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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

### CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, 15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file pto\_PLACENTA.txt, created 24

25 January 2001, having 26,548,337 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

#### Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., Proc. Natl. Acad. Sci. USA 70(4):1209-13 (1973); Gilbert et al., Proc. Natl. Acad. Sci. USA 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., Nature 308(5955):153-8 (1984).

More recently, however, the development of high
throughput sequencing methods and devices, in concert with
large public and private undertakings to sequence the human
and other genomes, has altered this investigational
paradigm: today, sequence information often precedes
understanding of the basic biology of the encoded protein
product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,

Science 252:1651 (1991); Williamson, Drug Discov. Today

4:115 (1999)). For nucleic acids sequenced by this

approach, often the only biological information that is

known a priori with any certainty is the likelihood of

biologic expression itself. By virtue of the species and

tissue from which the mRNA had originally been obtained,

most such sequences are also annotated with the identity of

the species and at least one tissue in which expression

appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches — and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species — there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, Science 280:995 (1998); Pennisi, Science 283: 1822-1823 (1999),

35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the C. elegans genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. C. elegans Sequencing Consortium, 10 Science 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of Arabidopsis predicts over 4000 genes, Lin et al., Nature, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the 15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many 20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence — and most importantly, but not exclusively, regions that

25 function to encode genes — to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., Proc. Natl. Acad. Sci. USA 88(24):11261-5 (1991); Xu et al., Genet. Eng. 16:241-53 (1994); Uberbacher et al., Methods Enzymol. 266:259-81 (1996); GENEFINDER, Solovyev et al., Nucl. Acids. Res. 22:5156-63 (1994); Solovyev et al.,

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Ismb 5:294-302 (1997); and GENESCAN, Burge et al., J. Mol.
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
however, to give high false positive rates. Burset et al.,
Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons from genomic sequence.
Ansari-Lari et al., Genome Res. 8(1):29-40 (1998)

Identification of functional genes from genomic

10 data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
need to be revised substantially downwards. Nature

15 405:311-199 (2000); Reeves, Nature 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically — and specifically, that permit the expression of regions predicted to encode protein — readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays: A Practical Approach

25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., Genomics 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

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et al., Cancer Res. (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast Saccharomyces cerevisiae. De Risi et al., Science 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single 10 exon genes, i.e., lack introns, Lopez et al., RNA 5:1135-1137 (1999); Goffeau et al., Science 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex 15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the 20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect, 30 particularly those with polygenic etiology.

#### Summary of the Invention

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35 The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.

35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single 30 exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The

nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome20 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention,

there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human placenta which is a nucleic acid molecule comprising
a nucleotide sequence as set out in any of SEQ ID NOs.: 1

13,232 or a complementary sequence or a fragment thereof
wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

13,233 - 26,232 or a complementary sequence or a fragment

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon

15 nucleic acid probe in accordance with the third or fourth
 aspects of the invention is between 3kb and 25kb in length.

It is preferred that said probe is no more than 3kb,
 suitably no more than 5kb, more suitably no more than 10kb,
 preferably 15kb, more preferably 20kb or, most preferably,

16 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

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the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in

20 a plurality of tissues and/or cell types using

hybridization to single exon microarrays having a probe

with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

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In a preferred embodiment, a peptide may be sencoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ 5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 26,233 - 38,837, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

## Detailed Description of the Invention

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### Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase
"nucleic acid microarray" include all the devices so called
in Schena (ed.), DNA Microarrays: A Practical Approach
(Practical Approach Series), Oxford University Press (1999)
(ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60
(1999); and Schena (ed.), Microarray Biochip: Tools and
Technology, Eaton Publishing Company/BioTechniques Books
Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray"
further include substrate-bound collections of plural
nucleic acids in which the nucleic acids are distributably
disposed on a plurality of beads, rather than on a unitary
planar substrate, as is described, inter alia, in Brenner
et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence

that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10<sup>7</sup>, preferably at least 10<sup>8</sup>, more preferably at least 10<sup>9</sup> liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display

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of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

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### Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;
FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1 x 10<sup>-30</sup>) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1 x 10<sup>-30</sup>) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

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Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained 5 in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence 10 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A 15 finite percentage of sequence data in the database will typically be erroneous, consisting inter alia of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can 25 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part 30 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

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Databases useful as genomic sequence database 100 35 in the present invention include GenBank, and particularly

include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, C. elegans, C. brigsii, Drosophila, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic

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assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the 5 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often 10 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the 15 functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within 20 the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

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FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and 35 facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or 5 interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of 10 functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 15 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified inter alia using gene prediction approaches, comparative sequence analysis 20 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, 25 corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic 35 sequence, the query will accordingly require that the

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sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a

15 required minimal individual genomic sequence fragment
length, such as 10 kb, more typically 20 kb, 30 kb, 40kb,
and preferably 50 kb or more, as well as an optional
further or alternative requirement that sequence from any
given clone, such as a bacterial artificial chromosome

20 ("BAC"), be presented in no more than a finite maximal
number of fragments, such as no more than 20 separate
pieces, more typically no more than 15 fragments, even more
typically no more than about 10 - 12 fragments.

Results using the present invention have shown

that genomic sequence from bacterial artificial chromosomes

(BACs) is sufficient for gene prediction analysis according

to the present invention if the sequence is at least 50 kb

in length, and if additionally the sequence from any given

BAC is presented in fewer than 15, and preferably fewer

than 10, fragments. Accordingly, query 20 can incorporate

a requirement that data accessioned from BAC sequencing be

in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, infra, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable 10 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,

including artifactual, sequence can be identified

algorithmically without comparison to external databases

and thereafter removed. For example, synthetic polylinker

sequence can be identified by an algorithm that identifies

a significantly higher than average density of known

restriction sites. As another example, vector sequence can

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be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be 5 removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired 10 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower 15 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

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Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, inter alia, addition of a unique sequence identifier, either derived 25 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as 30 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting 35 such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating

5 transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, infra, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the

15 multiple analyses required to achieve consensus can be done
in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the genespecific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible 5 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving 10 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequencespecific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such 15 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

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The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with

15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs

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predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are
thus input into one or more primer design programs, such as
PRIMER3 (available online for use at
http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal
of amplifying at least about 500 base pairs of genomic
sequence centered within or about ORFs predicted to be no
more than about 500 bp, or at least about 1000 - 1500 bp of
genomic sequence for ORFs predicted to exceed 500 bp in
length, and the primers synthesized by standard techniques.
Primers with the requisite sequences can be purchased
commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for 5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the 10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support

substrate.

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Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,

10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,

15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays

typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.

If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
high density microarrays constructed on planar substrates,
the methods of the present invention for confirming the
expression of ORFs predicted from genomic sequence can use
any of the known types of microarrays, as herein defined,
including lower density planar arrays, and microarrays on
nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.

30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high

5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by in situ synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived — either directly or indirectly — from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the de novo construction of "problem specific" libraries targeted at a particular biological question,

R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

5 expression only of those genes found in EST libraries,
shown herein to represent only a fraction of expressed
genes. Furthermore, such libraries — and thus microarrays
based thereupon — are biased by the tissue or cell type of
message origin, by the expression levels of the respective
10 genes within the tissues, and by the ability of the message
successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be

15 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, infra, the remaining population of genes identified from genomic sequence by the methods of the

20 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from

genomic material, a priori knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genomederived single exon microarrays of the present invention
lack homopolymeric stretches derived from message
polyadenylation, and thus can provide more specific signal.
Typically, at least about 50, 60 or 75% of the probes on
the genome-derived single exon microarrays of the present
invention lack homopolymeric regions consisting of A or T,
where a homopolymeric region is defined for purposes herein
as stretches of 25 or more, typically 30 or more, identical
nucleotides.

A further distinction, which also affects the

30 specificity of hybridization, is occasioned by the typical
derivation of EST microarray probes from cloned material.

Because much of the probe material disposed as probes on
EST microarrays is excised or amplified from plasmid,
phage, or phagemid vectors, EST microarrays typically

35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly

lack sequences drawn from plasmids and bacteriophage.

Preferably, at least about 85, 90 or more than 90% of exonincluding probes in the genome-derived single exon microarray of the present invention lack vector sequence.

With attention to removal of vector sequences through

preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-

20 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker

25 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include

30 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual 20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be 25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partiallyspliced message, probes disposed upon EST arrays will often
include multiple exons. The percentage of such exonspanning probes in an EST microarray can be calculated, on
average, based upon the predicted number of exons/gene for
the given species and the average length of the immobilized
probes. For human genes, the near-complete sequence of

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human chromosome 22, Dunham et al., Nature 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 10 75, 80, 85, 95 or 99% of probes deposited in the genomederived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

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Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genomederived single exon microarrays of the present invention 30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from in situ synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on in situ synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the in situ synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for in situ synthesis microarrays.

A further distinction is that the probes in in situ synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on in situ microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over in situ synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the in situ synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997).

only about 220 - 250 of the 6100 or so nuclear

genes in Saccharomyces cerevisiae - that is, only about 4
- 5% - have standard, spliceosomal, introns, Lopez et al.,
Nucl. Acids Res. 28:85-86 (2000); Spingola et al., RNA
5(2):221-34 (1999). Furthermore, the entire yeast genome
has already been sequenced. These two facts permit the
ready amplification and disposition of single-ORF amplicons
on such microarray without the requirement for antecedent
use of gene prediction and/or comparative sequence
analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as Saccharomyces cerevisiae, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the

25 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, infra.

mRNA can be prepared by standard techniques, see 35 Ausubel et al. and Maniatis et al., or purchased

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commercially. The mRNA is then typically reversetranscribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of 5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. 10 further described in Example 2, infra, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are 20 related to the original sequence.

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Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain 25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for 30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived 35 single exon microarrays of the present invention.

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In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate 5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidlynoncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' 20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

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In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered 35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing

5 information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate 10. that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide")

35 polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query — including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically — for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 — or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.

30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity 5 or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

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Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional 15 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method 25 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c 35 represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83

10 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue,

density, or texture of rectangles 83 can be used further to
report a measure of the bioinformatic reliability of the
prediction. For example, many gene prediction programs
will report a measure of the reliability of prediction.

Thus, increasing degrees of such reliability can be
indicated, e.g., by increasing density of shading. Where
display 80 is used as a graphical user interface, such
measures of reliability, and indeed all other results
output by the program, can additionally or alternatively be
made accessible through linkage from individual rectangles
83, as by time-delayed window ("tool tip" window), or by
pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as

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many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show 5 predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, 10 such function can usefully be indicated and userselectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the 15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional 20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an 25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 35 identifies the sequence included within the probe

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immobilized on the support surface of the microarray. noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the 5 probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of 10 expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting 15 thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be 25 predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified 30 in existing expression data bases.

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Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and 35 displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of

30 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to

35 depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed infra, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user

interface, rectangle 85 can be used as a link to further
information about the assay. For example, where the assay
is one for gene expression, each rectangle 85 can be used
to link to information about the source of the hybridized
mRNA, the identity of the control, raw or processed data
from the microarray scan, or the like.

gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented infra.

BAC sequence ("Chip seq.") 89 is presented, with the

20 physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence

25 that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG.

3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

## Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

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Using the methods and genome-derived single-exon

20 microarrays of the present invention, we have for example
readily identified a large number of unique ORFs from human
genomic sequence. Using single exon probes that encompass
these ORFs, we have demonstrated, through microarray
hybridization analysis, the expression of 13,232 of these

25 ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

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interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was 5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in 10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In 15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus 20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one 30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself in variety of phenotypic defects that vary in severity

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among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis, 10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought 15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease, 20 neurogenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must cooincide in the same individual or even the same cell for the disease to develop and/or progress.

A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may 35 be detected in placenta.

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The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be 5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based 10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof:

In one embodiment, the gene expression-profile is 15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

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In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the 30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in
Examples 1 and 2, the methods described enable ORFs which
15 are not present in existing expression databases to be
identified. And the fewer the number of tissues in which
the ORF can be shown to be expressed, the more likely the
ORF will prove to be part of a novel gene: as further
discussed in Example 2, ORFs whose expression was
20 measurable in only a single of the tested tissues were
represented in existing expression databases at a rate of
only 11%, whereas 36% of ORFs whose expression was
measurable in 9 tissues were present in existing expression
databases, and fully 45% of those ORFs expressed in all ten
25 tested tissues were present in existing expressed sequence
databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have

30 significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of 10 Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis, " Proc. Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology, " Arch. Biochem. 15 Biophys. 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays, " Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis 20 (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence, " Curr. Biol. 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis, " Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)). 25

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," Proc. Natl. Acad. Sci. USA 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci. USA 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol.

5 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," Cancer Res. 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents — whether in lead compound discovery or in subsequent screening of lead compound derivatives — the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in

Gerhold et al., Trends Biochem. Sci. 24(5):168-173 (1999)

and Zweiger, Trends Biotechnol. 17(11):429-436 (1999);

Schena et al.

The invention particularly provides genomederived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA

15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression.

Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, inter alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and

WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.
Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention

As mentioned earlier, when intended for use on a

When intended for use in solution phase 35 hybridization, however — that is, for use in a

will typically not contain a detectable label.

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message — a subset of target sequence that is much reduced in complexity as compared to genomic sequence — even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human cot1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

appended hereto presents, by convention, only that strand
25 of the probe and ORF sequence that can be directly
translated reading from 5' to 3' end. As would be well
understood by one of skill in the art, single stranded
probes must be complementary in sequence to the ORF as
present in an mRNA; it is well within the skill in the art
30 to determine such complementary sequence. It will further
be understood that double stranded probes can be used in
both solution-phase hybridization and microarray-based
hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic 5 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, inter alia, radioactive labels, such as <sup>3</sup>H, <sup>32</sup>P, <sup>35</sup>S, <sup>125</sup>I, <sup>131</sup>I; fluorescent 15 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

10

Green and other labels described in Haugland, Handbook of Fluorescent Probes and Research Chemicals, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates 20 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

25 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived 30 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 35 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific
5' primers used for genomic amplification had a first
common sequence added thereto, and the ORF-specific 3'
5 primers used for genomic amplification had a second,
different, common sequence added thereto, a single set of
5' and 3' primers can be used to amplify all of the probes
from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, inter alia, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, supra.

25

30 The invention particularly provides genomederived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays 35 comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived 5 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression 10 measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in 15 signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth

25 respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and

30 Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN:

10 0199637245); Jones, Amino Acid and Peptide Synthesis
(Oxford Chemistry Primers, No 7), Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

## 30 EXAMPLE 1

35

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

## Bioinformatics Results

All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:

GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs

("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb

window.

further study.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments

10 fewer than 250 bp in length do not bind well to the aminomodified glass surface of the slides used as support
substrate for construction of microarrays; therefore,
amplicons were designed in the present experiments to
approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/). A first

additional sequence was commonly added to each ORF-unique
5' primer, and a second, different, additional sequence was
commonly added to each ORF-unique 3' primer, to permit
subsequent reamplification of the amplicon using a single
set of "universal" 5' and 3' primers, thus immortalizing
the amplicon. The addition of universal priming sequences
also facilitates sequence verification, and can be used to

The ORFs were then PCR amplified from genomic

30 DNA, verified on agarose gels, and sequenced using the
universal primers to validate the identity of the amplicon
to be spotted in the microarray.

add a cloning site should some ORFs be found to warrant

Primers were supplied by Operon Technologies
(Alameda, CA). PCR amplification was performed by standard
techniques using human genomic DNA (Clontech, Palo Alto,

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CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). 5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) 10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median 15 size of 150 bp (n=9498). With an average amplicon size of 475  $\pm$  25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of 25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

20

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR 35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material

5 flanking coding regions could theoretically interfere with
hybridization during microarray experiments, subsequent
empirical results demonstrated that differential expression
ratios were not significantly affected by the presence of
noncoding sequence. The variation in exon size was

10 similarly found not to affect differential expression
ratios significantly; however, variation in exon size was
observed to affect the absolute signal intensity (data not
shown).

The 350 MB of genomic DNA was, by the abovedescribed process, reduced to 9750 discrete probes, which
were spotted in duplicate onto glass slides using
commercially available instrumentation (MicroArray GenII
Spotter and/or MicroArray GenIII Spotter, Molecular
Dynamics, Inc., Sunnyvale, CA). Each slide additionally
included either 16 or 32 E. coli genes, the average
hybridization signal of which was used as a measure of
background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt 25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e<sup>-100</sup>) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e<sup>-5</sup> to 1 e<sup>-99</sup>). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

of Predic	ted ORFs As	Deduced From Comparative
Analysis		·
V6 chip	V7 chip	Function Predicted from
		Comparative Sequence
		Analysis
96	115	Receptor
43	77 .	Zinc Finger
11	19	Homeobox
9	16	Transcription Factor
11	7	Transcription
57	61	Structural
39	56	Kinase
18	18	Phosphatase
31	52	Ribosomal
19	26	Transport
17	14	Growth Factor
12	5	Cytochrome
33	17	Channel
	Analysis V6 chip  96 43 11 9 11 57 39 18 31 19 17	Analysis         V6 chip       V7 chip         96       115         43       77         11       19         9       16         11       7         57       61         39       56         18       18         31       52         19       26         17       14         12       5

As can be seen, the two most common types of 10 genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

## EXAMPLE 2

15 Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays

prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)

Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100

cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial 15 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA+ mRNA performed using 1 µg oligo(dT)12-18 primer 20 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100μM dATP, 100 μM dGTP, 100 μM dTTP, 50 μM dCTP, 50 μM 25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup 30 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2  $\mu g/\mu l$  poly(dA), 0.2  $\mu g/\mu l$  human cot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

15 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the E. coli control genes.

25

The relative expression signal for these probes 30 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"

5 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is 20 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than 25 "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is 30 novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to le-99; black: E values > le-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

"novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

20

# Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown")

30 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of

35 0.2.

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As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonlyexpressed genes, which have a higher likelihood of being 5 found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' 10 or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for 15 incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

# Verification of Gene Expression

25

To ascertain the validity of the approach 20 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR 30 against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence 35 AL031734\_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology — which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays — to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further

25 studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

30

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray	Normal	Expressi	Homology	Gene Function
Sequence	ized	on Ratio	to EST	as described by
Name	Signal		present	GenBank
			in	
			GenBank	
AP000217-1	5.2	+7.7	High	S-100 protein,
	]			b-chain, Ca <sup>2+</sup>
				binding protein
				expressed in
			ļ	central nervous
				system
AP000047-1	2.3		High	Unknown
			{	Function
AC006548-9	1.7		High	Similar to
				mouse membrane
Ì				glyco-protein
				M6, expressed
			·	in central
				nervous system
AC007245-5	1.5		High	Similar to
				amphiphysin, a
				synaptic
				vesicle-
				associated
				proteim. Ref 21
L44140-4	1.2	+2.0	High	Endothelial
				actin-binding
	ļ			protein found
	Ì			in nonmuscle
		·		filamin
AC004689-9	1.2	+3.5	High	Protein
				Phosphatase
ļ				PP2A, neuronal/
				downregulates

				activated
				protein kinases
AL031657-1	1.2	+3.0	High	Unknown
				function/
				Contains the
				anhyrin motif,
				a common
			-	protein
				sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to
				the
				Synaptotagmin I
<u> </u>				protein in
				rat/present at
·				low levels
				throughout rat
				brain
AP000086-1	1.0	+2.7	Low	Unknown, very
				poor homology
				to collagen
AC004689-3	1.0		High	Protein
		,		Phosphatase
				PP2A, neuronal/
				downregulates
				activated
				protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca<sup>2+</sup> binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, Neurochem. Res. 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., Trends Biochem. Sci. 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the
highest (normalized) signal intensity in brain, regardless
of expression in other tissues, was assessed. In this
latter analysis, we found expression of many more common
genes, since the sequences were not limited to those
expressed only in brain. For example, looking at the 20
highest signal intensity spots in brain, 4 were similar to
tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2
were similar to actin (AL035701-2; AL034402-1), and 6 were
found to be homologous to glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
AC006064-K; AC035604-3; AC006064-L). These genes are often
used as controls or housekeeping genes in microarray
experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., J. Neurol. Sci. 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., Genomics

49(2):283-89 (1998))(AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature 5 (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.

10 The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparis	son of Expression Ra	atio, for each
tissue, of GAPDH		
	AC006064 (n = 4)	Control ( n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0:05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### 10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray

as above-described, a plethora of information was
accumulated, including full clone sequence, probe sequence
within the clone, results of each of the three gene finding
programs, EST information associated with the probe
sequences, and microarray signal and expression for

multiple tissues, challenging our ability to display the
information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate 30 synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. 15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very 20 good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following 25 colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 30 12 did not sequence verify.

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe
sequences. Each probe was completely sequenced on both
strands prior to its use on a genome-derived single exon

10 microarray; sequencing confirms the exact chemical
structure of each probe. An added benefit of sequencing is
that it placed us in possession of a set of single baseincremented fragments of the sequenced nucleic acid,
starting from the sequencing primer 3' OH. (Since the

15 single exon probes were first obtained by PCR amplification
from genomic DNA, we were of course additionally in
possession of an even larger set of single base incremented
fragments of each of the 13,232 single exon probes, each
fragment corresponding to an extension product from one of

20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon

probes on nucleic acid microarrays and then performing twocolor fluorescent hybridization analysis; significant

expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining

15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)

20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + 25 (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.

Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective

20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the

SEQ ID NO:. of the exon contained within the probe: "EXON

SEQ ID NO.:") from least similar to sequences known to be

expressed (i.e., highest BLAST E value), at the beginning

of the table, to most similar to sequences known to be

25 expressed (i.e., lowest BLAST E value), at the bottom of

the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The

peptide sequences for a given exon are predicted as
follows: Since each chip exon is a consensus sequence drawn
from predictions from various exon finding programs (i.e.
Grail, GeneFinder and GenScan), the multiple initial ORFs
are first determined in a uniform way according to each
prediction. In particular, the reading frame for predicting
the first amino acid in the peptide sequence always starts
with the first base of any codon and ends with the last
base of non-termination codon. Next, for each strand of the
exon, initial ORFs are merged into one or more final ORFs
in an exhaustive process based on the following criteria:
1) the merging ORFs must be overlapping, and 2) the merging
ORFs must be in the same frame.

The Sequence Listing, which is a superset of all

of the data presented in Table 4, further includes, for
each probe, the most similar hit, with accession number and
BLAST E value, from the each of the three queried
databases.

Table 4 further lists, for each probe, a portion

of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

'Using BLAST E value cutoffs of 1e-05 (i.e., 1 x  $10^{-5}$ ) and 1e-100 (i.e., 1 x  $10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, supra, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- 15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST 20 query of the EST database, with accession number and BLAST E value for the "hit";
  - (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- 25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

#### 30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

Page 1 of 550 Table 4

Single Exon Probes Expressed in Placenta	Top Hit Descriptor																																		
e Exon Probe	Top Hit Database Source																																		
Singi	Top Hit Acesston No.																																		
	Most Similar (Top) Hit BLAST E Value																																-		
	Expression Signal	150	9.68	3.01	10.9	1.92	4.94	1.03	1.67	8.53	1.57	2.66	3.39	2.83	3.75	1.48	10.5	0.84	98.0	0.94	1.55	6.88	0.87	0.87	1.69	0.61	1.86	9.0	5.14	1.24	1.76	1.78	4.12	7.28	3.31
	ORF SEQ ID NO:	26695						28008	28030	28036	28183	28285	28497	28616	29447	29713	29783		29912	-	30445	30500	30519	30520		30639	31064		31244	31255	31442	31443			H
	Exon SEQ ID NO:	13658		1			- 1		- 1	- 1	15082			16484	li	ı	1	16814	16908	17213	17457	17520	17639	17639	17597	17651	18088	18131	18279	18290	18574	18574	18735	18907	18735
	Prabe SEQ ID NO:	463	912	1070	1330	1645	1666	1764	178	1784	1939	2034	2234	2353	3255	3537	3804	3651	3747	4057	. 4314	4377	4396	4386	4457	4512	4958	8002	6157	5168	5371	5371	5538	5714	5796

Page 2 of 550 Table 4

Single Exon Probes Expressed in Placenta	Top Hit Descriptor																															Homo sepiens LSS gene, partial, exons 15, 16, 17 and 18	Haemophilus influenzae Rd section 31 of 163 of the complete genome	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2	Sulfolobus solfataricus 281 kb genomic DNA fragment strain P2
Exon Probes	Top Hit Database Source																															Ŋ	TN		Ę
Single	Top Hit Acession No.												,																				9.8E+00 U32716.1		
	Most Similar (Top) Hit BLAST E Vatue																															9.8E+00	9.8E+00	9.8E+00	9.8E+00 Y18830.1
	Expression Signal	4.22	1.61	1.92	1.01	1.25	1.25	1.42	1.42	1.18	1.18	1.44	1.14	0.78	0.76	3.82	0.56	1.51	0.88	0.74	0.74	2.32	1.78	2.79	1.73	1.36	1.36	2.09	1.58	2.08	1.5	18.82	1.5	0.48	0.48
	ORF SEQ ID NO:		ľ	32696		33228			33813	.34117	١			35684	H					37286	37287				1	37561			38746		31980			36575	
	Exon SEQ ID NO:	19048	L	18350	19708	19838	1				20641			ł	1 1			i. i				24005	1	1	. 1	. 1				<u> </u>	25628		i		1
	Probe SEQ ID NO:	5858	6148	6174	6546	629	6679	7275	7275	7569	7569	8251	8682	9061	9061	9734	8988	10086	10229	10843	10843	10922	11280	11348	11641	11749	11749	11792	12057	12623	12967	6177	8185	9944	9944

Page 3 of 550 Table 4 Single Exon Probes Expressed In Placenta

Page 4 of 550 Table 4

Single Exon Probes Expressed in Placenta	Most Similar (Top) Hit Acession (Top) Hit Details BLAST E No. Source Signal BLAST E Value	3.41 7.2E+00 [L12051.1 NT Lycopersicon esculentum Mill GTPasa (SAR2) mRNA crimplete cds		7.2E+00 BE179090.1 EST HUMAN	7.1E+00 P28168 SWISSPROT	П	7.1E+00 AL161595.2 NT	7.1E+00 P05850 SWISSPROT	2.76 7.0E+00 P48610 SWISSPROT   ARGININE KINASE (AK)	7.0E+00 O22469 SWISSPROT	6.9E+00 P35679 SWISSPROT	6.9E+00 P44834 SWISSPROT		1.64 6.8E+00 W03412.1 EST HUMAN Z207c11.r1 Scares malanocyta ZNbHM Home explans cDNA clone IMAGE 201880.5	6.8E+00 W03412.1 EST_HUMAN   Za07o11.r1 Soares melanocyte ZNbHM Homo sapiens cDNA clone  MAGE:291860	TOGGEN	6.8E+00 003570 SWISSPROT	8.6E+00 Q89028 SWISSPROT	6.6E+00 BF672421.1 EST HUMAN	6.6E+00 P51825 SWISSPROT	6.6E+00 Q9ZE07 SWISSPROT	SWISSPROT	6.6E+00 H29330.1 EST_HUMAN	SWISSPROT	6.5E+00 P03374 SWISSPROT	6.5E+00 BE866001.1 EST_HUMAN	6.2E+00 AY010901.1 NT	6.2E+00 6754621 NT	6.0E+00 BE780163.1 EST_HUMAN	6.0E+00 AP000006.1 NT	INT	6.0E+00 AE001882.1 NT	7.14 5.9E+00 AF165142.1 NT complete cds
	· 表 6 岁 2				4	'	4	_	<u> </u>				9	Θ	9	8	٩	®	°									┙					кò
	ORF SEQ Express ID NO: Signe	29238				33839							37219		34689		37053		33223		36912		37496				38574					373740	33197
}	SEO OR NO:	16218	16218	20307	20381	20381	22838	24745	23224	24584	21559	23594	23614	21174	21174	22409	23448	18600	19834	26226	23314	23314	23876		22457		22982				23765		19809
	Probe SEQ ID NO:	3042	3042	7174	7299	7289	9788	11668	10187	11528	8478	10559	10579	9092	8092	. 8333	10413	. 5398	6675	9234	10279	10279	5 5 5 5	11393	8382	10512	9943	10787	7181	10021	10732	10732	6650

Page 5 of 550 Table 4

					Singl	e Exon Probe	Single Exon Probes Expressed in Placenta
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Tap Hit Desoriptor
11933	24919		3.02	5.9E+00	.9E+00 BE958630.1	EST HUMAN	801645279F1 NIH MGC 56 Homo seniens CONA clare 1446 CE 3000454 51
3613			1.15		7861557 NT	E	Homo sablens DESC1 protein (DESC1) mRNA
7312		33865	0.74	ြိ	AF30204	NT.	Mus musculus immunoglobulin scavenger recentor in SR mRNA complete and
7312		33826	0.74	5.7E+00		N.	Mus musculus immunoslobulin scavenger receptor lask mRNA, complete cas
7742	20803		1.34	5.6E+00	.6E+00 P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11289	24355		203	5.6E+00	.6E+00 AB027305.1	LN L	Oppring carplo mRNA for lysozyme C. complete cds
11289		37997	2.03	5.6E+00	.6E+00 AB027305.1	L	Cyprinus carplo mRNA for lysozyme C. complete cds
11765	23951	37581	2.62	6.6E+00	.6E+00 Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
8384	- 1	32909	0.74	5.5E+00	.5E+00 P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
8982	23021		0.58	6.6E+00		SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE RICH OF YCODBOTTEIN)
11018	24097		1.48	5.5E+00	25.1	LN	Mus musculus DNA methyltransferase (Dmmt1) gene expres 30, 31, and 32
11763	23949	37578	232	5.5E+00		SWISSPROT	PNEUMOLYSIN (THIOL ACTIVATED CYTOLYSIN)
7069	20122	33536	1.11	5.4E+00		NT	Chicken alpha-cardiac actin gene
7069	20122	33537	1.11	5.4E+00		片	Chicken alpha-cardiac actin gane
7484	20559		1.04	5.4E+00		SWISSPROT	NEL PROTEIN PRECURSOR (NEL RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00 P50391		Г	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 11 (PP11)
8054	21137		1.62	5.45+00 091082		TOGODOLING	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
6668	22078	35818	0 83	5 4F+00	T	SWISSEND	SECULIAL LYZ]
6668	22078	35619	58.0	5 4F+00	Ť	SWISSPACE	NET FACIEIN BEST BEST BEST BEST BEST BEST BEST BEST
10242	23277	36870	1,45	5.4E+00 (	5.4E+00 Q17094	Т	RHODOPSIN
10242	23277	36871	1.45	5.4E+00	Γ	Т	RHODOPSIN
4906	18036	31024	1.47	5.3E+00	Γ	Г	Boyine Immunodeficiency-like virus surface envelope pene 57 end of cds
6817	19777		0.7	5.3E+00		SWISSPROT	HOMEOBOX PROTEIN CEH-20
8270	21352	•	3.39	5.3E+00 F		Г	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA FOLYMERASE CATALYTIC SLIBLINIT)
9184	22282		0.72	5.3E+00		LN	Homo sepiens HERPUD1 gene for stress protein Herp, complete cds
11928	24914	38616	1.51	€.3E+00 (	Г	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECIESOR
2280	18775		1.16	5.2E+00	Г	Γ	QV4-HT0691-270400-188-f09 HT0691 Homo serviers GDNA
10583	23618		0.98	5.2E+00 /	Г	Г	Droscophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cals
11470	24529		1.93	6.2E+00 Q10136	Г	SWISSPROT	HYPOTHETICAL 81.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
9162	22240	35784	0.94				RHODOPSIN
10030	23068	36667	1.33	5.1E+00 P09182			COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
8410	18684	32946	0.74			EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5
10397	23432		0.7		DE+00 BF308561.1 E	EST_HUMAN (	601890420F1 NIH_MGC_17 Hama saptens cDNA clone IMAGE:4131509 5'

Page 6 of 550 Table 4 Single Exon Probes Expressed in

Page 7 of 550 Table 4 Single Exon Probes Expressed in Placenta

Exon         ORF SEQ         Expression         Mode           SEQ ID         ID NO.         Signal         BM           NO:         20226         33658         1.67           22238         35783         5.3           23160         36769         1.03           23387         2386         0.47           20344         33789         0.98           21010         34523         3.8           21013         34524         3.8           21013         34524         3.8           21013         34523         2.88           21013         34524         3.8           22183         3473         2.88           22013         3648         2.25           22405         0.65         2.15           24285         0.55         2.15           24281         0.25         2.15           20130         33547         0.89           20130         33547         0.89           20130         33547         0.89           20130         33547         0.89           22153         36897         0.49           23498         3711         0		<del></del>	Т	Т	Т	7	1	7	Т	Т	Т	Т	T	Т	Т	_	_	Т	Т	_	Т	Ŧ	_	_	_	_	7	_	_	_	_		
Exon         ORF SEQ         Expression of Formation in Data (Top) Hit Accession in Diagram         Most Similar of Top) Hit Accession in Data (Top) Hit Accession in Diagram         Top Hit Accession of Top) Hit Accession in Data (Top) Hit Accession in Data (Top) Hit Accession in Diagram         Top Hit Accession in Diagram         Top Hit Accession in Data (Top) in Data	בילו הפפח ווו ד מספוונמ	Top Hit Descriptor	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE BICH OF YCOBBOTTEIN)	W87003X1 Sogres NFL T GBC S1 Home saniens cDNA clane IMAGE: 3361603 2	NUBBIN PROTEIN (TWAIN PROTEIN) (POLL DOMAIN SECTEIN 1) (PDAL1) (DROTEIN 1)	HEXOSE TRANSPORTER HXT8	601110727F1 NIH MGC 16 Home septens cDNA clone IMAGE:3351524 F1	YY1 PROTEIN PRECURSOR	Pathopecten vessoensis mRNA for calcineurin A complete cds	GENE 68 PROTEIN	GENE 68 PROTEIN	Pan troglodytes novel repetitive solo LTR element in the RNI 12 Izcus	50S RIBOSOMAL PROTEIN L4	602247938F1 NIH MGC 62 Hamo segiens cDNA clane IMAGE: 4233200 5	Rickettsla prowazekii strain Madrid E. complete genome: serment 4/4	CYCLIN-DEPENDENT KINASE INHIBITOR 18 (CYCLIN-DEPENDENT KINASE INHIBITOR P27)	(P27KIP1)	HYPOTHETICAL PROTEIN HVLF1	601507510F1 NIH_MGC_71 Hano sapiens cONA clane IMAGE:3909051 5'	GLC7-INTERACTING PROTEIN 1	SUCRASE-ISOMALTASE, INTESTINAL (CONTAINS: SILICRASE - ISOMALTASE)	SUCRASE-ISOMALTASE, INTESTINAL ICONTAINS: SUCRASE - ISOMALTASE 1	SUCRASE-ISOMALTASE, INTESTINAL (CONTAINS: SUCRASE: ISOMALTASE)	SUCRASE-ISOMALTASE, INTESTINAL ICONTAINS: SUICRASE: ISOMALTASE1	CELL DIVISION PROTEIN FTSY HOMOLOG	HYPOTHETICAL PROTEIN KIAA0144	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)	Jreaplasma urealyticum section 33 of 59 of the complete genome	JRICASE (URATE OXIDASE)	JRICASE (URATE OXIDASE)	CYTOCHROME C OXIDASE POLYPEPTIDE III	GENOWE POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN FANVELODE OF YEARD AND MANAGED ENVELORED FOR THE FANCE OF THE PROTEIN FOR THE FANCE OF THE PROTEIN FOR THE PROTE	AND AND AND AND AND HELD THE CONTROL OF THE PROJECT
Exon NO:         CRF SEQ Paression Signal         Most Similar (Top) Hit Top Hit Acession Signal ID NO:         Most Similar (Top) Hit Top Hit Acession Signal ID NO:         A.ZE+00 P13883           20228         33658         1.67         4.ZE+00 P13883           22238         33783         6.3         4.ZE+00 P13883           22340         33789         0.47         4.ZE+00 P13883           22391         34524         3.8         4.ZE+00 P13883           22013         34524         3.8         4.ZE+00 P13883           22013         34524         3.8         4.ZE+00 P13883           22013         34524         3.8         4.ZE+00 P28964           22013         34524         3.8         4.ZE+00 P28964           22013         34628         7.66         4.ZE+00 P28964           22013         34628         3.8         4.ZE+00 P28964           22013         34628         2.8         4.ZE+00 P28964           22013         34628         2.28         4.ZE+00 P28964           22013         34628         0.65         4.ZE+00 P28964           22013         34648         0.65         4.ZE+00 P28964           2218         2.28         4.ZE+00 P28964           2218			SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	SWISSPROT	Z L	SWISSPROT	SWISSPROT	N	SWISSPROT	EST HUMAN	LN		SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT		Г	Г	Г	Г		SWISSPROT	SWISSPROT	SWISSPROT		TOGGSSIMS
Exan NO:         ORF SEQ ID NO:         Expression Signal         Mos ID NO:           20226         33656         1.67           20228         35783         5.3           23160         36759         1.03           23384         34723         3.8           21013         34524         3.8           21013         34524         3.8           21013         34524         3.8           21013         34524         3.8           21013         34524         3.8           22013         36498         2.25           23405         0.62         2.15           24283         1.2.26         0.62           24283         1.2.26         0.62           24283         0.65         0.62           24283         0.65         0.65           20130         33546         0.69           20130         33547         0.99           20130         33546         0.65           22013         35697         0.45           22498         3711         0.45           22498         3711         0.45           22499         3711         0.45	6	Top Hit Acession No.	P13983	AI809013.1	P31368	P40886	BE253868.1	023810	AB041523.1					BF692425.1	AJ235273.1		P46414	P09716	BE885880.1	P38229	062653	062663	062653										
Exon ORF SEQ         Express Signal NO:         CRF SEQ         Express Signal NO:			4.2E+00	4.2E+00	4.2E+00	4.2E+00	4.1E+00	4.1E+00	4.1E+00	4.1E+00	4.1E+00	4.1E+00	4.1E+00	4.1E+00	4.1E+00		4.1E+00	4.1E+00	· 4.1E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00	4.0E+00		4.0E+00 P07564
SEG ID ORI 20286 22346 22408 22408 22408 22548 22408 22408 22408 22408 22408 22408 22408 22408 22408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408 225408		Expression Signal	1.67	5.3	1.03	0.47	0.98	7.68	0.64	3.8	3.8	2.88	0.61	2.25	0.55		0.62	2.15	12.26	0.72	0.93	0.93	0.99	0.99	+	0.49	0.65	9.0	0.45	0.45	1.59		2.88
<u> </u>					L		33786	34386		34523	34524										33546	33547	33546	33547	33881	35697	36783	37014	37111	37112	37677		38524
Probe SEQ ID NO: NO: 10322 10352 10373 10373 10368 10368 10368 10368 10368 10464 10464 10464 11762			20226		Ш	Ш					_ 1		- 1	22913	23405			24196	- 1	- 1	- 1	- 1	- 1	- 1	- 1	- 1	- 1		23489	23469	23048		24832
		Probe SEQ ID NO:	6911	9160	10122	10352	7261	7839	7960	7963	7963	8101	9740	9873	10370	,	10314	11124	11214	3635	5675	5275	7077	787	7330	9074	10148	10368	10464	10484	11762		11843

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							1	$\neg$			т-	_		_	Α,	_	_,	_	_,	_								_	_
Single Exon Probes Expressed in Placenta	Top Hit Descriptor	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS	INST, NSZA, NSZB, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6))	Nahaciim Ahlingsa anna 60 for alaca I atti	Mus musculle saminal varieta constant and in the constant and in t	MRo-BN0020-30050-008-bot BN020-01-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0	MR0-BN0070-300500-028-h05 BN0070 Homo sepiens chiva	Dictyostellum discoideum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds	Hüman hereditary haemochromatosis region, histone 24-like protein gene, hereditary baemochromatosis	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	THE TOTAL INVALATION INVALATION IN AIDB-RPSF INTERGENIC REGION	Turnen with class II lymphocyte antigen (DPw4-beta-1) gene, exon 2	Kidevis iliniva id my muscardic receptor	Halinobarder miles obtain 100 and a stop ass	HYPOTHETICAL DEOTEIN Microse	HUMSUPY135 Human brain cONA Homo scalars - PMM -1.	Streotococcus oralis partial antidene for worthing shows the contractions of the contraction of the contractions of the contractions of the contra	Melancolus sancunipas antomocovinus complete accessors answerses, strain NCI C7864	Arabidopsis thaliana DNA chromosome 4 contin frament No 30	Thermoplasma soldophilum complete genome: segment 3//5	Mus musculus faminin heta 2 name, wore 12 32 agricuit (1)	202120541E1 NIH MCC Re Homer Control of the Complete Cas	602120551F1 NIH MGC 56 Home canient clivia c	Gallus galius mRNA for hymoxia-indicible forter 1 airks - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	AV761056 MDS Home sensions CDMA close MDS I select to Indiana CDS	601901866F1 NIH MAC 19 Hams seniors and All All HAMS	HUM000TB08 I iver Heio/3 cell line. Home engles about 1	HUM000TB08 Liver Heng2 cell line Home septem CDNA done to 8	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
e Exon Prob	Top Hit Database Source	1000M	SWISSPROT	Į.	ŀ	EST HUMAN	EST_HUMAN	Ę		NI	TO LOCAL PIN	2 2	Į.	Į	SWISSPROT	EST HUMAN	NT		LN	LN	Z L	T HUMAN	Т	Т	EST HUMAN	Т	Т	Т	П
Sing	Top Hit Acession	0 7 8	P35611	3.9E+00 X84518.1	3.9E+00 AF055466.1	3.9E+00 BE814357.1	3.9E+00 BE814357.1	3.9E+00 AF298209.1			-	T	Ī	-			3.8E+00 AJ390961.1	9631294 NT		3.7E+00 AL445065.1		-	T		3.6E+00 AV761055.1	3.6E+00 BF316316.1			5
	Most Similar (Top) Hit BLAST E		4.0E+00 P35611	3.9E+00	3.9E+00	3.8E+00	3.9E+00	3.9E+00	L	3 95+00 103/328	3 95+00	3.9E+00 X65865 4	3.9E+00 Y18000.1	3.8E+00	3.8E+00 Q57830	3.8E+00 D44725.1	3.8E+00	3.8E+00	3.7E+00/	3.7E+00/	3.7E+00 U43541,1	3.7E+00	3.7E+00	3.7E+00	3.6E+00	3.6E+00	3.6E+00 D12367.1	3.6E+00 D12367.1	3.6E+00 △
	Expression Signal	600	1.34	9	0.87	2.92	2.92	0.93		4.43	4.25	2.44	2.77	1.53	1.05	1.12	9.0	11.65	12.79	0.83	1.04	2.11	2.11	1.87	3.76	0.78	0.86	0.86	3.67
	ORF SEQ ID NO:	38525		29770		32270	32271	33322	33380	33570	34088	35128	37524		33057	35244			30277		36017	38450	38451		20814	31440	35364	35365	35464
	SEQ ID NO:	24832	25113	16755	17681	18967	18967	19927	10092	20149	20592	21593	23902	15813	19885	21707	23037	25100	17282	2030	22454	24765	24755	25196	13796	18572	21828	21828	21826
	Probe SEQ ID NO:	11843	12133	3591	444	5775	6775	6772	6829	7013	7519	8512	11674	2893	6520	8627	0000	12120	4129	7316	8378	11716	11716	- 2260	8	8369	8748	8749	8847

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21926 22904 22904 22904 22904 22904 22904 22904 22904 22904 22904 22904 21851 21781 21781 21781 21864 21965 22986 21965 22986 21965 21965 21965 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968 21968
9864 9864 9864 9864 9864 9864 9864 9864

Page 10 of 550 Table 4 Single Exon Probes Expressed In Placenta

					Billo	777111777	Single Extri Flobes Expressed in Flacenca
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4138	13707	28735	0.78	3.2E+00	2E+00 X96422.1	M	D.reito zp-50 POU gene
							Homo saplens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1),
4850	17983	30971	0.95	3.2E+00	4502404 NT	L L	mRNA
5686	18880	32170	1.16	3.2E+00	.2E+00 P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5686		32171	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00 P12783	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912		2.49	3.2E+00		SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	Ι.	32966	1.91	3.2E+00		SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6438	J .			3.2E+00 P18831		SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837		0.86	3.2E+00	3.2E+00 P04276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7852		34513			Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 ganes
7952	21002					NT	Chlemydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230			5.28		P13061	SWISSPROT	PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9730	1				M36383.1	NT	S.cerevisiae threonine deaminase (ILV1) gene, complete cds
10345	,				AB016081.2	NT	Oryzlas latipes OiGCB gene for guenylyl cyclase C, complete cds
12219	J				L33836.1	LΝ	Sus scrofa choline acetyltransferase gene, promoter region
2996	1	32503		L	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7647		34095	0.91	_	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7804	20956				3.1E+00 AF303225.1	NT.	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8279	J,	34880	0.51	3.1E+00 P40985	P40985	SWISSPROT	PROBABLE UBIQUITIN~PROTEIN LIGASE HUL4
8801	21880				P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-1 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
8801	Ι.		5.14		P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-1 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
0450	27876		4.5	3 15+00 014957		TORDROWS	GLJTAMATE (NIMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (NIMETHYL D'ASPARTATE RECEPTOR SUBTYPE 20) (NR20) (NIMDAR20)
9526				1_	001149	SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR
10100	23138	36739	0.76		7624769	Ę	Chlorella vulgaris chloroplast, complete genome
10183	1			3.1E+00 Q10125	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10543	23578	37187				SWISSPROT	DEOXYHYPUSINE SYNTHASE (DHS)
	L.						GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN), MATRIX PROTEIN
11751	23937		. 245	3.1E+00 P33515	P33515	SWISSPROT	(ENVELOTE FRO I EIN M), MANON ENVELOTE FRO I EIN E, NONS INOOTONAL FRO I EINS INS.), NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
							retinoic ecid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971
11771			2.49		3.1E+00 S56660.1	LZ	ĵu (
13019	25870		1.17		3.1E+00 U77666.1	N <sub>T</sub>	Brassica rapa polien coat protein homolog (BAN103) gene, complete ods

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					2010		Single Lyones Lybessed in Flacelina
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2899	16078				. 8923984 NT	NT	Hamo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
25.22	18654			3.0E+00 X53096.1	X53096.1	TN	S.aureus genes encoding Saus6i DNA methyltransferase and Saus8i restriction endonuclease
9899	19844	L				IN	Corynabactarium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
9899	19844	L	0.82	3.	0E+00 X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7306	20388	L		3.	0E+00 P18408	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7346			0.7	(C)	0E+00 Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	ļ		1.62	6	0E+00 X67838.1	IN	B.napus DNA for myrosinase
	1						S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET
10501	23536	37146	0.58	ю	0E+00 Q58605	SWISSPROT	SYNTHETASE)
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2)
				•			(ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE,2) (ROS-GC2) (GUANYLATE CYCLASE)
11259	24328	37967	4.96	e,	0E+00(P51842	SWISSPROI	(1) (2)
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEWBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE
11259		37968	4.98		0E+00 P51842	SWISSPROT	F) (GC-F)
11885	ł			1_	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2087	1	l			AE002225.2	L	Chlamydophila pneumoniae AR39, section 53 of 94 of the complete genome
7049	1	33518	1.65	乚	Z36879.1	Į.	Figringial gdcsPA gene for P-protein of the glycine deavage system
7380	1			L	014514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360				L	2.9E+00 014514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20684		6.19		P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8052	24135	34655	0.57		9E+00 P05844	SWISSPROT	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
							STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2;
8052	21135	34656	0.57		P05844	SWISSPROT	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8289	21371	34892	0.81	L	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4153059 5'
9438	ı				AJ002153.2	ΤN	Saguinus oedipus gene for seminal veskde secreted protein semenogetin i
1486		27722	4.77		AF186398.1	NT	Buxus harlandii maturase K (matk) gene, partial cds; chloroplast gene for chloroplast product
1662	14814		3.14		AL161552.2	MT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7480	20535	34010	5.05		R393724 NT	NT	Mus musculus endomucin (LOC53423), mRNA
9813			0.6	l I	BE5651821	EST_HUMAN	601342758F1 NIH MGC_53 Home septens cDNA clane IMAGE:3684807 5
10928	20636		1.53		8393724 NT	M	Mus musculus endomucin (LOC53423), mRNA
240					6679306 NT	Ā	Mus musculus per-hexamer repeat gene 3 (Phvx3), mRNA
240		26491		1 1	2.7E+00 6679306 NT	N	Mus musculus per-hexamer repeat gene 3 (ค่านว3), mRNA

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6134		32652		L	2.4E+00 P02843		VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538		34085	0.71	Ш			602120856F1 NIH_MGC_58 Hamo sepiens cDNA clone IMAGE:4278012 5
7538	20611	34086				EST_HUMAN	
883 483	ı				1 1	SWISSPROT	CD271, RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416					SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406					.	NT	Helicobacter pyloni, strain J99 section 47 of 132 of the complete genome
8852	ı				AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-d05 PT0004 Homo saplens cDNA
8206	22107	35648			P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHIN-B)
10244	1	L				SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	١.			L		SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313		Ŀ		L		NT	H.seplens CTGF gene and promoter region
10449				L.	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10528	1				BE326702.1	EST_HUMAN	hre3f06.x1 NCL_CGAP_Kid11 Homo saplens cDNA clone IMAGE:3133187 3'
10528	1	37170		L	BE326702.1	EST_HUMAN	hre3f06.x1 NCI_CGAP_Kid11 Fomo septens cDNA clone IMAGE:3133187 3'
10818	23851			L	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11335	1	38047	1.36		Y14079.1	NT	Bacilius subtilis chromosomal DNA, region 75 degrees: glpPFKD operon and downstream
11640		38413	2.44		AF168652.2	Ę	Fregaria x ananassa cytosolic ascorbata peroxidase (ApxSC) gene, ApxSC-c ellele, complete cds
1282	1			L	Γ	F	G.domesticus artificial single chain antibody gene (L3)
4237	17383			L	2.3E+00 AJ401081.1	N	Bos taurus partial cytb gane for cytochrome b
	l.				4 27 7 E	NAME IN TOR	J7340F Human fetal heart, Lembda ZAP Express Homo sapiens cDNA clone J7340 6' similar to PROLYN CARROXYPEPTIDASE
7640	1	24459		⊥.	ROZBESA NT	TN TN	Rettus novecious ATPase. Ca++ transporting. ublautous (Ato2a3), mRNA
1111	26221		2.37	1_	2.3E+00 P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7958	1_					Z	M.mazsi dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9310	22386	35938			835317	ĮN.	Polypterus ornatipinnis mitochondrion, complete genome
9371	ı				011127	SWISSPROT	ALPHA-(1,3) FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
11041		l			Q07078	SWISSPROT	ANNEXIN VII (SYNEXIN)
12075	25056	38763	2.14	L	2.3E+00 BF641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Hcmo sapiens; cDNA clone IMAGE:4068173 5
12075	ı				BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_68 Hcmo capienc cDNA clone IMAGE:4068173 5
12445	l				BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Hcmo sapiens cDNA clone IMAGE.3918843 5'
4128			1.06		AF020528.1	TN	Megnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572				D67071.1	Ę	Rat gene for regucalcin, excn1 (non-coding excn)

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Single Exon Probes Expressed in Placetica	ORF SEQ Expression (Top) Hit Acession Database ID No. Signal BLAST E No. Source	2 30554 4.12 2.2E+00 D67071.1 NT Ret gene for regucalcin, exan1 (non-codinglexan)	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LI	31637 11.22 2.2.E+00 (088307	32478 1.83 2.2E+00 BE927220.1  EST_HUMAN	32479 1.93 2.2E+00 BE927220.1	32711 9.39 2.2E+00 BE250383.1 EST_HUMAN	33013 2.87 2.2E+00 Q00336  SWISSPROT	33278 3.14 2.2E+00[P51459 SWISSPROT	3.4 2.2E+00[AA594574.1 [EST_HUMAN	34017 0.83 2.2E+00 AA137027.1  EST_HUMAN	34332 11.91 2.2E+00 AA449012.1	34427 0.68 2.2E+00 P54918 SWISSPROT	34896 0.65	A CORNECTION OF THE CORNECTION	34697 0.00 2.2E-100 BE30 1300.1 E.S.I. TOWNERS	2 12 2 2F+00 004708   SWISSPROT	36890 1.12 2.2E+00 Al280373.1	36891 1.12 2.2E+00 Al290373:1	36941 3.04 2.2E+00 BF246782.1 EST_HUMAN	37315 2.8 2.2E+00 AF183416.1 NT	37536 3.3 2.2E+00 P07911 SWISSPROT	38605 6.04 2.2E+00[P10407  SWISSPROT	26795 13.2 2.1E+00 AF132812.2 NT	1.19
		30554	31636	31637	32478	32479	32711	33013	33278		34017	34332	34427	34898	7007	34087		36890	36891	36941	37315	37536	38605	26795	
	Exan SEQ ID NO:	17572	18658			5 19160	_				0 20545			4 21376		-	25880								8 16841
	Probe SEO ID NO:	4432	5458	5458	597	5975	618	648	673(	.602	747	778	786	8294			9768	10269	10258	10301	1067;	1172	11915	583	. 3678

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Probe SEQ ID NO:	E CO	ORF SEQ	Expression	Most Similar	Top Hit Acession	Top Hit	
6260		Ω O O	Signal	(Top) Hit BLAST E	Š	Database	Top Hit Descriptor
8260	<u> </u>		,	Value	•		
	19434		76.0	2.1E+00 P75357		SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20260	33698	3.51	2.1E+00 O70159		SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7160	2013012	33744	7.0	2 15+00	4503430 NT	þ	Homo sapiens dysferlin, limb girdle musculin dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
2				3			yy08a10.s1 Soares melanocyte 2NbHM Horno sapiens cDNA clone IMAGE:270818 3' similar to gb:M55654
7191	20058	33468	5.88	· 2.1E+00	2.1E+00 N29575.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
8694	21774		2.43	2.1E+00	2.1E+00 AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sepiens cDNA clane NT2RM2000671 5'
1223	14383	27444	1.32	2.0E+00	2.0E+00 AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1223	14383			2.0E+00	2.0E+00 AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1366	ŀ	27595		2.0E+00	2.0E+00 AF204927.1	N	Oryctolegus cuniculus Na+,K+-ATPase beta 1 subunit mRNA, complete cds
1606	14759			2.0E+00 P25582		SWISSPROT	PUTATIVE RRINA METHYLTRANSFERASE SPB1
2216	16360	28480	72	2.0E+00	2.0E+00 Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type i
2216	_		7.2	2.0E+00	2.0E+00 Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type i
9,0	l		7	00430.0	,	TOT HIMAN	hi13co5.x1 NCL_CGAP_GU1 Homo sapiens cDNa clone IMAGE:2972168 3' similar to gb:X01677 cl. YCERAI DEHYDE 3-PHOSPHATE DEHYDROGENASE LIVER (HUMAN):
27	1			20.70.7	T		HIRACES AT NOT CRAP GLIT Homo saplens CDNA clone IMAGE: 2972168 3' similar to ob: X01677
4216	17365	30354	1.7.1	2.0E+00	2.0E+00 AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
	1		8			TOGGGGIA	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE O YCODBOTEINS E1 AND E21
77.1	1		2		Ī	DA PENNS	The state of the s
8214	╝		4	2.0E+00		z	Escapriona con 01st Cuts, map position at 40 min., compute cus
8214			4	2.0E+00		· LN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8214	21296	34817	7	2.0E+00	2.0E+00 AB008676.1	NT	Escherichia coli 0157 DNA, map position at 🕫 min., complete cds
9122	22201	35743	3.04	,	2.0E+00 F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117808
12815	26022	31670	6.76	2.0E+00	5834843 NT	ΝT	Gallus gallus mitochondrion, complete genome
5715	18908	32202	4.28	1,9E+00	E154389 NT	NT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5715	18908	32203	4.28	1.9E+00	F154389 NT	TN	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6225	19400		12	1.9E+00		EST HUMAN	601679636F1 NIH_MGC_78 Homo septens cDNA clone IMAGE:3949881 5'
6782	19947		0.92		1.9E+00 AW845689.1	EST_HUMAN	MR0-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA
6889	20040		<u>ę.</u>	1.9E+00 Q63627		SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8653	21733	35272	2.21	1.9E+00 P02467		SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR
8653	21733	35273	•	1.9E+00 P02467		SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8859	l .l		3.32		06.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
9095	22174		1.86	1.9E+00   O51781	·	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	970	1,	9E+00 AA669125.1	EST_HUMAN	ab94a04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone INAGE:854574 3' similar to contains Alu repetitive element;contains element L1 L1 répetitive element;
10790	23823	37447	29'0	1.9E+00	1.9E+00 AF248269.1	NT	Homo saplens gag-pro-pol precursor protein gene, partial-ods
3162	16337	28346	1.89	1.8E+00 P21004	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16385		2.15	+	8E+00 U04356.1	TN	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3180	18385	28371	2.16	-	8E+00 U04356.1	ΤΝ	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988				-	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02		1.8E+00 BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clane IMAGE:4127364 6'
6528	1			Ė	1.8E+00 BF683327.1	EST.HUMAN	602/139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288272 5'
6879	20031	33441	1.15		1.8E+00 BF305852.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7204	20069		122	-	8E+00 P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		8.0	<del>-</del>	8E+00 P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE- (GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308		34043		_	8E±00 D11360	SWISSPROT	RETROVIRUS-RELATED POL POLYPROITEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCI EASEI
3	1						RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE;
8308					8E+00 P11369	SWISSPROT	ENDONUCLEASE]
9066			2.28	1.	8E+00 O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
. 9376	i		0.78	1	8E+00 R31042.1	EST_HUMAN	yh72c08.r1 Soares placenta Nb2HP Homo capiens cDNA done IMAGE:135278 5
9462			0.82	1	.8E+00 AW880004.1	EST_HUMAN	QV0-0T0030-070300-148-a03 OT0030 Horno sapiens cDNA
9888	23034	36626	0.47	1	8E+00 P06828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR (CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1)
10054		1		_	8E+00 P27050	SWISSPROT	CHITINASE D PRECURSOR
10480	L			-	8E+00 AF111849.1	IN	Homo sapiens PRO0530 mRNA, complete cds
10777			0.78	1	8E+00 P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12575	25994		4.97	-	8E+00 AF314264.1	TN	Chlamydomonas reinhardiil alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12667	25444		6.01	1	9508404 NT	NT	Rattus narvegicus Actin-related protein complex 1b (Arpc1b), mRNA
13005		31854	1.45	1	.8E+00 BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Home sapiens ::DNA done IMAGE:4048251 5'
1132	14297	27352	1.68	-	7E+00 080114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2345				-	7E+00 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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					3.6	2001	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2445	15573	28702	1.49	-	7E+00 AI141087.1	EST_HUMAN	oz43h05x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878137 3'
	<u>l_</u>						LEVANSUCRASE (BETA-D-FRUCTOFU, ANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL
4681	17718	30701	0.98	1.	7E+00 Q60114	SWISSPROT	TRANSFERASE)
5730		32218		-	7E+00 BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo capiens cDNA
5730	18923	32217	1.73	٦.	7E+00 BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo saplens cDNA
6141				1.	7E+00 Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
GRAZ	1	33230	. 0.87	1 7F+00	7F+00 P35818	SWISSPROT	PYRUVATE DEHYDROGENASE (LIPOAMIDE))-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7367				-	7E+00 Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7367	L	L		-	7E+00 Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2: AMD1 INTERGENIC REGION
8038	21121	34641	1.1	1.7E+00	7E+00 AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	ı	L	1.08	1.7E+00	6755715 NT	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
8252	ı	L	0.61	1.7E+00	7E+00 BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Brn87 Homo sepiens cDNA clone IMAGE:4214669 5'
8739	l	35352	0.76	-	7E+00 AF245513.1	Ŋ	Hippoglossus hippoglossus interferon Inducible Mx protein (Mx) mRNA, complete cds
8828	ı		1.63	1.	7E+00 BF308000.1	EST_HUMAN	801894255F1 NIH_MGC_17 Hamo sapiens oDNA clone IMAGE:4140084 5'
8901	21980	35519		1.		TN	M.musculus Ank-1 mRNA for erythroid ankyrin
8901				۱.	7E+00 X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9014	52093	35633	1.03	1.	7E+00 U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	26859	35981	2.44	1.7E+00	7E+00 O60479	SWISSPROT	HOMEOBOX PROTEIN DLX+3
9350	25859	35982	2:44	1.7E+00	7E+00 O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9800	3 22846		-	1.7E+00	7E+00 AF161380.1	NT	Homo septens HSPC262 mRNA, partial cds
10375	5 23410		0.54	1	7E+00 AW853681.1	EST_HUMAN	EST365751 MAGE resequences, MAGC Homo sapiens cDNA
10857	23890	37509	0.47	1.	7E+00 BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Hcmo saplens cDNA clone IMAGE:3890464 5'
10857	23890	37510	0.47	1.	7E+00 BE878260.1	EST HUMAN	601488170F1 NIH_MGC_69 Hcmo sapiens cDNA clone IMAGE:3890464 5
11898	3 24884	L	1.67	_	7E+00 W22424.1	<b>EST_HUMAN</b>	67B7 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
	l						tu82d07.x1 NCI_CGAP_Gas4 Homo sapieris cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1
12523	3 25356		1.94	1.	7E+00 AI678443.1	EST_HUMAN	MSR1 repetitive element;
2080		L	19.53	1	6E+00 AF199339.1	NT	Homo sapiens lens epithelium-denved growth factor gene, alternatively spliced, complete cds
2101		L	4.14	_	6E+00 AF077374.1	NT	Home seplens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2107	L	L		1	.6E+00 Y11344.1	TN	Mus musculus ST6GalNAcili gene, exon 2
2357			0.97	•	.6E+00 X98373.1	IN	B.napus gene encoding endo-polygalacturonase
3026	16202	28225	1.22	<del>-</del>	6E+00 W 38426.1	EST_HUMAN	zd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gbD28805 N-ACETYLLACTOSAMINE S'YITHASE (HUMAN);
1,1							

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Tap Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
. 3857	17017		1.08	1.	6E+00 AB026898.1	TN	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17294		6.05	٦.	6E+00 BF570077.1	EST HUMAN	602186095T1 NIH_MGC_45 Hcmo sapiens cDNA clone IMAGE:4310591 3'
4472	17012	30590	1.25	1.6E+00	6E+00 AF155827.1	LN	Homo capiono proliferation-accociated SNF2-like protoin (SMARCA6) mRNA, complote ode
4472	17612	30591	1.25	1.6E+00	6E+00 AF155827.1	IN	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	65'0	1.6E+00	6E+00 AF127897.1	MT	Samiri boliviensis olfactory receptor (SBO27) gene, partial cds
5184	18316	31284	2.83	1.6E+00	6E+00 Y11344.1	IN	Mus musculus ST6GalNAcill gene, exon 2
5194	18316	31285	2.83	1.8E+00	6E+00 Y11344.1	NT	Mus musculus ST6GalNAcill gene, exon 2
5948	19134	32447	2.38	1.6E+00	6E+00 L04808.1	Į.	Brachydanlo rerio MHC class 11 DA-beta-2"01 gene, 3' end
8035	19218	32540	0.78	1,	6E+00 AF005631.1	NT	Homo sapiens transglutaminase type I (Tgrisel) gene, promoter region
6286	19759	33147	0.91	1.6E+00	6E+00 BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Horno sapiens cDNA
6849	20002	33411		1	6E+00 AW 294881.1	EST HUMAN	UI-H-BIZ-ahr-b-04-0-UI.s1 NCI_CGAP_Sub4 Homo saplens cDNA done IMAGE:2727511 3'
7394	20472	33938	2.37	1.6E+00	GE+00 BE697267.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Hcmo saplens cDNA
8219	21301		1.3	Ψ.		SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8574	21655	35198	3.3	1	6E+00 AJ297131.1	된	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222 NT	NT	Homo sepiens hypothetical protein PR0097,1 (PR00971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222 NT	NT	Homo saplens hypothetical protein PRO097,1 (PRO0971), mRNA
9272	22348		0.49	٦.	6E+00 BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Hamo sapiens cDNA clane IMAGE:3605647 5'
8659	25857		1.05	1.	6E+00 X52046.1	LΝ	M.musculus COL3A1 gene for collagen alpha-l
8659	25857	34616	1.05	1.	8E+00 X52048.1	ΝΤ	M.musoulus COL3A1 gene for collagen alpha-l
9786	.22826		0.7	· 1.6E+00	6E+00 AF043466.1	N	Thermognærobacter ethandicus D-xylose-binding protein (xylF) gene, complete cds
9835	22974	99598	1.49	٦.	6E+00 T41290.1	EST_HUMAN	ph6b6_19/1TV Outward All-primed hncDNA library Homo saplens cDNA clone ph6b6_19/1TV
10388	23423	37029	1.09	٦.	6E+00 AW835844.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo saplans cDNA
10388	23423	37030	1.09	1.	6E+00 AW835844.1	EST_HUMAN	QV4-LT0016-080200-100-d07 LT0018 Homo sapiens cDNA
10552	23587	37195	0.52	1	.6E+00 AF037352.1	¥	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37728	1.77	1.6E+00	6E+00 P54817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSIEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
11082	19278	32540	4.8	1.	6E+00 AF005631.1	NT	Homo sepiens transglutaminase type i (Tgatel) gene, promoter region
12008	24991	38698		1	6E+00 AF104313.1	TN	Homo saplens unknown mRNA
33	13271	26275		1	5E+00 U53449.1	NT.	Rattus norvegicus jun dimenzation protein 2 (jdp-2) mRNA, complete cds
241	13463	26492	2.44	1.5E+00	.5E+00 AE002201.2	۲	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome
636	13821		1.81	1.5E+00	6752961 NT	<u> </u>	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2481	15608			-	5E+00 AJ131402.1	Į.	Potato virus A RNA complete genome, Isolate U
2584	16709	28828	2.02	1.5E+00	6678350 NT	M	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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Probe SEQ ID 1	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vælue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3208	15608	28732	1.75	1.5E+00	.5E+00 AJ131402.1	LNT.	Potato virus A RNA complete genome, Isolete U
.3462	16629	29849	0.77	1.6E+00	.6E+00 AE001945.1	N	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
							tt12/10.x1 NCI_CGAP_GC6 Home sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237
5846	19036	32342	0.71	1.5E+00	.5E+00 AI655301.1	EST_HUMAN	HKF-1.;
5846	10038	32243	0.74	4 55+00		FST HIMAN	tt12/10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' sImilar to TR:000237 000237 HKF-1
8538	19899	33072		1.5E+00	5E+00 R17879.1	EST HUMAN	yg10e02.r1 Soares infent brain 1NIB Homo sapiens cDNA clone IMAGE:31683 5'
7278	20361		,	1.5E+00	L	EST_HUMAN	601478745F1 NIH_MGC_68 Homo saplens; cDNA clone IMAGE:3881555 5'
7311	20383	33853	16.24	1.5E+00 P47179		SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393		16.24	1.5E+00 P47179		SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575		0.61	1.5E+00	.5E+00 AA889259.1	EST_HUMAN	ak26110.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:14071153'
7769	90806	34347	0.00	1 5F+00	5F+00 A1003254 1	NAMUH TSE	an07b11.s1 Stratagene schizo brain S11 Hcmo sapiens cDNA clone IMAGE:1684893 3' similar to db:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8313	21395	34920	6.0	1.5E+00		EST HUMAN	601509586F1 NIH MGC_71 Homo eaplens, cDNA clone IMAGE:3911181 5
8367	21448	34971	0.5	1.5E+00		NT	Homo saplens mRNA for KIAA1454 protein, partial cds
8846	21825	35463	1.09	1.6E+00	5E+00 K02138.1	NT	Mouse germline igM chain gene, mu-delta région
9218	22288		0.48	1.5E+00	5E+00 AB038518.1	INT	Homo sapiens hGPib alpha gene for platelet glycoprotein ib alpha, complete cds
9334	22410	35963	0.51	1.6E+00	5E+00 BF217818.1	EST_HUMAN	601882682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5
9884	22733		0.85	1.5E+00	5E+00 R81928.1	EST_HUMAN	yi03h01.r1 Soares placenta Nb2HP Homo suplens cDNA clone IMAGE:147697 5'
9832	22875	36459	9.1	1.5E+00	5E+00 AW375897.1	EST_HUMAN	QV3-CT0192-281099-008-d09 CT0192 Homo saplens cDNA
10064	23102	36705		1.5E+00	SE+00 BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo saplens cDNA
10258	23293			1.5E+00	.5E+00 BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
10389	23434	37040		1.5臣+00	.5E+00 AA017689.1	EST_HUMAN	za38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5
10339	23434	37041		1.5E+00	5E+00 AA017689:1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo capiens cDNA done IMAGE:361306 5
11684	24683	38373	3.4	1.5E+00	:1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 3'
11834	24823		89'4	1.5E+00		NT	Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11829	24915	38817		1.5E+00	.5E+00 A1400798.1	EST_HUMAN	tg94d09.x1 NCL_CGAP_CLL1 Homo saplents cDNA clone IMAGE:2116433 3'
11929	24916	38618		1	.5E+00 AI400798.1	EST_HUMAN	tg94d09.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:2116433 31
12515	26095	31662		1.	6E+00 D63480.1	TN	Human mRNA for KIAA0148 gene, partial cds
12765	25508		3.92	1	AL445065.1	N	Tharmoplasina aoldophilum complete genome; segment 3/5
12888	25589		2.17	1.5E+00	6978492 NT	NT	Rattus norvegicus 5 - Lipoxygenase (Alox5), inRNA
13220	25794	Ц		1.5E+00	.5E+00 BF223935.1	EST_HUMAN	7q82b08x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13268		-	1.4E+00	7661685 NT	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	13268	26272	2.27	1.4E+00	7661685 NT	ΝΤ	Homo sapiens DKFZP58GM0122 protein (DKFZP58GM0122), mRNA

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Homo sapiens caveolin-1/-2 locus, Contig1, ID7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and WSB1 protein (WSB1) genes, complete cds. Fugu rubripes neuroffixonatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and LAMININ BETA-2 CHAIN PRECURSOR (S.LAMININ)
LAMININ BETA-2 CHAIN PRECURSOR (S.LAMININ)
GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) he23/05.x1 NCI\_CGAP\_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) x333112.1 Scares infant brain 1NIB Homo sciptens cDNA clone IMAGE:34345 67 RC1-BT0313-301299-012-105 BT0313 Homo septens cDNA NT Scaloporue undulatus omithine transcarbamylase (OTC) mRNA, complete cds EST\_HUMAN 602133135F1 NIH\_MGC\_81 Homo sapiens cDNA clone IMAGE:4288137 6' EST\_HUMAN IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA EST\_HUMAN IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA w445g07.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3 602156687F1 NIH\_MGC\_83 Homo saplens oDNA clone IMAGE:4297656 6 Helicobacter pylori glutamine synthetase (glinA) gene, complete cds Top Hit Descriptor Homo saplens Mad4 homolog (MAD4) mRNA CM0-NN1005-140300-286-h06 NN1005 Homo saplens cDNA CM0-NN1005-140300-286-h06 NN1005 Homo sepiens cDNA CM3-NN0006-300300-132-b12 NN0006 Horno sapiens cDNA Homo saplens mRNA for KIAA0905 protein, complete cds Homo sapiens Xq pseudoautosomal region; segment 1/2 Homo sapiens mRNA for KIAA1157 protein, partial cds Human papillomavirus type 7 genomic DNA DNA TOPOISOMERASE III ALPHA Single Exon Probes Expressed in Placenta repetitive element; SYNAPSIN II EST\_HUMAN EST\_HUMAN EST HUMAN EST HUMAN SWISSPROT EST\_HUMAN SWISSPROT SWISSPROT Top Hit Database Source SWISSPROT 눋 눋 눋 눌 뉟 5453733 Top Hilt Acession 1.4E+00 AW900465.1 1.4E+00 BF681547.1 Q92777 AW893057.1 1.4E+00 AW 467760.1 1.4E+00 AF064564.2 AF064564.2 AW900455. AB032983.1 1.4E+00 AF134844.1 1.4E+00 BF575545.1 1.4E+00 BE145374.1 1.4E+00 BE145374.1 I.4E+00 AJ133269.1 1.4E+00 R20459.1 1.4E+00 BE064667.1 AJ271735.1 ġ U67922.1 1.4E+00 AB03298 1.4E+00 P55268 1.4E+00 P55268 X74463.1 1.4E+00 P07683 1.4E+00 1.4E+00 1.4E+00 1.4E+00 1.4E+00 4E+00 1.4E+00 1.4E+00 (Top) Hit BLAST E Most Similar Value 0.65 0.88 0.88 22 8 8 3.83 9.39 80. 3.07 86. 0.97 1.51 Expression Signal 33078 33079 33614 34005 34063 36072 37052 37102 29055 29056 31705 33988 28964 30484 32939 ORF SEQ ÖΝΘ 20515 23492 SEQ ID 15482 17513 19705 20588 20588 21611 15947 15947 17843 19578 19705 23482 15541 18687 18839 20631 22371 ÿ 7614 9432 Probe SEQ ID 4370 4370 5317 5045 6409 6542 6542 6542 8994 9295 8388 10412 4708 10457 2351 2411 2734 2833 2833 7438 8530 ë

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					ignic.	EXOIL FIORE	Single Exoll Flobes Explessed in Flacelia
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390		-	.4E+00 D83441.1	TN	Pandorina colemaniae chloropiast rocL gene for ribulose bisphosphate carboxylase, partial cds
10744		37391	96'0	-	4E+00 D63441.1	IN	Pandorina colemaniae chioropiast rbcL gene for ribulose bisphosphate carboxylase, partial cds
10852	23885			<del>-</del>	4E+00 Q07283	SWISSPROT	TRICHOHYALIN
11499	i	38232			.4E+00 AB006682.1	NT	Hamo sepiens APECED mRNA for AIRE-i, complete cds
11691	24689		3.46	1.4E+00	4E+00 BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	L		3.46	1	4E+00 BE962107.2	EST_HUMAN	801655184R1 NIH_MGC_65 Homo sapieris cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	4E+00 U30790.1	۲N	Preumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711				1.4E+00	4E+00 U30790.1	L	Preumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359			2	1.4E+00	.4E+00 AL181500.2	N	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	۱_		2.99	1.4E+00	11545838 NT	Į.	Homo saplens cutaneous T-cell lymphoma lumor antigen se70-2 (SE70-2), mRNA
684	13775		1.96	-	.3E+00 Z73640.1	LN ⊢N	M.mucedo gene encoding 4-Dinydromethyktrisporate dehydrogenase
925		27164	2.79	1.35+00	.3E+00 AJ271192.1	ĻΝ	Cantharellus sp. partial 25S rRNA gene, Isolate Tibet
1153	14317	L			.3E+00 Y19213.1	TN	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27549	14.38	1.35+00	4507998 NT	LN	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482		14.36	-	TN 8662059	N.	Hano sapiens zinc finger protein 157 (HZF22) (ZNF167) mRNA
1387	l			-	.3E+00 U61730.2	F	Ook lacryma-jobi dihydrodipicolinata synthase (dapA) gene, complete cds
164	14783		2.35	-	3E+00 AE002338.2	Ę	Chlamydia muridarum, section 66 of 85 of the complete genome
	1						Oyptinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serins protease (MASP)
2316			2.38	+	3E+00 AB030447.1	μ	and MASP-related protein, complete cds
2615	15739		1.81	1.3E+00	BE96673	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapients cDNA clone IMAGE:3915945 31
3005	16180	29201	98'0	1.3E+00	6755621 NT	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
							Fugu rubripes gamma-aminobutyrio acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane
3686	16848	29857	1.14	_	3E+00 AF016494.1	L.	protein (Foo), syntypus vestured sociated integral intentionally protein (VAVIIF-1), proteingen Christians enhancer protein (PCOLCE) genes, complete o>
5631	l				3E+00 P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5827	19017	32322	0.58		.3E+00 M27138.1	Z	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	١.			_	3E+00 AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo saplens cDNA
6142			7.56	-	3E+00 AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Honto sapiens cDNA
6547	ŀ		1.14	1.3E+00	SE+00 M33498.1	LN	D.melanogaster no-on-transient A gene produot, complete odo
0689	i		0.71	-		SWISSPROT	HYPOTHETICAL GENE 84 PROTEIN
6928			0.58	-	3E+00 P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	3 20206	33634	1.04	-	.3E+00 M13918.2	TN	Homo sepiens fibronectin receptor alpha-subunit precursor (ITGAS) mRNA, partial cds

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Probe NO: 7092 7092 7092 7092 8907 8907 8907 8907 8907 8907 8907 8907	Exon SEC ID NO: NO: 20188 20332 20332 21675 21675 22423 22423 22423 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 22789 2278	33610 33776 33776 34162 35126 35269 356976 35977 36977 36976 36976 36976 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 36977 369777 36977 36977 36977 36977 36977 36977 36977 36977 369777 36977 36977 36977 36977 36977 36977 36977 36977 369777 36977 36977 36977 36977 36977 36977 36977 36977 369777 36977 36977 36977 36977 36977 36977 36977 36977 3697	Expression Signal 1.16 0.88 0.88 0.89 0.51 0.51 0.51 0.51 0.51 0.51 0.51 0.51	Most:	DE 538819.  No. No. No. No. SE538819. SE538819. SE538819. SE538819. SE538819. SE538819. SE538819. SE538811. SE53881. SE53881. SE53881. SE53881. SE53881. SE53881. SE53882. SE5382. SE53882. SE53882. SE53882. SE53882. SE53882. SE53882. SE53	Top Hit Diabese Source EST HUMAN SWISSPROT HUMAN SWISSPROT HUMAN NT EST HUMAN NT	Top Hit Detaileses Source TOPAPIOSES Professed in Fracentia Top Hit Descriptor  Top Hit Detaileses Source Source Source Source  EST HUMAN Gene CANA done TOBAPORES Professed Canada Cana
10435	-				3E+00 AE004392.1	Z	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10435	1 1				.3E+00 M28953.1	F F	Cempylobacter jejuni kanamyoin phosphotrainsferase (aphA-7) gene, complete cds Homo sapiens chromosome 21 segment HS21C102
10838	1 1	37493			3E+00 A1990946.1 ES 3E+00 8923637 NT	EST_HUMAN NT	ws32e10.x1 NCI_CGAP_GC6 Homo sapleris cDNA clone IMAGE:2498922.3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE; Homo saplens hypothetical protein FLJ20707 (FLJ20707), mRNA
	ļ						

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					Bill	ממון וומאין מ	القاد المعمد المعمدة الله العمدالة
Probe SEQ ID NO: .	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.48	1.3E+00	7949159 NT	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	L	37507	0.48	1.3E+00	7949159 NT	LZ	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	L	37515	0.45		.3E+00 H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NbHBst Homo saplens cDNA clone IMAGE:183076 3'
10861	L		0.45	-	.3E+00 H42881.1	EST_HUMAN	ye88o03.c1 Scares breact 3NbHBct Hamo capiene cDNA clone IMAGE:183076 31
10832	<u> </u>		4.05	1	.3E+00 Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	24	Ĺ	.3E+00 P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	.3E+00 Z18892.2	NT	Mus musculus desmin gene
11619	24870		1.43		1.1	EST_HUMAN	xp09e03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11831	24820	38511	2.73			NT	Human mRNA for KIAA0085 gene, partial cds
11823	ı	38610		١		NT	Bacillus subtilis genomic DNA 23.9kB fragment
11894	1		1.35	-	.3E+00 L31891.1	LN	Arabidopsis thaliana 3-ketoacyt-acyt carrier protein synthase III (KAS III) mRNA, complete cds
12604	25347		3.81		.3E+00 AF187873.1	Z	Cavia porcellus inwardiy-rectifying potassiuni channel Kir2.2 (KCNJ12) gene, complete cds
12698	1	32022			.3E+00 BF348043.1	EST_HUMAN	602023185F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158452 5
12707	l		1.98	_	.3E+00 P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	ı		1.53	Ĺ	1.3E+00 AF187035.1	NT	Sturntra lillum cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
							Naphthalanesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCil) gene, complete
13200			1.34	_		NT	ods
13231	25981		1.63		.3E+00 AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
299	13853	26881	8.73	٣	.2E+00 AA676246.1	EST_HUMAN	222408.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:431535 3'
848	14024	27082	1.52	-	.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
. 846				Ĺ	.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
846	14024		1.52		.2E+00 P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
904	14078		1.21	1.2E+00	8924234 NT	NT	Homo sapiens hypothetical protein PR03077 (PR03077), mRNA
1187	14349	27407	7.6		1.2E+00 AF080245.2	NT	Elesis oleifera sesquiterpene synthase mRN4, complete cds
1232	14391	27453	1.7.1	1.2E+00	.2E+00 AJ252242.1	NT	pea seed-borne mosaic virus complete genoine
1232	14391	27454	1.71	1.2E+00	.2E+00 AJ252242.1	. TN	pea seed-borne mosaic virus complete genoine
2068	_	28323	1.02		.2E+00 AF140631.1	TN	Hamo sepiens G-protein coupled receptor 14 (GPR14) gene, complete ods
3179	16354	29359	1.06		.2E+00 AB020681.1	TN	Homo seplens mRNA for KIAA0874 protein, partial cds
3234	16408		7.01	1.2E+00	1.2E+00 AL161563.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	29422	7.01	1.2E+00	1.2E+00 AL161563.2	NT .	Arabidopsis thaliana DNA chromosome 4, ocntig fragment No. 63
3358	16530		3.57		1.2E+00 P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	28825	0.61		1.2E+00 AF188740.1	NT.	Homo sepiens LHX3 gene, Intron 2
3804	16964	29967	9.16		1.2E+00 U75902.1	TN	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4084	L		1.87		1.2E+00 BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g08_1 FT0175 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta	Top Hit Descriptor	Recommunis gene for pyrophosphate-dependent phosphofructokinase beta subunit	HUMHW01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01	H.sapiens ENO3 gene for musche specific enolase	Homo sapians klotho gane, exan 1	Mus musculus ld gene, exon 1	PM0_ST0264-161199-001-d01 ST0264 Horns saplens cDNA	PM1-HT0422-160200-007-g10 HT0422 Homo saplens cDNA	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds	Maze mitochondrial F-0-ATPase proteolipid (subunit 9) gene	Homo sapiens chromosome 21 segment HS21C003	Bacillus halodurans genomic DNA, section £/14	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06	Human mRNA for KIAA0227 gene, partial cds	QV0-BN0042-170300-163-g12 BN0042 Horno saplens cDNA	UI-HF-BR0p-ajk-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'	Gellus gallus alpha 1 (V) collegen mRNA, ccmplete cds	Homo saplens chromosome 21 segment HS21C013	Homo sapiens chromosome 21 segment HS21C013	Homo saplens hypothetical protein FLJ10749 (FLJ10749), mRNA	wf64h11.x1 Soares_NFL_T_GBC_S1 Home expiens cDNA clone IMAGE:2359481 3' similar to 9W P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1;	Xylelia fastidiosa, section 32 of 229 of the complete genome	Xytella fastidiosa, section 32 of 229 of the complete genome	H.parahaemolyticus hphlM(A), hphlM(C), hphlR and menB genes	Homo sepiens hypothetical protein FLJ10749 (FLJ10749), mRNA.	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA	R unicornis complete mitochandrial genome	African swine fever virus, complete genome	E faecalis pbp5 gene	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'	qd85c03.x1 Sogres_testis_NHT Homo sapiens cDNA clone IMAGE:1739260 3'	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLO6A14), mRNA
Exon Probes	Top Hit Database Source		EST_HUMAN			NT.	EST_HUMAN P		NT IN	VI LN		NT E	EST_HUMAN 7		EST_HUMAN C	EST_HUMAN L		1 LN	F		EST HUMAN S		N L					d IN				EST_HUMAN o	
Single	Top Hit Acessian No.				11	2E+00 M38686.1	2E+00 AW817817.1	2E+00 BE160761.1		2E+00 M10408.1	1.2		2E+00 AA077909.1	1E+00 D86980.1	1E+00 AW995393.1 :	.1E+00 AW575889.1		1E+00 AL163213.2	1E+00 AL163213.2	8922641 NT	1E+00 AI808360.1	_	1E+00 AE003886.1	.1E+00 X85374.1	8922641 NT	6765205 NT	5835331 NT	.1E+00 U18466.1	.1E+00 X78425.1	6978530 NT	1E+00 BE960184.1	1E+00 AI138582.1	11419739 NT
	Most Similar (Top) Hit BLAST E Value	1.2E+00 Z32850.1	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00
	Expression Signal	3.79	2.13	3.6	0.82	1.69	1.51	7.69	3.13	1.68	17.76	1.74	2.66	1.11	1.23	1.21	2.74	.8.86	8.86	1.02	0.99	1.16	1.16	0.92	1.03	0.72	6.82	3.45	2.06	1.49	14.33	1.32	0.9
	ORF SEQ ID NO:	36224				38158	38400		37556	38788	31768			26703	28045	28192		29594		29757	23844	28974	28976		30220			31204		31599			32740
	Exon SEQ ID NO:	22653		23173	23587	24493	24707	24743	23930	25081	25884	ı	25703	13671	14951	1	•	16579	16679	16740	l	ľ.	L		17210		ı	18235	ı	18023	18924	18942	19392
	Probe SEQ ID NO:	9598	9808	10135	10532	11432	11627	11668	11744	12101	12471	12491	13218	478	1802	1948	2017	3409	3409	3575	3870	3812	3812	3920	4054	4130	4331	5107	5180	5422	5731	2260	6217

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Single Exon Probes Expressed in Placenta	Top Hit Descriptor	Petroselinum crispum cytosolic glucosa-6-phasphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds	χI	w776e11.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2301548 3	Human PBI gane, complete cds	Human PBI gene, complete cds	LOW TEMPERATURE ESSENTAL PROTEIN	Taenia solium immunogenic protein 1 s/6 mr.NA, partiai cas	Dichostelium discoldeum isopertienyi pyrophosphate isomerase (Uipi) mixivA, complete cas	Xenopus lævis modopsin gene, complete cds	Cavia cobaya mRNA for serine/threoine kinase, complete cds	Marchantia polymorpha genee for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rKNA and 26S rKNA	Girardia tigrina mRNA for homeodomein transcription factor (so gene)	Homo sapiens chromosome 21 segment HS;21C018	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds	V.certeri Algai-CAM mRNA	Plautia stali Intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete ods	DNA GYRASE SUBUNIT B	DNA GYRASE SUBUNIT B	af26g08.s1 Soares_total_fetus_Nb2HF8_6w/Homo saptens cDNA ctone IMAGE:1032830 3' similar to WP:G42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME I	ar26g08.s1 Soares_total_fetus_Nb2HF8_9w;Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;	Raftus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6	Xenopus laevis rhodopsin gene, complete cds	Agaricus bisporus mikina (or tyrosinase
Exon Probes	Top Hit Database Source	NT Pe		T HUMAN		╗	ISSPROT					M TN		Ĭ		<u>&gt;</u>	<u>a</u>	SWISSPROT D		EST_HUMAN W	SWISSPROT 3		Г	EST_HUMAN W		×	
Single	Top Hit Acession No.	E+00 AF012862.1	1	+	IE+00 D89501.1	1				DE+00 U23808.1	DE+00 D88425.1	E+00 AB021684.1	0E+00 AJ251660.1	0E+00 AL163218.2	4.1	1.0E+00 X80416.1	0E+00 AB006531.1		0E+00 P48355	0E+00 AA628453.1	0E+00 P24008	0E+00 P24008	0E+00 014228	.0E+00 AA628453.1	.0E+00 AF222781.1	.0E+00 U23808.1	.0E+00 AJ223816.1
	Most Similar (Top) Hit BLAST E Value	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 P48355	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
	Expression Signal	2.83	2.03	3.99	1.38	1.38	1.82	3.58	1.86	1.84	2.1	-2.78	1.4	7.14	2.28	1.35	1.33	1.11	1.11	0.95	4.51	4.51	0.95	1.18	0.73	0.75	1.61
	ORF SEQ ID NO:	38083	38084	38409	38552	38553		32070			26374		26800	26910			28037		28804		29129		١	29463			29939
	Exon SEQ ID NO:	24427	24427	l_	24858	24858	25312	26371	25980	13337		L	13781	L	L	16037	14944	1	1		16117	18117	1	1	L.	H	16933
	Probe SEQ ID NO:	11368	11368	11637	11870	11870	12441	12547	12689	ē	118	431	88	8	989	1417	1785	2554	2554	2621	2940	2840	3032	3260	3469	3688	3772

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					· C	مساوره سردان المحمد	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
4180	17330	30322	1.12	1.0E+00	0E+00 AF223391.1	TZ.	Homo sepiens calcium charnel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	Ĺ			1.0E+00	8922246 NT	Ē	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	•	31568		1.0E+00	1.0E+00 Z97022.1	칟	Hordeum vulgare gene encoding cystains proteinass
5971	19157	32472	4.38	1.	0E+00 AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1	0E+00 AF248054.1	된	Bos taurus micromolar calcium ectivated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds.
6077	18259		1.74	1.0E+00	.0E+00 Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fregment No. 6
6241	ı	32763	4.85	4	0E+00 P04501	SWISSPROT	FIBER PROTEIN
6248	ı			-	0E+00 AW452782.1	EST_HUMAN	Ui-H-Bi3-ak-d-08-0-Ui.s1 NCI_CGAP_Sub5 Homo sepiens cDNA clone IMAGE:3068969 3'
8618		33167	2.04	'L	.0E+00 U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6871	1			١	.0E+00 AF104669.1	INT	Homo saplens cell cycle protein (PA2G4) gene, exons 2 though 5
6767	18923		1.07	1.0E+00	.0E+00 P46508	SWISSPROT	SRB-11 PROTEIN
6785	l	33349	0.82	1	.0E+00 BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3936382 57
6795			0.82	1.0E+00	.0E+00 BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3936382 6'
6916	20231			1.0E+00	.0E+00 Y11204.1	NT	V.carteri gene encoding volvoxopsin
7288	20371	33828	1.15	1	.0E+00 S52770.1	Ę	Insulin-like growth factor-binding protein 4 [crittle, pulmonary artery endothelial cells, mRNA, 2028 nt]
	l						B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7647					.0E+00 P20273	SWISSPROT	(BL-CAM)
7889		Ì_	1.51	1.05+00	.0E+00 AF192531.1	L	Home sapiens endethelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20965	34462	6.02	-	.0E+00 AA775191.1	EST_HUMAN	ac79b08.s1 Strategene lung (#937.210) Homo saptens cDNA clone IMAGE:808791 3'
8019			0.72	-	.0E+00 BF679213.1	EST_HUMAN	602/153792F1 NIH_MGC_83 Home sapiens cDNA clone IMAGE:4284727 5
8148	21230		1.65	_	.0E+00 BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Home sapiens cDNA clone IMAGE:3848005 5
8148		34750	1.85	_	.0E+00 BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3848005 5
8335	1			_	.0E+00 D10852.1	TN	Rettus norvegicus mRNA for N-acetyglucosaminytransferase III, complete cds
						i	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-
8545	2,626	35163	2.69		.0E+00 Q02207	SWISSPROT	DAIDATION FROTEIN (WITT) INVALUDES! ZEINOTEVONTITION TAGE; UST TIENOTEVONTITION TAGE; UST TIENOTEVONTITION TAGE
	1						PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-
9700	24.07	26,64	03.0	*	05+00	TORGSIMS	OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA IDEHYDROGENASE 1
900				-	COLEAN!	011100110	

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		-			Billo	מממני ו ווסעדום	טווקום דאטון וטפס דאט פספס ווון ומספס אוון ומספ אוון ומספס אוון ומ
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8672	21752		1.07	1.0	E+00 P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	95.0	1.0	E+00 Q9Y6T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8708	21788	35322			1.0E+00 Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8735	Į.		1.82		1.0E+00 BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
8776	21855	35397	1.15	7.	DE+00 U42720.2	NT	Simian Immunodeficiency virus Geg protein (3eg) gene, complete cds; Pol protein (pol) gene, partial cds; and VII protein (vf), Vpr protein (vpr), Tet protein (tet), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (net) genes. >
8922	22001	36640	1.8	1.0E+00	E+00 M38427.1	LΝ	Human immunodeficiency virus type 1 (HIV-1), Isolata SF33,
9471	22528	36091	1.95	1.0	E+00 BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA done IMAGE:3899421 5'
9682	ட	38301		1.		, LN	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9682			1.62	1.0	6753429 NT	l. I	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9810				1.0	DE+00 AV689554.1	EST_HUMAN	AV689554 GKC Homo saplens CDNA clone GKCCYA11 5'
9816	22855	38434		)'L	E+00 U44852.1	IN	Xencous laevis zona pellucida C glycoprotein precursor (xIZPC) mRNA, complete cds
9816	,			1.0	E+00 U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein[precursor (xIZPC) mRNA, complete cds
10318			0.82			NT	Homo capiens MHC binding factor, beta (MHCBFB) mRNA
10318		36962	0.82	1.0E+00	5174562 NT		Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10408		37050	69'0	1.0	DE+00 A1077820.1	EST_HUMAN	oy/5d07.s1, Soares_senescent_flaroblasts_NbHSF Homo sepiens cDNA clone IMAGE:1065901.3*
10633		37175		۱۲	E+00 AV768825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW C04 5'
10694		37333	19.71	1.0	DE+00 AA004982.1	EST HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 6'
10894		37334	19.71	1.	0E+00 AA004982.1	EST_HUMAN	2h94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5
10728	<u> </u>	37368	1.22	Ĭ	E+00 L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11218	24285	37924	1.37	1.0	DE+00 S90825.1	FZ	PBR1=proline-tich protein (Intran 3) [human, Genomic, 898 rtt]
							z163b11.51 Soares_fetal_liver_spleen_1NFLS_S1 Homo septens cDNA clone IMAGE:435453 3' similar to
11342	24405	38054	1.48	-	0E+00 AA701494.1	EST_HUMAN	contains Alu repettive element;contains element MER38 repettiive element;
11825	24814		1.62	1,	0E+00[L47613.1	NT	Picea glauca EMB13 mRNA
12329	Ш	-	5.49	11	DE+00 P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12876	L		2.67		1.0E+00 AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Horno sapiens cDNA
3693		150	9.		9.9E-01 AF174685.1	N	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5752		32246	8.8	9.9E-01 P49857	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

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Probe SEQ ID 8 NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Тор Hit Descriptor
2990	19175	32488	0.83	9.9E-01	.9E-01 Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.9E-01	.9E-01 U65667.1	IN	Lycopersicon esculentum putative MI1 copy 1 nematode-resistance gene
9755	22693		2.14	9.9E-01	.9E-01 Q28642	SWISSPROT	82 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26753	1.17	9.8E-01	.8E-01 P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N'ACETYLCLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	9.8E-01 AJ003108.1	IN	Callitrix Jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.28	· 9.8E-01	.8E-01 AF174644.1	Г	Xencpus laevis rac GTPase mRNA, complete cds
3903	17062	30081	0.67	9.8E-01	9.8E-01 BE957439.2	EST_HUMAN	601653383R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3903	17062		29.0	9.8E-01	.8E-01 BE957439.2	EST_HUMAN	601663583R2 NIH_MGC_55 Homo saplens cDNA clone IMAGE:3838461 3'
1			:	L		ļ	Enterchacterlaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-
7349	20429	33890	4.42	9.8E-01	.8E-01 AJ302158.1	Z	like protein, Isolate Jivisos
-			,	L	7 0170001		Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- lity meeting in plats. Moss
7349	20429	33891	4.42	9.85-01	9.8E-01 AJ302158.1	NAM II IMAN	IIIKE DOUBUI, ISOUBER JANSOS 601458337F1 NIH MGC 66 Homo sapiens DNA clone IMAGE:3860049 5'
1050	1000	0,010	1	9.00	0104010.1	1444	60146893751 NIW MGC AR Home company CONA clone IMAGE GROOMS ST
1823	24005	343/B	1.14	"	9.6E-01 DP034010.1	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
2160	2013	İ	5 5	Ϊ,	20000 1 10 300	TOTAL PARTY	AGEGOR OF NOT COAD CODE Homo company of Not Alone INACCE 11271847 3
10653	23687		7.02	"	AA825565.1	EVI TOMAN	OCCOUNTS IN THE CONTRACT OF THE PROPERTY OF TH
11242	24311	37948		၈	.8E-01 BE258705.1	EST_HUMAN	601110238F1 NIM MCC_10 Homb septens curve gione live cone live cone
11242	24311	37949	1.84	G.	.8E-01 BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3350750 5
							Home saplens XZ8 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
12554	25377		2.43	9.8E-01	.8E-01 U52111.2	IN	protein Lios (MTL) ody, CezzyCarindouringeparcein protein furiase ( (Chwinz), Geaule (ransporte) (COM) adrenolaukodystrophy protein >
T.							Drosophila malanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d
7309	20391	33851	2.73	9.7E-01	9.7E-01 U26716.1	ᅜ	and e, partial cds
8701	21781	35314	1.8	9.7E-01	9.7E-01 AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.54	9.7E-01	9.7E-01 M90544.1	NT	Saimonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35661	0.73	9.7E-01	9.7E-01 BE799822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Horno saplens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01		EST_HUMAN	ULH-BI4-api-0-07-0-UI.s1 NCI_CGAP_Sub8 Homo septens cDNA clone IMAGE:3085140 3'
13208	25789		3,17	9.7E-01	9.7E-01 AL'114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4558	17696	30876	0.74	9.6E-01		NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558	17696	30676	92'0	9.6E-01	9.6E-01 AF197925.1	NT	Bromus înermis putative cytosolic phosphoglucomutace (pgm1) mRNA, complete ode
4580	17717	30700	1.28	9.6E-01	3.6E-01 AW789674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homp sapiens cDNA
5872	19062			9.6E-01	.6E-01 Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5872	19082		3.61	9.6E-01	9.8E-01 Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
6889	20038	33447	9.0		9.6E-01 Z97341.2	NT	Arabidopsis thallana DNA chromosome 4, ESSA I FCA contig fragment No. 6

PCT/US01/00663

WO 01/57272

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	Top Hit Descriptor	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds	601441338T1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3916184 3'	601817814F1 NIH_MGC_68 Homo capienc cDNA clane IMAGE:4041363 5	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slo30a4), mRNA	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'	N.crassa valyl-tRNA synthetase (cyt-20/un-3) gene	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	Mus musculus carbonic anhydrase 4 (Car4)! mRNA	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA	7o58e00.x1 NCI_CGAP_KId11 Homo sapleins cDNA done IMAGE:3578219.3' similar to SW:NU6M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;	601334943F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3688714 51	601820312F1 NIH_MGC_58 Homo sepiens cDNA clane IMAGE:4052018 5'	yeS2f01.st Sogres fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:121369 3' similar to contains. Au repositive element;	Homo saplens hypothetical protein FLJ20043 (FLJ20048), mRNA	AB200GBR Infent brain, LLNL array of Dr. M. Scares 1NIB Home saplens cDNA clone LLAB200GB 5"	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Home sapiens cDNA clone LLAB200G8 5'	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)	ob71g08.s1 NCI_CGAP_GCB1 Home sapiens cDNA clone IMAGE:1336862 3'	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cd3	P80-COILIN	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds	Hamo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA	Homo sapiens neurexin III-apha gene, partial cds	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds	Danio rerio LIM class homeodomain protein/(lim5) mRNA, complete cds	Xenopus lasvis gene for aidolase, complete cds
	Top Hit Database Source	TN	TN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	TN	LN	TN	ΤN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	L	EST_HUMAN	EST_HUMAN	F	SWISSPROT	EST_HUMAN	M	SWISSPROT	ᅜ	TN	NT .	NT	F	NT	۲N	ΙN
,	Top Hit Acesslon No.	11440298 NT	9.3E-01 AF271207.1	9.2E-01 BE622702.1	3F129973.1	7105410 NT	9.2E-01 BF037586.1	M84703.1	9.2E-01 AL161565.2	6671677 NT	11430963 NT	2E-01 BF593251.1	9.2E-01 BE563811.1	3F132402.1	196675.1	TN 8923068	1E-01 T26418.1	126418.1	36033.1	9.1E-01 Q61704	AAB06623.1	U72995.1	P38432	AF050113.1	9.0E-01 7661625 NT	AL161515.2	8G22310 NT	AF099810.1	AF017729.1	9.0E-01 L42547.1	D38621.1
	Most Similar (Top) Hit BLAST E Value	9.3E-01	9.3E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01 M64703.1	9.2E-01 /	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.1E-01	9.1E-01 8	9.1E-01	9.1E-01 T26418.1	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01 P38432	9.1E-01	. 9.0E-01	9.0E-01	9.0E-01	9.0E-01	9.0E-01	9.0E-01	9.0E-01
	Expression Signal	2.09	1.22	3.92	0.01	1.58	4.97	0.65	0.98	1.31	3.6	1.64	1.76	1.5	1.52	1.49	1.28	1.28	1.54	3.25	17.46	2.81	9.0	19.67	9.0	0.73	89.0	1.43	13.05	0.82	1.42
	ORF SEQ ID NO:	31861		28505			32624	33320	36484	36582		37269		38707			29468	29469		33183	34300	34473	37023		29472		30367		31218		
	Exon SEO ID NO:	25683		16484	<u></u>	L	_	18925	22800	22988	<u> </u>	23661	L	25006		1	16449	16449	l	ı	20810			_	16451	L	17368			1 1	20651
	Probe SEQ ID NO:	13039	13049	3311	4999	5835	6109	6770	9860	9949	10472	10627	10883	12022	1654	2183	3276	3275	6296	6635	7750	7916	10379	12595	3277	3439	4219	4498	5127	7551	7579

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
9549	Ł				9.0E-01 AF086761.1	NT	Danio rento semaphorin Z1a mRNA, complete cds
10035	23073	36673	0.48			NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1,41	9.0E-01	0E-01 AF146793.2	L	Mus musculus neuromedin U precursor (Nriu) geno, partial odo; tPhLP (Tphlp) gene, partial odo; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
581A	1			, a		Ŀ	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chiromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6378	1						Rabbit MHC fragment RLA-DF DNA
6590	25827	33134		_		EST_HUMAN	601882708F1 NIH_MGC_57 Hamo sepiens cDNA clone IMAGE:4096216 5'
6590	L	L			8.9E-01 BF217939.1	HUMAN	801882708F1 NIH_MGC_57 Hamo septens cDNA clone IMAGE:4095216 51
						Ė	Oithone nana cytochrome-c oxidase subunit i (coxi) gene, partial cds; mitochondrial gene for mitochondrial nording
12080	25080	35237	27.0		A PE-01 AF208007.1	Į,	Xylalia fastidiosa, section 90 of 229 of the complete genome
12423	Ŀ	L		L		LN.	Chlamydophila pneumoniae AR39, section 21 of 84 of the complets genome
4664		L		L	028350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489		31706			8.8E-01 AF310617.1	N	Pseudorables virus Ea glycoprotein M gene, complete cds
7701	20758		0.69		M81182.1	Ę	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436			1.07	L	8.8E-01 7656978 NT	TN	Homo sapiens cell death-inducing DFFA-Ilke effector B (CIDEB), mRNA
11337	L	38049			Z28337.1	TN	M.asrughosa (HUB 5-2-4) DNA from plasmid PMA1
1	l		7 58			EST HIMAN	oc38h11.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone INAGE:1352037 3' similar to contains Alu repetitive element:contains element MER22 repetitive element ;
12240						N	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
477	L	L		L	İ	N.	Homo sepiens SOS1 (SOS1) gene, partial cds
2475	١.		96.0		5901893 NT	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2938	_	5 29127	5.32		8.7E-01 AA595863.1	EST_HUMAN	nn05ff1.s1 NCI_CGAP_Pr4.1 Homo sepieris cDNA clone IMAGE:1076877
							Pseudomonas aeruginosa topoiscmerase (t/p), putative transcriptional regulatory protein OhbR (ohbR), ortho- habbanaseta 1.2-diovarenses nata-ISP proficio OhbA (ohbA), OhbC (ohbC), ortho-halobenzoata 1.2-
6120	18246	- 10	4.12		AF121970.1	Ē	dioxygenase alpha-ISP protein OhtbB (ohtbB), and put>
8229	1_	34831			AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9130					A1239456.1	EST_HUMAN	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo capiens cDNA done IMAGE:1846786 3'
9130	22209				8.7E-01 AI239456.1	EST_HUMAN	qh38eQ6.x1 Soares_NFL_T_GBC_S1 Hom5 sapiens cDNA done IMAGE:1846786 3'
9339	L		2.07	L	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
10511	23546	37156	1.08		.7E-01 BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'

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	Top Hit Acession Database No. Source	EST_HUMAN	8.7E-01 BF383970.1 EST_HUMAN   QV0-NN1021-100800-337-c03 NN1021 Horito sapiens cDNA	EST_HUMAN	8.7E-01 BF107694.1 EST_HUMAN   601823694R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043664.3'	n AV681898.1 EST_HUMAN AV681898 GLC Homo saplens cDNA clone GLCGYGO7 3'	LN.	EST_HUMAN	Homo saplens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous	LN	Ψ	8.6E-01 X66647.1 NT Chicken lipoprodein lipase gene	TN	polygratein [Coxsackle B4 vinus CB4, hostenitice, E2, originally derived from Edwards CB4 human strain, REDA Complete, 7397 ntl	ž	8.6E-01 AF143732.1 NT Grus caredensis recombination activisting protein 1 (RAG-1) gene, partial cds	NT	NT	INT	NT			NT	EST_HUMAN	IN AL161572.2 NT Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	SWISSPROT	SWISSPROT	5E-01 AJ243213.1 NT Homo eaplens partial 5-HT4 receptor gene, exons 2 to 5	3E-01 AB008799.1 NT Cyanidium caldarium gene for SigC, complete ods	TN	11418543 NT	9507008 NT	4E-01 AF083975.2 INT   Fowl adenovirus 8, complete genome
Piling Park				Г			Γ		TM 050024	2		Γ												EST		Γ					11418543 NT	9507008 NT	
	Most Similar (Top) Hit BLAST E Value	8.7E-01	8.7E-01 E	8.7E-01 E	8.7E-01 B	8.7E-01 A	8.6E-01	8.6E-01 V	i i	8.6E-01 A	8.6E-01	8.6E-01	8.0E-01	8 6E-01 S	8.6E-01 A	8.6E-01 A	8.6E-01 ⊁	8.6E-01	8.6E-01	8.6E-01	8.6E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8.5E-01 F	8.5E-01 F	8.5E-01	8.5E-01	8.5E-01	8.5E-01	8	8
	Expression Signal	1.08	5.87	3.32	3.32	2.8	2.39	3.14		1.51	1.31	10.02	10.02	6	1.96	1.98	9.0	1.82	0.56	45.0	2.11	1.46	1.1	2.36	0.57	0.92	28.0	99.0	1.49	1.49	5.29	6:39	0.68
	ORF SEQ ID NO:	37157	37782	L	L			27123		29875	L	L	L	33042	L	33410	L		34834				33427	34243	34784	L	L	35315					30989
	SEQ ID NO:	23546	24145	25017		25940	13681	14057	,,,,,	_L		L	l	25826		Ι.		21194		L	L	15635	20018	L	21262	L			23593			1	18008
	Probe SEQ ID NO:	10511	11070	12034	12034	12652	487	881		3710	3804	6019	6019	8028	6848	6848	7696	8112	8232	9887	12856	2509	6866	7894	8180	8613	8613	8702	.10558	10558	12577	12585	4873

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ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal BLASTE No. Source	31871 2.75 8.4E-01 L78726.1 NT	31872 2.75 8.4E-01 L78728.1 NT	34553 0.57 8.4E-01 AF061142.1 NT	3.42 8.4E-01 AJ248287.1 NT	26988 2.17 8.3E-01 M93437.1 NT	29347 3.46 8.3E-01 AL161508.2 NT	30069 0.69 8.3E-01 AB010879.1 NT	30273 3.17 8.3E-01 Y19177.1 INT	31464 2.32 8.3E-01 AL161540.2 NT	NVIII IT LOCAL	4 8.3E-01/A1791852.1 EST_HUMAIN	36958 1.32 8.3E-01 AF098070.1 NT	37063 3.9 8.3E-01 AF108133.1 NT		37627 2.18 8.3E-01 AE000903.1 NT	1.66 8.3E-01 7212472 NT Phytophthora infestans mitochondrion, complete genome	38317 8.95 8.3E-01 AF020503.1 NT	28369 2.72 8.2E-01 AB000489.1 NT	1.32 8.2E-01 AF145589.1 NT	0.95 8.2E-01 AW376990.1 EST_HUMAN	30174 0.68 8.2E-01 AB014574.1 NT	30381 0.7 8.2E-01 Z72684.1 NT	30382 0.7 8.2E-01 Z72584.1 NT	31311 1.19 8.2E-01 AB000489.1 NT	33332 0.59 8.2E-01 X95283.1 NT	33333 0.69 8.2E-01 X95283.1 NT	33681 0.76 8.2E-01 AJ010142.1 NT	33595 3.19 8.2E-01 AW379433.1 EST_HUMAN		33986 4.48 8.2E-01 Z12128.1 NT	35258 0.55 8.2E-01 BE263145.1 EST_HUMAN	36856 0.81 8.2E-01 AB014630.1 NT	28807 4 84 8 2F-01 AF052859 1
	31871	31872	34553		26986	29347	ŀ					36958	37063				38317		L													ļ_	
Exan SEQ ID NO:	11 25808	1_		L	L	1	ı	20 17274	ı	1		16 23351	ı	l l	11 23994	<u>L</u>	84 24637	L	L	L	L	47 17393		<b>L</b>	L	L	上		L	7419 25844	8639 21719	23266	L
Probe SEQ ID NO:	56	8	7991	10163	1	31	3912	4	5383		88	103	10423		10911	10930	11684	2111	2158	2744	4	4247	42	5217	67	6781	8	٦		7	8	10231	A9004

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					Billio		
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10428	23463		0.54	8	2E-01 AF223888.1	NT	Oncorhynchus ishawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23463	ĺ	0.54		.2E-01 AF223888.1	TN	Oncorhynchus Ishawytscha Isolata T-20 somatolactin precursor gene, exon 1
10598	23631		3.78	8	2E-01 Q9JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10596	23631			8		SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11942	24928	38631		8	ZE-01 L101Z7.1	NT .	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12030	25013			8	2E-01 P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018					EST_HUMAN	yw14d02.r1 Soares_placenta_8to9weeks_2lylbHP8to9W Homo sapiens oDNA done IMAGE:252195.5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12607	25406	32048	3.01		8.2E-01 AJ001261.1	۲	Mus musculus mRNA for NIPSNAP2 protein
2817	15931				8.1E-01 AF191839.1	LΝ	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	16712	ŀ			8.1E-01 AF055068.1	ŇŦ	Homo septens MHC class 1 region
3547	16712	29724		8.1E-01	.1E-01 AF055066.1	ΝŢ	Homo saplens MHC class 1 region
4730	17866		0.63	8.1E-01	4506290 NT	뉟	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA
_							MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
5825	18015					SWISSPROT	(MELANOCORTIN-1 RECEPTOR) (MC1-F.)
6445	18612		0.89		8.1E-01 U16780.1	NT	Mus musculus putative collagen alpha-2 (XI) chain (COL.11A2) gene, partial cds
6759	19915		2.17	8.1E-01 Q13491	Q13491	SWISSPROT	NEURONAL MEMBRANE CLYCOPROTEIN M8-B
63/9	18915	ŀ	2.17	8.1E-01 Q13491		SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7681	20746		0.7	8	.1E-01 047477	SWISSPROT	CYTOCHROME B
							Drosophile melanogaster putetive inorganic phosphate cotransporter (Picot) gene, partial ods; putative sodium
8085	21177	34693	1.1	8.1E-01	1E-01 AF022713.2	Ę	cialificativa de practica de la productiva del la productiva de la productiva della productiva della product
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium
							channet (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-
8095	21177	34694	1.1	8.1E-01	.1E-01 AF022713.2	N.	enriched protein (gprs) gene, partial cd>
8808	21887			8.1E-01	8.1E-01 AP001517.1	N	Bacillus halodurans genomic DNA, section 11/14
8808	21887	35429	0.91	8.1E-01	.1E-01 AP001517.1	N	Bacillus halodurans genomic DNA, section (17/14
							xn01h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA done IMAGE:2692469 3' similar to SW:LYAR_MOUSE
							Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN.; contains MER22.b1:PTR5 repetitive
8969	22048		1.14	ω.	.1E-01 AW242647.1	EST_HUMAN	element;
10330	23385		0.58	8	1.1E-01 P06425	SWISSPROT	PROBABLE E4 PROTEIN
							KK9972F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to
10623	23667	37267	0.52			EST_HUMAN	ESI(CLONE COPELT)
10769			0.54		8.1E-01 AE001226.1	Į,	Treponema pallidum section 42 of 87 of the complete genome

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Single Exon Probes Expressed in Placenta	Top Hit Descriptor	RCO-TN0080-220800-025-d10 TN0080 Horiro saplens cDNA	RCC-TN0080-220800-025-d10.TN0080 Horino saplens cDNA	Thermotoga maritima section 23 of 136 of the complete genome	Staphylooocous aureus partial pta gene for phosphate actyltransferase allele 15	Bos taurus futb and rtif genes	802072473F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4215091 5'	Saimiri boliwensis olfactory receptor (SBO27) gene, partial cds	Mus musculus gene for oviducial glycoprotein, camplete cds	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit	Mus musculus myosin IXb (Myo9b), mRNA	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA	Rice stripe virus RNA 3 '	QV3-OT0065-280600-250-c09 OT0065 Homo saplens cDNA	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds	CREB-BINDING PROTEIN	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	Ureaplasma urealyticum section 31 of 59 of the complete genome	Homo saplens mRNA for KIAA1452 proteinį partial cds	Haemophilus influenzae Rd section 54 of 163 of the complete genome	Oryctolagus cuniculus mRNA for mitsugumin29, complete ode	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, compilete cds	Gallus gallus SOX8 trenscription factor (SOX8) mRNA, complete cds	601192033F1 NIH_MGC_7 Homo sapiens ¿DNA clone IMAGE:3535785 5'	Mus musculus embigin (Emb), mRNA	Mus musculus embigin (Emb), mRNA	Mus musculus enabled handog (Drosophilia) (Enah), mRNA	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	Chrysomya bezziana pertirophin-48 precursor, gene, complete cds	Humen mRNA for prostacyclin cynthese, complete odo	P.sativum GR gene	Giardia lambila variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds	SMALL HYDROPHOBIC PROTEIN	AV700860 GKC Homo sapiens cDNA clone GKCDRE123'
Exon Probe	Top Hit Database Source	EST_HUMAN	EST_HUMAN	LZ.	NT	NT	EST_HUMAN	. LN	NT	NT	NT	EST_HUMAN	NT	EST_HUMAN	LN	SWISSPROT	Ŋ	F	L	5	Ę	ΤŃ	ÌN	EST_HUMAN	LN	NT	TN	IN	LN	IN	N	NT	NT	SWISSPROT	EST_HUMAN
Single	Top Hit Acession No.			8.1E-01 AE001711.1		8.0E-01 AJ132772.1		8.0E-01 AF127897.1		CB3739.2	7667352 NT	8.0E-01 AW901489.1	8.0E-01 Y11095.1			292793	.9E-01 D11476.1	.9E-01 AE002130.1	.9E-01 AB040885.1	.9E-01 U32739.1	.9E-01 AB004816.1	.9E-01 AF130459.1	.9E-01 AF228664.1	.9E-01 BE263612.1	6753745 NT	6753745 NT	6753753 NT	.9E-01 Z47210.1	.8E-01 Z47210.1	.9E-01 AF139718.1	.9E-01 D38145.1	.9E-01 X90998.1	.9E-01 U01912.1	918719	.9E-01 AV700860.1
	Most Similar (Top) Hit BLAST E Value	8.1E-01	8.1E-01	8.1E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01 XB3739.2	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.8E-01 P19719	7.9E-01
	Expression Signal	2.62	2.62	2.22	2.02	10.2	1.95	1.32	1.29	6.77	<b>-</b>	2.68	1.21	0.48	0.48	1.43	0.75	0.92	28.32	1.06	9.03	4.11	3.67	78.0	0.84	0.84	0.68	0.93	0.93	0.66	0.68	2.68	3.24	5.43	1.17
	ORF SEQ ID NO:	38459	38460	32102		26549		29334	28272	30775	31196		.35338		37483	37802	26697				28603	Ŀ	29784		30852	30853		31325	31326		23003	34903		36887	
	Exan SEQ ID NO:	24764	24764	25221	13404	13516	15233	16322	16557	17791	18224	21281	21802	23660	23860	24287	13681	1	1	14839	15463	15469	16769	17557	17869	17869	18331	ļ	•	18402	19642	21382	22811	23280	ı
	Probe SEQ ID NO:	11772	11772	12303	181	682	2083	3146	3387	4655	2096	8179	8722	10636	10827	11198	466	733	1635	1687	2337	2338	3605	4416	4734	4734	5210	5235	5235	5283	6475	8300	9747	10255	10296

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Table 4
Single Exon Probes Expressed in Placenta

$\vdash$							
Probe SEQ ID 8	SEQ ID NO:	ORF SEQ ID NO:	Expression Signai	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hit Descriptor
10729	23762	37369	0.78	7.9E-01	.9E-01 AB000631.1	TN	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10845	23878			7.9E-01	.9E-01 P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8	24325		1.75	7.9E-01	7662471	NT	Homo capiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	38218	1.84	7.9E-01	7.9E-01 P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
888	14074		1.49	7.8E-01	.8E-01 Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sepiens cDNA done c-1kh04
2349	15480			7.8E-01	.8E-01 AW859567.1	EST HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17956	30942		7.8E-01	.8E-01 U87305.1	INT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271			1	.8E-01 AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Harino sapiens cDNA
6194	19370	32721		1		TN	Sphenodon punctatus alpha enolase mRNA  partial cds
8348	19518	32876	2.28	_	.8E-01 P05231	SWISSPROT	INTERLEUKIN-8 PRECURSOR (IL-8) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
16	19761	33136			.8E-01 AL445066.1	NT TN	Thermoplasma acidophilum complete genomie, segment 4/3
8688	21768	35299		7.8E-01	.8E-01 BF108927,1	EST_HUMAN	7154405.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
봈	22508			7.8E-01	.8E-01 Y10159.1	NT	D.discoideum racGAP gene
9633	22598			7.8E-01	4826873 NT	NT	Homo sapiens nucleoparin 214kD (CAIN) (NUP214), mRNA
10329	23364		1.28	4	.8E-01 Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12671	28033		1.82	7	.8E-01 L28280.1	NT	Arebidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
146	13371	26403	5.78	7	.7E-01 AF184345.1	Ę	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Asipha) dan major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
744	13925			7	.7E-01 AF050157.1	支	butyrophilin-like (N-59), butyrophilin-li>
2776	15892	29003	1.34	7.7E-01	7.7E-01   O33916	SWISSPROT	CITRATE SYNTHASE
3438	16806		0.89	7.7E-01	8383408 NT	Ę	Homo eaplens UDP-N-acetyl-apha-D-galactosamine:polypeptide N-acetylgalactosaminyfransferase 7 (GaINAc-T7) (GALNAC-T7), mRNA
3689	16851	28859		1	.7E-01 AF118085.1	Ę	Homo saplens PRO1975 mRNA, complete ods
4516	17655			_	.7E-01 AF199488.1	F	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
919	17855				7.7E-01 AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32169		7	.7E-01 P16663	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
18	18872	32160	1.39		.7E-01 P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	L	.7E-01 R08600.1	EST_HUMAN	yr24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
10049	23087		0.68		.7E-01 AB021134.1	NT	Daphnia magna hemoglobin gene clusier (dhb3, dhb1 and dhb2 genes), complete cds
12462	25317		7.14	7.7E-01	11497621 NT	ᅜ	Archaeoglobus fulgidus, complets genome

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
6224	19399	32748	5.26	7.6E-01	.6E-01 AF059510.1	IN	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	19399	32749	5.26	7.6E-01	.6E-01 AF059510.1	NT	Arabidopsis thaliana 3-methylorotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6847				7.6E-01	.6E-01 P37838	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
0669			0.74	7.6E-01	.6E-01 AI263399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Home saplens cDNA clone IMAGE.2030879
6890				7.6E-01	-	EST_HUMAN	aq14b12x1 Stanley Frontal NS pool 2 Home saplens cDNA clone IMAGE:2030879
7196	20061	33472	0.84	7.6E-01	.6E-01 U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
3800	21227	39876	V# +	7	AE 04 AE448703 2	. F	Mus musculus neuromedin U precursor (Ninju) gene, partial ods; tPhLP (Tphlp) gene, partial ods; CLOCK (Clock) nene complete ods: PHT27 (PR27) dene complete ods: and H5AR (H5ar) nene complete ods:
300	1			10.1	200000	-	(Verenty gardy order) and the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the compan
2 2 2	ı	34924		7.05-01		2 1	International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Control and International Cont
8218	21400	34925	86.2	/.bE-01		Z	was mascalas gaviiin (Aawi-perang), mova
8520	21601	35137	6.53	7.6E-01	.8E-01 Q01098	SWISSPROT	GLUTAMÁTE [NMDA] RECEPTOR SUBUINIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE: RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35138	0.53	7.6E-01	.6E-01 Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NRZC) (NMDAR2C)
9167	1	36789	1.33	7.6E-01	6753577 NT	NT	Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA
9479				7.6E-01	.6E-01 P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9479	22536			7.6E-01	.6E-01 P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411		7.6E-01	.6E-01 X86347.1	NT	H.aspersa mRNA for neurofilament NF70
11639	24719	38412	2.29	7.6E-01	.6E-01 X86347.1.	NT	H. espersa mRNA for neurofilament NF70
12010	24885		278	7.6E-01	.6E-01 AL161592.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	28157		8.21	7.8E-01	.8E-01 AB020702.1	LN	Homo sapiens mRNA for KIAA0895 protein, partial cds
979	13719		1.31	7.5E-01	.5E-01 AL163301.2	NT	Homo saplens chromosome 21 cagment HS21C101
.597	13787		1.08	7.5E-01	.5E-01 AF020503.1	Ŋ	Homo sapiens FRA3B common fragile regiojr, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7690	20755	34240	9.0	7.5E-01		IN	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12521	25354		5.2	7.5E-01		NT	Homo sapiens dentin statophosphoprotein precursor (DSPP) gene, complete cds
	l						b114b08.x1 NCI_CGAP_Bm25 Home sapients cDNA clone IMAGE:2167577 3' similar to contains Alu
1154	- 1			7.4E-01		EST HOMAN	repetitive element contains element MIR repositive element ;
2419		28676		7.4E-01		LN.	Homo sapiens mRNA for KIAA0534 protein, partial cds
3820	16980		26.0	7.4E-01	.4E-01 AF112538.1	NT .	Malva pusilla actin (Act1) mRNA, complete cds

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Singie Exon Probes Expressed in Pracenta	Top Hit Descriptor	Vibrio cholerae phage CTXchil Calculta-rstR-e (rstR-a) and Calculta-rstR-b (rstR-b) genes, complete cds	Homo sepiens chromosome 21 segment HS21C048	Arabidopsis thailana DNA ohromosome 4, oontig fragment No. 61	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51	602018456F1 NCL_CGAP_Brn67 Homo sapiens cDNA done IMAGE:4154340 5'	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated	EXVIII FON 5730726F1 NIH MGC 19 Home seniens cDNA clone IMAGF 3834174 5	medical and Christian and other form of the contains a DNA clear IMA CE-625207 3' similar to	ZPOTROTIS STREETS ENTROTREET CHI BY 1223 FROME SEPENS COUR CHIEF INTOCHOUSE PASSES 5 STITIGHT IN SWITCHOOL WOUSE PASSES T-COMPLEX PROTEIN 1, THETA SUBUNIT;	Homo sapiens NY-REN-45 antigen (LOC51/133), mRNA	Mus musculus complement component 1 inhibitor (C1nh), mRNA	ta13h01 x1 NCI_CGAP_Lym5 Hamo saptens cDNA clone IMAGE:2043885 3'	Aeropyrum pernix genomic DNA, section 5/7	Borrella burgdorferi (section 52 of 70) of the complete genome	Homo saplens HT017 mRNA, complete cds	Mus musculus antigen (CD72) gene	Mus musculus antigen (CD72) gene	Lycopersicon esculentum mRNA for ubiquitin activating enzyme	D.melanogaster Ohc mRNA for clathrin heavy chain	V.alginolyticus sucrase (scrB) gene, complete cds	V.alginolyticus sucrasa (scr.B) gene, complete cds	2/25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'	2/25508.s1 Soares_fetal_liver_spleen_1NFI.S_S1 Homo sapiens cDNA clone IMAGE:431799 3'	Rattus norvegicus initiation factor-2 kinase (elF-2a) mRNA, complete cds	N: tabacum NelF-4A13 mRNA	Gallus gailus gene for melanocortin 2-receptor, complete cds	Fowlpax virus, complete gename	Giardia Intestinalis variant-speciffo surface protcin (vop417-8) geno, vop417-8/A-1 allole, complete odc	Human mRNA for KIAA0309 gene, partial cds	602035589F1 NCI_CGAP_Bm64 Homo sapiens cDNA done IMAGE:4183222 5'	Homo saplens IA-2 gene, intron 18
Exon Probe	Top Hit Database Source	TN.	NT	TN	NT	EST_HUMAN		NI COT UIMAN	NUMBER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE	EST_HUMAN	LN TN	LN L	EST_HUMAN	NT	NT	LN	NT	IN	IN	NT	NT	Į,	EST_HUMAN	EST_HUMAN	LN	E	NT NT	NT	N	IN	EST_HUMAN	LΝ
Sing	Top Hit Acessian No.	7.4E-01 AF133310.1	7.4E-01 AL163246.2	7.4E-01 AL181551.2	7.4E-01 AL161551.2	7.4E-01 BF346266.1		7.4E-01 UB/860.1	1,4,500.	7.4E-01 AA187988.1	11424933 NT	6763217 NT	7.4E-01 AI472841.1	7.3E-01 AP000062.1	7.3E-01 AE001188.1	7.3E-01 AF225421.1	36772.1	.35772.1	7.3E-01 AJ011418.1	214133.1	7.3E-01 M26511.1	7.3E-01 M26511.1	7.3E-01 AA678019.1	7.3E-01 AA678019.1	29281.1	X79140.1	7.2E-01 AB009605.1	7.2E-01 AF198100.1	7.2E-01 AF065606.1	7.2E-01 AB002307.1		7.2E-01 AF108093.1
	Most Similar (Top) Hit BLAST E Value	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.4E-01		7.4E-01 U8/860.1	2	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.3E-01	7.3E-01	7.3E-01	7.3E-01 L36772.1	7.3E-01 L35772.1	7.3E-01	7.3E-01 Z14133.1	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.2€-01 L29281.1	7.2E-01 X79140.1	7.25-01	7.25-01	7.2€-01			7.2E-01
	Expression Signal	0.71	8.12	1.25	1.25	1.01		45	8.0	1.24	0.7	3.69	1.17	0.73	0.8	2.38	6.6	5.5	0.93	0.69	7.25	7.26	3.29	3.29	1.86	3.43	1.98	1.27	2.36	1.35	1.57	0.73
	ORF SEQ ID NO:	30176	30551	34628		35451		90000		36990	37256				30856	30941	33287	33288		34163	34268	34269	L	38449	Ŀ	28257	28781	28323	29717	29866		
	Exan SEQ ID NO:	17167	17569	21110	21110	21913		27989	1100	22432	23647	26133	25213	17238	17873	17955	19897	19897	26841	20687	20782	20782	24754	24754	14031	15152	15657	18311	16705	16863	17132	17323
	Probe SEQ ID NO:	4010	4429	8027	8027	8834		8910	0070	9357	10813	12170	12287	4083	4738	4822	6741	6741	7243	7817	7718	7718	11714	11714	854	2012	2532	3135	3541	3702	3975	4173

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					i Biris		
Probe SEQ ID SI NO:	Exan SEQ ID NO:	ORF SEO ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4892	18022	31007	2.68	7.2E-01	.2E-01 D90314.1	ᅜ	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
-				1	,		Homo eapiens transcription factor IGHM enthancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,
5225	18347	31317	1.07	7.2E-01	.2E-01 AF 1957/9.1	N	compare cas, and c-type cactum channer at
<u> </u>							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM6 protein, T54 protein, JM70 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,
5225	18347	31318	1.07	7.2E-01	2E-01 AF196779.1	NT	complete cds; and L-type calcium channel a>
5308	18425	31395	0.65		.2E-01 AL181583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
82	20441	33903		_	.2E-01 U69633.1	노	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8648	21728	35265		_	2E-01 AF236061.1	F	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
į.	22241			7.2E-01	2E-01 AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
<u> </u>	23583	37192		1	.2E-01 BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4275381 5'
	24056	37690		_	ZE-01 U82623.1	N	Rattus norvegicus cytocentrin mRNA, complete cds
L	18401	31530	1.51	_	.2E-01 U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
12737	25489		4.37	_	2E-01 AP000063.1	¥	Aeropyrum pernix genomic DNA, section 6/7
12784	26075		1.48	_	2E-01 Y10168.1	N	B.thuringlensis PK1 & cap genes, putative
┞	Γ						Rena catesbelana mRNA for builfrog skeletal muscle calcium release channel (nyanodine receptor) alpha
710	13892	26928	11.37	_	7.1E-01 D21070.1	N	lisoform(RyR1), complete ods
3130	16306	28320	16.1	7.1E-01	7.1E-01 AJ270777.1	M	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
Z	17487	30453	3.07	7.1E-01		LN	Mus musculus otogelin (Olog), mRNA
4324	17467	30454	3.07	7.1E-01	7305360 NT	LN	Mus musculus otogelin (Otog), mRNA
6909	19261	32579	1.73		7.1E-01 BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83
6909	19251	32580	1.73		.1E-01 BF681034.1	<b>EST_HUMAN</b>	602165438F1 NIH_MGC_83 Hamo sapient cDNA clone IMAGE:4296344 5
ı	20182	33606	6,48	_	.1E-01 U36232.1	TN	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds
8934	22013	35552	1.12		7.1E-01 BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Hoino sapiens cDNA
34	22013	35553			.1E-01 BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Hoino saplens cDNA
82	23097	36700				EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10621	23655	37265	1.1	_	.1E-01 M12961.1	N	Human T-cell receptor germline gamma-chtin J2 gene
12505	25935		2.64	_	.1E-01 AA421492.1	EST_HUMAN	Zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	ļ	0.85	7		IN	Homo sapiens mRNA for KIAA0614 protein, partial cds
1267	14416	27480	0.95		.0E-01 AB014514.1	TN	Homo saplens mRNA for KIAA0614 protein, partial cds
25.24	15847		- 20		0F-01 N62412 1	EST HIMAN	yz73e07.s1 Soares_multiple_scierosis_2NtHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Atu recettive element:
7	1	١			1402712.1	10000	

Page 42 of 550 Table 4 Single Exon Probes Expressed in Placenta

Probe   Earn   Opt SEC   Expression   Mides   Shmilar   Top HI Acession   Top HI Devotrice   Top HI Devotrice   Top HI Devotrice   Top HI Devotrice   Top HI Acession   Top			_		_				_		_											_									
Expn NC:         ORF SEQ ID D NO:         Expression Signal Signal         Most Similar I Cab Hit Acession I Cap) Hit I Cab Hit Acession I Signal         Tob Hit Acession I Cap) Hit I Cab Hit Acession I Cab Hit I Cab Hit Acession I Cab Hit I Cab Hit Acession I Cab Hit Acession I Cab Hit I Cab	Top Hit Descriptor	yz73e07.s1 Soares_multiple_sclerosis_2Nbi-IMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;	Hama sapiens chromosame 21 segment HS21C101	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete ods	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, mtlF, and mtlD genes, complete cds	Clostridium acetobutylicum mannitol-specific phosphot ansferase system (PTS) system, mtlA, mtlR, mtlF,	and mtID genes, complete cds	AV763842 MDS Homo capiens cDNA clone MDSCHE04 5'	AV763842 MDS Homo saplens cDNA clone MDSCHE04 5'	Bacterlophage N15 virlon, complete genome	Condida albicans equalene epoxidase (CAERG1) gene, complete eds and translational regulator gene, partial cds	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial	spo	nn28a09.s1 NCI_CGAP_Gas1 Homo saplens cDNA clone IMAGE:1085176 3'	Chlamydia muridarum, section 3 of 85 of the complete genome	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811	601465594F1 NIH_MGC_67 Homo sapient cDNA clone IMAGE;3868943 5'	Branchiostoma belcherl BbNA3 mRNA for notochord actin, complete cds	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'	Strongylocentrotus purpuratus myosin V, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	Arabidopsis thaliana DNA chrcmosome 4, contig fragment No. 69	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds	Musa acuminata pectata lyase 1 (PL1) mRNA, complete cds	601880580F1 NIH_MGC_65 Homo capient cDNA clone IMAGE:4109419 5'	Homo sapiens DAN gene, complete cds	Homo sapiens DAN gene, complete ods	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
Exon NO:         CRF SEQ Signal         Expression (Tay) Hit Vertue         (Tay) Hit Vertue         Top Hit Applie           16647         28771         1.29         7.0E-01         NB2412.1           18251         2.32         7.0E-01         NB22412.1           18251         2.32         7.0E-01         NB22412.1           21654         8.52         7.0E-01         NE00075           22582         38150         0.58         7.0E-01         NF0888.1           24443         38102         1.47         7.0E-01         NF0888.1           24443         38103         1.47         7.0E-01         NF0888.1           24443         38103         1.47         7.0E-01         US988.1           14466         27224         6.3         6.8E-01         US987.4           16696         2949         1.77         7.0E-01         US987.4           16696         2949         1.77         6.8E-01         H7737.3	Top Hit Database Source	EST_HUMAN	ŊŢ	F	NT L	Ę		Ę	EST_HUMAN	EST_HUMAN	LN	F		Ę	-	. LN	NT		ΤN	TN	EST HUMAN	NT	NT	NT	TN	TN	NT	EST_HUMAN	Ν	NT	SWISSPROT
Exon ORF SEQ Expression (Tory) Hit Nost Strailar SEC ID ID NO: Signal Vatue Vatue 18251 28771 1.29 7.0E-01 19256 0.89 7.0E-01 19256 0.89 7.0E-01 24443 38102 1.47 7.0E-01 14495 27252 86.3 6.9E-01 14495 27255 6.3 6.9E-01 14495 27255 6.3 6.9E-01 14495 27255 6.3 6.9E-01 14295 33029 1.12 6.9E-01 19250 33029 1.12 6.9E-01 19250 33029 1.12 6.9E-01 21250 34720 0.85 6.9E-01 22447 3692 36520 0.56 6.9E-01 22447 3692 36520 0.56 6.9E-01 22936 39620 0.56 6.9E-01 24692 38259 2.11 6.9E-01 24692 38259 2.11 6.9E-01 24692 38259 2.11 6.9E-01 24692 38259 2.11 6.9E-01 24692 38259 2.11 6.9E-01 24692 38259 2.11 6.9E-01 24692 38259 2.11 6.9E-01	Top Hit Acesston No.	V62412.1	4L163301.2	AB021316.1	AE000253.1	153868.1		J53868.1	AV763842.1	AV763842.1	9630464	169874.1		J69674.1	AA593530.1	AE002271.2	Y17373.1	BE782751.1	AB035682.1	Y18278.1	BE298188.1	AF248863.1	AL161573.2	AL161573.2	AF118046.1	AF206319.1	AF206319.1	BF242367.1	D89013.1	D89013.1	Q99958
Exon ORF SEQ Express SEC 1D ID NO: Signs NO: 16847 28771 18251 18251 22582 38150 24443 38102 24443 38102 24443 38102 24443 38102 24443 38103 24465 25862 2586 25065 18097 18097 18097 18097 18097 18097 21250 34769 21250 34769 21250 34769 22462 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 38620 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22836 22828 22836 22828 22836 22828 22828 22828 22828 22828 2282	Similar p) Hit AST E	7.0E-01	7.0E-01	7.0E-01	7.05-01	7.05-01		7.0E-01	7.0E-01	7.0E-01	7.0E-01	8 9F-01		6.9E-01	8.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01					6.9E-01	6.9E-01	6.8E-01
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Exan ORF SE SEC ID NO: NO: NO: 14162 272 16866 278 386 24407 380 24437 380 24437 380 24437 380 24893 385 13580 288 15348 284 16058 284 16058 284 16236 286 14820 3318 284 16236 286 14820 3318 284 16058 284 16236 286 14820 3318 284 16058 284 16236 286 14820 3318 284 16058 284 16236 286 14820 3318 284 16058 284 16236 285 14820 3318 284 16058 284 16236 285 14820 3318 284 16058 284 16236 285 14820 3318 284 16058 284 16236 285 14820 3318 284 16058 284 16058 284 16058 285 14820 3318 284 16058 285 14820 3318 284 16058 285 14820 3318 284 16058 285 14820 3318 284 16058 285 14820 3318 284 16058 285 14820 3318 284 16058 285 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3318 14820 3	Expression Signal Signal 1.94 1.43 1.43 1.43 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.97 1.98 1.97 1.98 1.97 1.98 1.97 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 1.98 .	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- I 광명조 12161 41c16181 81억1억1억1억1억1 - 91 - 81 - 61 - 61억1 - 1 - 61억1년1억1억	ਲ D	ORF SEQ Expression ID NO: Signal 27212 1.84 27212 1.84 2.7212 1.84 2.7212 30815 0.62 2.4 38056 2.4 38056 1.97 38594 1.97 28559 30.38 28594 1.97 28559 30.38 28594 1.97 28559 30.38 28594 1.97 28559 30.38 28594 1.97 28559 30.38 28594 1.97 38594 1.97 28599 6.16 282399 6.16 282399 0.62 31894 1.44	ORF SEQ Expression (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO: Signal Acade (Top) His ID NO:	OPF SEQ Expression (Top) Hit Top Hit Acc ID NO: Signal Value RLAST E No. Value 27212 1.84 6.8E-01 AF017784.7 6.8E-01 D00917.1 6.8E-01 D00917.1 6.8E-01 D00917.1 6.8E-01 D00917.1 6.8E-01 AA834475.1 8056 2.4 6.8E-01 AA837636.2 2.4 6.8E-01 AA8376375.1 80050 2.4 6.8E-01 AA8376375.1 80050 2.4 6.8E-01 AF038239.1 80057 2.4 6.8E-01 AF038239.1 80057 2.4 6.8E-01 AF038239.1 80057 2.4 6.8E-01 AF10520.2 80050 30.38 6.7E-01 AF10520.1 AF213884.1 6.8E-01 AF10520.1 AF213884.1 6.8E-01 AF10520.1 AF213884.1 6.8E-01 AF10520.1 AF213884.1 6.8E-01 AF10520.1 AF213884.1 6.7E-01 AF213883.1 6.7E-01 AF213883.1 6.7E-01 AF213883.1 6.7E-01 AF213883.1 6.7E-01 AF213883.1 6.7E-01 AF2138	Most Similar   Top Hit Acession   Top Hit Acession   Top Hit Acession   Top) Hit   Top Hit Acession   Top

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Top Hit Descriptor	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	Gallid herpesvirus 2, complete genome	Gallid herpesvirus 2, complete genome	601660177R1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3905778 3'	601660177R1 NIH_MGC_71 Homo seplens cDNA clone IMAGE:3905778 3'	Pseudomonas aaruginosa PA01, section 167 of 529 of the complete genome	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	Human placental protein 14 (PP14) gene, ccmplete cds	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA	N-ACETYLGLUCOSAMINYL-PHOSPHATIOYLINOSITOL BIOSYNTHETIC PROTEIN GP11	EST48065 Fetal spleen Hamo sepiens cDNA 3' end	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds	Homo capiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds	Homo sapiens sema domain, seven thrombespondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA	Cablcans random DNA marker, 282bp	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haamochromatosis Aut a. u.) gene BoBet name, and soditim photoshate transporter (NDT3) same commiste eds.	Mile milecula Unesia linké choir 9 (VIS) MONA	Mus Hussenson national tight of such a 1002, in the complete menume	Settlement and University of Action 1970 and the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Co	Pseudomonas agruganosa FAO, secular 19/di 329 di una complete ganoma.	AV704700 ADB Homo sentiens cDNA clone/ADBCAE11 5	Homo septems chromosome 21 segment HS21 C078	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds	Mus musculus gane for Tob2, complete cds	Homo sapiens interleukin 10 receptor, alphal(IL10RA) mRNA	Homo saplens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	Phaseotus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
Top Hit Darabase Source	TN TN			EST_HUMAN 6	EST_HUMAN 6	NT	H LN	NT TN		SWISSPROT	EST_HUMAN E	LN	NT			1				T	TOU HOWAN	T	H IMAN					TN.	IN TN
Top Hit Acession No.	6.7E-01 AE001486.1	9635035 NT	9635035 NT	6.7E-01 BE966241.2	6.7E-01 BE966241.2	6.7E-01 AE004606.1	.7E-01 AE001488.1	6.7E-01 M34046.1	6.7E-01 BF354649.1	014357	6.7E-01 AA342521.1	.6E-01 AF075240.1	.6E-01 AF189339.1	4508880 NT	.6E-01 Y07669.1	1000 0000 0000	091320.1	IN //C0000	6.6E-01 AE004436.1	6.6E-01 AE004458.1	6E-01 AV000000.3	8E-01 At 18278 2	SE-04 AL 1418408 4	5E-01 M75140.1	.5E-01 M75140.1	.5E-01 AB041225.1	4504632 NT	.5E-01 AJ272265.1	.6E-01 U28921.1
Most Similar (Top) Hit BLAST E Value	8.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	8.7E-01 014357	6.7E-01	6.6E-01	6.6E-01	6.8E-01	8	0 10 0	9.96-01	0.05-01	0.05-01	6.8E-01	0.05-01	A REDA	A REAL	6.5E-01	6.5E-01	8.5E-01	6.5E-01	6.5E-01	°
Expression Signal	0.79	1.3	1.3	69.0	0.59	3.97	0.94	1.01	2.06	2.75	2.48	76.0	1.13	1.18	4.58	9	2.40	3.02	0.62	0.62	3.7	50.00	. 2.51	202	2,02	5.5	1.73	7.71	2.88
ORF SEQ ID NO:	32594	32983	32984	33304	33306		34042		37900		38649	28819	28989					32330				5000			26849				31268
Exan SEQ ID NO:	19265		_	L	19910	20543	20570		L	Ĺ	Į	16696	15880	]	J		L	19629			⊥	2005	1	1		j	}	ļ	18286
Proba SEQ ID NO:	6083	6453	8453	6754	8754	7468	7495	10348	11196	11748	11859	2570	2765	3578	3748		4220	5402	12/2	7272	7997	0.00	4000	840	640	3519	4148	4397	5174

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					)		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hit Descriptor
5559	25807	31795	. 1	6.6E-01 P18480	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4)
6865	20017	33426	1.3	6.5E-01	3.5E-01 D88348.1	LN	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7760	}		0.74	Ĭ	3.5E-01 X04769.1	NT	Murine ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7846	1		08.0	· 6.5E-01	3.5E-01 AI799882.1	EST_HUMAN	wc48a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321642 3'
10042	23080		0.86	9.5E-01	9.5E-01 T78904.1	EST HUMAN	yd21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10542		37186	2.53	6.5E-01	8.5E-01 AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10889	23954	37583	2.55	1	8.5E-01 H87583.1	EST_HUMAN	yw17708.r1 Soares_placenta_8tb9weeks_2NoHP8to9W Homo sapiens cDNA clone IMAGE:252515 5
10925			2.98		8.5E-01 AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo saplens cDNA clone IMAGE:1100748 3'
11030	L				3.5E-01 AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo septens cDNA clone PLACE1007810 5
. 11800	<u> </u>	28.88	R 43	6.5F-01	8 5F-01 AF014115.1	Ė	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12568	L	L				EST HUMAN	hv74a10.x1 NCI_CGAP_Lu24 Homo sepients cDNA clone IMAGE:3179130 3'
12840	L		3.83			FN	S.cerevisiae chromosome IV reading frame QRF YDL097c
282	L	26613			6.4E-01 U48848.1	ĮŅ.	Drosophila melanogaster 8kd dynetn light chain mRNA, complete cds
3545	16710	29721	4.42		6.4E-01 U48854.2	IN	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3984	17122	30126	1.48		8.4E-01 AB046827.1	NT.	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30731	0.74		6.4E-01 Y12488.1	Ψ	M.muscalus whn gene
4814	17751	30732	0.74		8.4E-01 Y12488.1	M	M.muscalus whn gene
8812	L	36432	1.58		AE0012	占	Treponema pallidum section 63 of 87 of the complete genome
10221	23257		9.0		11418320 NT	M	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10294	23329	36933	7.31	6.4E-01	6.4E-01 U82828.1	L	Homo sapiens ataxia telangiectasia (ATM) gane, complete cds
10309						EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens/cDNA clone IMAGE:4291128 6
12693	25461		19.53		12.1	EST_HUMAN	AV759212 MDS Homo sepiens cDNA clone/MDSCGC09 5
44	13843	26682	3.76			SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
548	13741	28765	1.85		6.3E-01 U32689.1	. TN	Haemophilus influenzae Rd section 4 of 183 of the complete genome
2230	15364	28493	3.29		6.3E-01 U81136.1	NT	Shigella fleweri multi-antibiotic resistance focus
2646	15769	28884	3.65		6.3E-01 U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2646	15769				6.3E-01 U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16257		0.63		6.3E-01 Y17275.1	뒫	Lycopersicon esculentum p69a gene, complete CDS
6189	19365	32713	0.84		6.3E-01 BE093906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Horno sapiens cDNA
6733					6.3E-01 L27798.1	뒫	Streptococcus dysgalactiae (mag) gene, complete cds
6733	19889	33282	1.01		[27798.1	보	Streptococcus dysgalactiae (mag) gene, complete cds

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					III III	EXOLI LIONG	Single Extra Flobes Expressed in Fracelina
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8718	21798		3.44	6.3E-01	6.3E-01 BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3959351 5'
9087		35712		6.3E-01	\$62927.1	NT ·	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9421		36062	0.65	6.3E-01	BF21698	EST_HUMAN	601884050F1 NIH_MGC_57 Hamo saptens oDNA clone IMAGE:4102596 5
9620	L.	36245	3.14	6.3E-01	1N 1257288	TN	Variola virus, complete genome
9620	22675	38248	3.14	8.3E-01	9627521 NT	NT	Variola virus, complete genome
10142			0.68	6.3E-01	6.3E-01 AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10641	L	37285	1.59	6.3E-01		NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10747	L	37393	1	6.3E-01		TN	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	6.3E-01 AW795395.1	EST_HUMAN	PMC-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
44046			4 78	8 3E 04	0.08777745.1	EST HIMAN	nroghoßist NCI_CGAP_Co10 Hamo sapien's cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLARK :
11820		İ		63E-01	6.3E-01 Al904160.1	EST HUMAN	CM-BT043-090299-046 BT043 Homo sapiens cDNA
11709				6.3E-01 P47003	l	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11888	L			6.3E-01		SWISSPROT	HYPOTHETICAL 15,3 KD PROTEIN IN VIMA12-APN1 INTERGENIC REGION
12086	ŀ			6.3E-01	9838361 NT	N	Beta vulgaris mitochondrion, complete genome
12262	ŀ	31548	15.92	6.3E-01	9910283 NT	TN	Mus musculus keratin complex 2, gene 5g (Krt2-5g), mRNA
12358	. 25257		1.6	6.3E-01	6.3E-01 AF105227.1	L	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12582	L		4.27	6.3E-01	6.3E-01 X83528.1	ΙN	C.limicola pscD gene
5991		32497	2.15	6.2E-01	6.2E-01 Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7664	20731			6.2E-01	6.2E-01 AF022253.1	NT	Mus musculus calclum-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7715	25852	34288	1.16		AL021127.2	Į.	Mus musculus chromosome X contigA; putritive Magea9 gene, Celtractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8497	1				6.2E-01 H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2135423'
1000	l	ŀ	0		8 7E 04 AE034444 4	5	Lycopersicon esculentum cytosclic Cu,Zn supercodde dismutase (Sod) gene, partial cds; and dehydroquinate dehydroquinate dehydroquinate.
2000	200	34608	,		A 25-01 AF 0344 11.1	EST HIMAN	601336146F1 NIH MGC 44 Homo saplents oDNA clone IMAGE:3690010 5
8040	Т				8 25 04 M24484 4		Human pulmonary surfactant-essociated protein SP-B (SFTP3) mRNA, complete cds
OL/A	1				A 404544 0	L.	Azabidoneis theliana DNA chromosoma 4 conflictraciment No. 23
10283	23318	36919	6.83		6.2E-01 AL161511.2	Ž	אל מתחקום בי היים ביותר ביותר בי בי בי בי בי בי בי בי בי בי בי בי בי
10426	23461	37067	0.63	6.2E-01	11420783 NT	FZ	Homo sapiens potassium voltage-gated chennel, Shab-related aubfamily, momber 1 (KCNB1), mRNA
10426	23464	37068	0.63	6.2E-01	11420793 NT	TN	Homo sepiens potessium voltage-gated cheinnel, Shab-related subfamily, member 1 (KGNB1), mRNA
10758	23789	37405	5.75	6.2E-01 P27410	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesston No.	Top Hit Database Source	Top Hit Descriptor
10758	23789	37406	5.75	6.2E-01	8.2E-01 P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
2468			6.27	6.1E-01	6678076 NT	١	Mus musculus secreted acidic cysteine rich glycoprotein (Sparo), mRNA
5653	l	ŀ	1.33	6.1E-01		F	Cænorhabdilis elegans N2 CeMyoD (hih-1) alternatively spliced genes, complete cds
2009	20145		3.4	6.1E-01		TN	Rat TRPM-2 gene, complete cds
7009	ı		3.4	6.1E-01	6.1E-01 M64733.1	ΙN	Rst TRPM-2 gene, complete cds
7160	20283	33736	0.67	6.1E-01	6.1E-01 AW105663.1	EST_HUMAN	xd50h03.x1 NCI_CGAP_0v23 Homo saplejrs cDNA clone IMACE:2597237 3° similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7254	l		0.69	6.1E-01	6.1E-01 Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041		6.1E-01	35.1	۲	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
9668	1		1.51	6.1E-01	11431065 NT	N	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
8995		35613	1.51	6.1E-01	11431065 NT	LN	Homo saplens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
8615	<u>'</u>		20.44	6.1E-01	6.1E-01 AF236117.1	LN	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9615			20.44	6.15-01	6.1E-01 AF236117.1	N	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36688	1.05		8.1E-01 AE004462.1	TN	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
10252	23287	36883		8.1E-01	8.1E-01 AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cos
10833	23866	37489	0.47	6.1E-01	6.1E-01 AF026993.1	TN	Sus scrofa neural cell adhesion malecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38718	1.77	6.1E-01	6.1E-01 S83182.1	FZ	hyaluronan-binding protein=hepatocyte grov/th factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25018	38719	1.77	6.1E-01	6.1E-01 S83182.1	ᅜ	hyaluronan-binding protein=hepatocyte grov/th factor activator homolog [human, plasma, mRNA, 2408 nt]
13062	25695		1.16	6.1E-01	X95287.1	NT	M.mazel orfA, orfB, and orfC of archaeal ABC-transporter system
507	13701	26730	1.79	6.0E-01	6.0E-01 D87675.1	NT	Hamo sapiens DNA for emyloid precursor protein, complete ods
575			4.74	8.0E-01	TN 66623939 NT	NT	Home sapiens adapter-related protein compilex 3, mu 2 subunit (CLA20), mRNA
1393				6.0E-01	6.0E-01 AF065253.1	L'	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3917	17078				6.0E-01 AJ233396.1	L	Viral hemorrhagic septicemia virus N, P, Mi G, Nv, L genes, French strain 07-71
4305	17448		1.26		8.0E-01 AF058895.1	LN	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5655	18597	31567	1.96		6.0E-01 P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753		2.5		6.0E-01 AW139713.1	EST_HUMAN	UI-H-Bi1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6999	19828	33216	2.74		6.0E-01 U38813.1	NT	Musca domestica insecticide susceptible strain voltage-sensitive sodium channel mRNA, complete cds
9800	19966	33355	0.68		6.0E-01 Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD138 ANTIGEN)

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					יונים י	באינו דוטאק	Single Extri Flores Explessed III Flaverina
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Sœurce	Top Hit Descriptor
6955	20268	33705	0.77	6.0E-01		NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
9369	ı	L	77.0	6.0E-01		NT	Strongylocentrotus purpuratus kinesin light chain Isoform 2 mRNA, complete cds
7509	1		6.49	6.0E-01		NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	1	L	4.15	6.0E-01	6.0E-01 P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315			4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028		36684	1.57	6.0E-01	6.0E-01 AB008193.1	NT	Homo sepiens genes for leukotriene B4 receptor BLT2, laukotriene B4 receptor BLT1, complete cds
10480			1.04	6.0E-01 Q01497	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10594	23629		19.0	6.0E-01	BE837779.1	EST HUMAN	RC2-FN0094-190700-017-d08 FN0094 Homo saplens cDNA
11312	L_		1.38		AJ131892.1	۲	Gallus gallus mRNA for Hyperion protein, 419 kD isotorm
11312	Ŀ	38022	1.38		6.0E-01 AJ131892.1	NT	Gallus gallus mRNA for Hyperlon protein, 419 kD Isoform
11848	L		2.74	6.0E-01	AI420623.1	EST_HUMAN	#08/07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3
12663		32052			11421663 NT	. 1	Homo capiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mKNA
12781	25523		1.46		AA706087.1	EST_HUMAN	298g05.s1 Soares fetal liver spicen 1NFUS S1 Homo sapiens cDNA clone IMAGE:452770 3
12953	ı		1.44	6.0E-01	5803136 NT	LN T	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12998	25963	31788	5.46		B055303 NT		Mus musculus cGMP-Inhibited phosphodiesterase (Pde3a), mKNA
13032	ı		8.12		BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sepiens cDNA
1025	1	1			5.9E-01 U32701.1	ΝΤ	Haemophilus influenzae Rd secton 16 of 163 of the complete genome
3343	16518				AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	1	29531		L	5.9E-01 AL163267.2	NT	Hamo sapiens chromosome 21 segment HS21C067
	1				2000	Ę	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cyte
3916	6/0/1	30007			AF182756 1	F	Rettus norvegicus cenexin 2 mRNA, partial cds
5280	1	31374	0.65	1	5.9E-01 AF026566.1	E	Ovis aries SRY gene promoter region
7038	1				4 9F-04 AF085440 2	L	Home saplens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33962			5.9E-01 AB023486.1	TN	Homo sepiens gene for histamine H2 receptor, promoter region and complete cds
7558	1			L	5.9E-01 X68801.1	N.	G.gallus gene for skeletal alpha-actinin, excn EF2
8188	ı				.9E-01 D90911.1	LN	Synechacystis sp. PCC8803 complete gename, 13/27, 1576593-1719643
8839	ı	35456	0.48	မ	.9E-01 D12922.1	IN	Legionella pneumophila gene for iron superioride dismutase, complete cds
9743	ĺ	36385		L.C	.9E-01 AF063204.2	NT	Chlamydla trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete ods
1917	<u> </u>	l	0.84	ľ	.9E-01 P06463	SWISSPROT	E6 PROTEIN
10391	1 23426	3 37033			5.9E-01 P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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					,		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10908	23991	37624	2.24	6.9E-01 Q9X0(3	Q9X0l3	SWISSPROT	THYMIDYLATE KINASE (DTWP KINASE)
10916	23999	37632	1.71	5.9E-01	AF197944.1	IN	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete ods
11203	24272		2.76	5.9E-01	5.9E-01 AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Hano saplens cDNA
11469	24528		1.98	6.95-01	5.9E-01 AF064626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.78	5.9E-01	5.9E-01 L42320.1	NT	Orycidagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549	25372		1.92	6.9E-01	6.9E-01 AB017705.1	NT	Aspergillus oryzae pyrG gene for crobdine-5", phosphate decarboxylase, complete cds
12789	25533		4.82	5.9E-01 P34926	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101		1.28	5.8E-01	5.8E-01 P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_58 Homo septens;cDNA clone IMAGE:4076131 5
4637	17773	30753	3.59	5.8E-01	5.8E-01 AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphalase, complete cds
4917	18047		2,22	6.8E-01	5.8E-01 AF110846.1	NT	Megaselia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5490	18689		1.02	5.8E-01	5.8E-01 AE002152.1	IN	Ureaplasma urealyticum section 53 of 59 of the complete genome
5848	18842	32123	0.81	5.8E-01	5.8E-01 Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.8E-01	5.8E-01 D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFtjiwara) Homo saplens cDNA clone GEN-500E06 5'
6442	18609		0.58	5.8E-01	5.8E-01 D50801.1	NT	Shigella sannal DNA for 28 ORFs, complete cds
6952	20265		2.37	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprobain [rats, mRNA, 1030 nt]
				Lo	7 7 6 7 7 7	140741171 1100	yri91503.s1 Soares adult brain N255HB557 Homo saplens oDNA clone IMAGE:175757 3' similar to
ŝ	2 2		707	0.00	05-01   14   15/ 1   1	NICALO I CU	SECTION OF THE TOTAL PROPERTY OF THE WAY CHARGOSTON
8278	21360		0.08	5.8E-01	5.8E-01 AI280051.1	EST_HUMAN.	–, јг
8278	21360		0.68	5.8E-01	AI280051.1	EST HUMAN	qn85610x1 Sogres, NFL   _GBC_S1 Hamp sepiens cLINA Glane IMAGE: 1853 / 18 3
. 8385	21466		2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8385	21466	34992	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8092	22171	_	10.4	5.8E-01	5.8E-01 AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9172	22250		1.23	5.8E-01	027368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9173	22251	35794	0.57	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F48F2.2 IN CHROMOSOME X
92.6	22835		62.0	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5
11237	24306	37943	7.26	5.8E-01	AJ243213.1	NT	Homo saplens partial 5-HT4 receptor gene, exons 2 to 5
11291	24357		3.36	6.8E-01	6.8E-01 BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sepiens cDNA clane IMAGE:4284403 5'
11407	24468		1.44	5.8E-01	5.8E-01 BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6755253 NT	INT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3205	16469	29488	1.46	5	7E-01 Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3593	16757		2.84	ທ	7E-01 AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1;aminocyclopropane-1-carboxylate synthase, complete cds
RABE	10652	33014	441	5 7E-01	5.7E-01 BF035413.1	EST HUMAN	601454962F1 NIH MGC 68 Homo saplene cDNA clone IMAGE:3858590 5'
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					18.5		Single Lyones Lybrosod in Fracelina
Probe E SEQ ID SI NO:	Exon O NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	20003	33412	0.92	5.7E-01	.7E-01 AA194201.1	T_HUMAN	z/38c06.r1 Soares_NhHMPu_S' Homo sapiens cDNA clone IMAGE:665674 5'
L.	18519	31512	1.15		3.7E-01 AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
L_	20991	34501	1.88	Ì	5.7E-01 P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
L	21239		0.55	ì		NT	Mus musculus Kong1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
	23042	36634	1.13	1	5.7E-01 AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
L	23042	36635	1.13	1			Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37481	0.91	5.7E-01	5.7E-01 BF540962.1		602067712F1 NIH_MGC_58 Hano sapiens cDNA clone IMAGE:4066810 5
L	25192		1.29		5.7E-01 BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-802 HT0736 Homo saplens cDNA
	25675		1.31	5.7E-01		EST_HUMAN	601654814R1 NIH_MGC_57 Homo saplent; cDNA clone IMAGE:3839763 3'
<u> </u>	16817	29635	1.1		5.6E-01 AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	28636	1.1		5.6E-01 AB018283.2	NT.	Homo seplens mRNA for KIAA0740 protein, partial cds
l	17140	30152	0.59		5.6E-01 AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
	17497	30476	77.0	5.6E-01	5.6E-01 D83135.1	NT	Chicken TBP gene, exan8, complete ads
5006	22082	35625	4.11	5.8E-01	5.8E-01 AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
	22082	35626	4.11	5.6E-01	5.6E-01 AV684703.1	EST_HUMAN	AV684703 GKC Homo saplens cDNA clone GKCFSF05 5'
L	227.17	36285	1.13		5.6E-01 AB038782.1	NT	Homo sepiens MUC3A gene for intestinal much, partial cds
_	25123		7.84		5.6E-01 BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Hcmo sapiens cDNA clone IMAGE:3915457 5
L							ng75g10.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7
12272	25204	38362	1.39		5.6E-01 AA493535:1	EST_HUMAN	repetitive element;
12661	17146	30152	2.38		Я.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
_	25460		2.66		6.6E-01 P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
L	25758		3.64		5.6E-01 BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4271334 5
	14397	27459		5.5E-01	8393912 NT	ΙΝ	Rattus norvegicus Propicnyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
						1	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL
2766	15881	28890	8.3		5.5E-01 P03341	SWISSPROT	PROTEIN P30; NUCLEOPROTEIN P10]
	ļ	·	,		770000	Todasinis	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL DEOTEIN PAGENI ICE FORROTEIN P401
2766	15881	28991			103341	SWISSPRO	VIOLUTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
2986	16161	29178	1.17		5902085 NT	ħ	Homo saplens superkiller viralicidic activity 2 (5. cerevisiae nomotog)-like (5. NV2L), mikivA
3134	16310		1.57		5.5E-01 H48219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178265 3
3308	16480	29501	2.93		5.5E-01 AF227240.1	Ę	Rabbit oral papillomavirus, complete genome
3783	16944	29951	1.34		5.5E-01 P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
6249	18370		1	5.5E-01	5.5E-01 AF063866.1	LN.	Melanoplus sangulnipes entomopoxvirus, complete ganome
2269	18388	31356	1.01		5.5E-01 U69097.1	Ę	Bos faurus MHC class II beta-chain BoLA-(VIB1 gene, partial cds

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		cds; PT2),	ods; PT2),						RNA	RNA	enes,		gres,									~~ ~				T	
Single Extil Flobes Expressed III Flacenia	Top Hit Descriptor	Mts musculus major histocompatibility locus class ill region:butyrophilin-like protein gene, partial cds; Notch4, PBXQ, RAGE, lysophatidio acid acyl transferase-alpha, palmitoy-protein thloesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex	Mus musculus major histocompatibility locus class III region:butyrophilin-tike protein gene, pertial cds; Notche, PBX2, RAGE, tysophetidic acid acyl transferase-alpha, palmitoyi-protein thioesterase 2 (PPT2), PREB, PP, and tensecin X (TNX) cenes, complex.	Carassius auratus gene for gonadotropin II beta subunit, complete cds	QV3-HT0468-170200-090-b05 HT0458 Homo sapiens cDNA	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds	[EST02935 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCQ35	601811077R1 NIH_MGC_48 Homo saplens cDNA clone IMAGE:4054003 3	Homo capiens KIAA0929 protain Msx2 interacting nuclear target (MINT) hamolog (KIAA0929), mRNA	Homo sepiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Pseudomonas syringae pv. tometo strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes,	complete ads; and unknown genes	Pseudomonæs syringae pv. tometo strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes	QV4-NN0040-070400-160-c04 NN0040 Homo saplens cDNA	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome	Drosophila melanogaster mRNA for 15,151 bela carotene dioxygenase (beta-diox gene)	PM2-CN0030-030200-003-c10 CN0030 Homo saplens cDNA	Rattus norvegicus gene for TIS11, complete cds	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3	S.cerevisiae RIB3 gene encoding DBP synthase	S.cerevisiae RIB3 gene encoding DBP synthase	MITOCHONDRIAL TRIFUNCTIONAL ENEYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENDYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA	DEHYDROGENASE]	602076545F1 NIH MGC 62 Home capients cDNA clone IMAGE:4243590 3	NITRATE REDUCTASE (NADPH) (NR)	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAV) COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COMIN OF THE COM	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEXOSIN PEXVI CHAIN)
EXOIL FIORE	Top Hit Database Source	ΝΤ	Ė	5 5	EST_HUMAN	N	EST HUMAN	EST_HUMAN	Z	Ę	!	Ę	LN	EST_HUMAN	NT	TN	EST_HUMAN	NT	EST_HUMAN	ΤN	TN		SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT
ignic	Top Hit Acesslan No.	5E-01 AF030001.1	4 A C C C C C C C C C C C C C C C C C C	APO15596 1	5.5E-01 BE163243.1	U88415.1	T05047.1	BF129507.1	7 <del>05</del> 7266 NT	7657266 NT		4E-01 AF232008.1	4E-01 AF232006.1	4E-01 AW896087.1	4E-01 AE002247.2	4E-01 AJ276682.1	.4E-01 AW842327.1	5.4E-01 AB025017.1	5.4E-01 BE988592.2	4E-01 Z21619.1	.4E-01 Z21619.1		Q64428	5.4E-01 BF572536.1	.4E-01 P36858	.4E-01 Q60675	3.4E-01 Q60675
	Most Similar (Top) Hit BLAST E	5.5E-01	i i i	9.00.0	5.5E-01	5.5E-01	5.5E-01	6.6E-01	5.4E-01	6.4E-01		5.4E-01	6.4E-01	5.4E-01	5.4E-01		5.4E-01	5.4E-01	5.4E-01	5.4E-01	5.4E-01		5.4E-01 Q84428	5.4E-01	ι.		5.4E-01
	Expression Signal	0.59		0.09	0.47	0.56	0.83	1.64	8.11	8.11		1:01	1.01	2.21	2.8	2.82	0.83	0.83	0.77	1.98	1.98		1.47	2.69			2.76
	ORF SEQ ID NO:	33950		1688	35291		37230			26405		26808	26809			28594							34039				
	Exon SEQ ID NO:	20483	ŀ	20463	1	1	ı	24467	Į.	13372	1	13788	13788	l.		ı		ı	i	ı	1	<u> </u>	20567	ı	24387	i I	24908
	Probe SEQ ID NO:	7405		7405	8676	6966	10588	11408	147	147		298	88	1300	2473	2329	5774	6320	7170	7490	7490		7492	10195	11334	11920	11920

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Probe SEQ ID NO:	SEO D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2213	15347	28476	2.85	5.2E-01	5.2E-01 AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16364	29369	21	5.2E-01		NT	Chiamydophila abortus strain S26/3 POMP9/1A and POMP90A precursor, genes, complete cds
3309			1.05	6.2E-01	6.2E-01 D73443.1	NT	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds
3491			1.61	5.2E-01	5.2E-01 AL116780.1	IN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3530	16695	29706	2.01	5.2E-01	5.2E-01 AA984165.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:1616504 3'
373	l		74.0	5 2F-01	5 2F-01 AF020269 1	, <u>F</u>	Medicago sativa chloroplast malate dehydrogenase pracursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
7							Homo sepiens chromosome Xo28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
							(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin
3724	16885	29891	0.87	5.2E-01	,	NT	(CALT), NAD(P)H dehydrogenase-iike prote/n (NSDHL), and LI>
4729	ł	30846	0.61	5.2E-01	52947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5770	18962	32263	0.92	6.2E-01	.1	EST HUMAN	zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9932		36562	0.87	5.2E-01	5.2E-01 X02218.1	TN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9832		36563	0.87	5.2E-01		NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	<u>!_</u>	38772	0.49	5.2E-01	5.2E-01 AA194518.1	EST_HUMAN	zq05b09.r1 Stratagene muscle 937209 Homo saplens cDNA clone IMAGE:628793 5'
10233	23268	36858	1.32	5.2E-01	5.2E-01 AF143952.2	IN	Homo sapiens PELOTA (PELOTA) gene, complete cds
131.08	<u> </u>		483	5.2F-04	5 2F-01 P18516	TORISSIMS	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR- DELTA)
2	1	26B44	2.5	5 1F-01	-	Ę	Human adrenodoxin reduciase gene, exons 3 to 12
199		26878	ľ	5.1E-01	2	¥	Polyangium vitellinum (strain PI vt1) 16S rRt\A gene
965	1	26879		5.1E-01	5.1E-01 AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1684			1.02	5.1E-01	5.1E-01 X87885.1	TN	R norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	5.1E-01 AI858495.1	EST_HUMAN	w39b12x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2427263 3'
4303	17446	30432	2.89		5.1E-01 P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5179	L		9.0		5.1E-01 BE091796.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo saplens cDNA
6352	l	32879	-	6.1E-01	5.1E-01 BE541088.1	EST HUMAN	601063808F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5
8408	19575		6.0		5.1E-01 AV712326.1	EST HUMAN	AV712326 DCA Homo saplens cDNA clone DCAAUF07 5
¥ 7067		33528	1.35		5.1E-01 R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo septens cDNA clone IMAGE:1468723'
8770		35389	0.84	5.1E-01	5.1E-01 AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-e01 ST0023 Hoino sapiens cDNA
8770					5.1E-01 AW806881.1	EST HUMAN	QV4-ST0023-160400-172-e01 ST0023 Homo capiens oDNA
9886		36510	4.85		5.1E-01 J05412.1	M	Human regenerating protein (reg) gene, complete cds
6886	22829		36.6		5.1E-01 W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp5091-cleaved sublibrary Homo saplens cDNA not directional
10363	ı				5.1E-01 M94579.1	F	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25874		3.49		5.1E-01 BF030207.1	EST HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828767 5

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					igno	באסוו ו וכמס	
Probe SEQ ID (9 NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6161	18337	32682	2.67	4.9E-01	.9E-01 AF020831.1	TN	Homo saplens diacylglycerol kinase 3 (DAGI(3) gene, exon 10
6161	18337	32683	2.67	4.9E-01		IN	Homo saplens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7610	20680	34156	1.61	4.8E-01	.BE-01 AB040051.1	IN	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934		0.86	4	.9E-01 Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934		0.88	7	.9E-01 Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9180	22268		1.96	4	9E-01 BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Hamo saplens cDNA clane IMAGE:4102503 5'
				:			hc90c02x1 Soares_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE:2807286 3' similar to TR:095714
9389	22484	36028	J	4	AW339	905.1 EST_HUMAN	096714 HERC2 ;
9486	26228		2.2		10946863	F	Mus musculus uno13 homolog (C. elegans)/1 (Uno13h1), mRNA
10524	23559	37166	1.05		4.9E-01 AF053880.1	NT	Mus musculus adenyly cyclase 1 (Adcy1) clDNA, partial cds
12197	25154		2.61	4.9E-01	4.9E-01 AF176912.1	NT	Homo saplens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
13085	28174		4.94	7	.DE-01 AA613582.1	<b>EST_HUMAN</b>	nq22e11.s1 NCI_CGAP_Co10 Home saplens cDNA done IMAGE:1144652 3'
13094	25714	31939	1.69	4	.9E-01 AL163301.2	Į,	Homo sapiens chromosome 21 segment HS21C101
13181	25788		1.27	4.9E-01	11431438 NT	١	Homo espiens eukaryotio translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4452	17502		0 69	10-E8-01	4504850 NT	LV.	Homo sepiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
							Construction of the second second second (CDO44) are a construct for majoric manufactor
5624	18818	31892	9.66		4.8E-01 J02987.1	Į.	oscoristottiyos cerevisses) sporuseuon procein (ar o'i') gene required to menore recommisseo), compressods
6817	19970	33378	0.69	4	.8E-01 U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Trint1) gene, complete cds
6827	18980			4	.8E-01 AA659878.1	EST HUMAN	nu85f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7469	20544		1.83	4	5031650 NT	NT	Homo sapiens reproduction 8 (D8S2298E) inRNA
7845	2000	34403	1.06	·	1.8E-01 AL163209.2	N	Homo sapiens chromosome 21 segment HS21C009
7938	20388		3.69	4	.8E-01 AL161492.2	F.	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7938	20988		3.59	4	.8E-01 AL161492.2	F	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
							y77110 y5 Sogres breast 2NbHBst Homo saplens cDNA clone IMAGE:154785 6' similar to contains element
808	21171	34686	1.81	_		EST_HUMAN	MER8 repetitive element ;
9448	22562		1.05		1.8E-01 BE155148.1	EST_HUMAN	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
10212	23248		0.55	4	.8E-01 BF568633.1	EST_HUMAN	602184267F1 NIH_MGC_42 Homo saplens cDNA clone IMAGE:4300048 5'
10966	24047		1.9	4	.8E-01 X83502.1	IN	S.cerevisiae ORFs from chromosome X
12279	25208		1.56	4	.8E-01 AL163227.2	M	Hamo sapiens chromosome 21 segment H\$210027
12509	25918		5.78	4	.8E-01 AF227568.1	M	Trypanosoma cruzi transposon VIP II SIRE repoat region
3142	ı		65.0	7	.7E-01 AF192387.1	NT	Felis catus feline leukemia virus subgroup. C receptor (FLVCR1) mRNA, complete cds
6644	19803	33190	8.07	*	.7E-01 BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7186	. 20051		0.84	4	.TE-01 AI204374.1	EST_HUMAN	qf72a09xf Scares_testis_NHT Homo sepiens cDNA clone IMAGE:1755544 3'

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Top Hit Descriptor	hbe811 Human pancreatic islat Homo sapieris cDNA clone hbc811 Send hbc811 Himan pancreatic islat Homo sapieris cDNA clone hbc811 Send	Raftus norvegicus Spermine binding protein (Sbp), mRNA	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds	RC6-NT0029-240400-011-E08 NT0029 Homo saplens cDNA	601511333F1 NIH_MGC_71 Hcmo sapiens cDNA clone IMAGE:3912488 5	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'	602081103F1 NIH_MGC_81 Home septens cDNA clone IMAGE:4245481 5'	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5	601900234F1 NIH_MGC_19 Hcmo sapiens cDNA clone IMAGE:4129472 5'	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'	INTERFERON REGULATORY FACTOR 3 (IRF-3)	INTERFERON REGULATORY FACTOR 3 (IRF-3)	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5	ph59h02.x1 Sources fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:1849011 3' similar to	IK:O18338 O1838 BU I ROFFILIN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR-015338 Q15338 R1TVRODHII IN	MEIOSIS SPECIFIC PROTEIN HOP	Anolis schwartzi cytochrome b gene, partial cds. mitochondrial gene for mitochondrial product	PM0-BN0260-120600-001-F07 BN0260 Homo sepiens cDNA	Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the	complete genome	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein,	complete cds	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein,	complete cds	Murine cytomegalovirus e1 protein gene, complete cds	nh04h05.s1 NCI_CGAP_Thy1 Homo capicins cDNA clone IMAGE:943363 cimilar to contains Alu rapatitive	element, contains element L i openiwe element.	602130953F1 NIH MGC 36 Homo Sapiens CUNA Crone IMAGE: 4267826 3	co76b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 AUP-RIBOSYLATION FACTOR 4 (HUMAN);
Top Hit Database Source	П	NICANOL II		T	EST_HUMAN RC	EST_HUMAN 60			EST_HUMAN   60		EST_HUMAN 60		SWISSPROT IN	EST_HUMAN 60	-	EST HUMAN	HP NAME TO TOO	T	Τ	T HUMAN		NT CO	5	NT			NT TN		Т	EST_HUMAN 60	EST_HUMAN RI
Tap Hit Acessian No.	1.7E-01 T11414.1	3981501	1.7E-01 AF102673.1			4.7E-01 BE887763.1	_			4.6E-01 BF313593.1	4.6E-01 BF313603.1	4.6E-01 Q90643		4.6E-01 BE734781.1		4.8E-01 AI247679.1	A 01047010 4	P20050	24.1			4.8E-01 AE000894.1		4.6E-01 U62332.1			4.6E-01 L07320.1		4.6E-01 AA4935/7.1	4.6E-01 BF697389.1	4.6E-01 AA932237.1
Most Similar (Top) Hit BLAST E Value	4.7E-01	4.7E-01	4.7E-01	4.7E-01	4.7E-01	4.7E-01	4.7E-01	4.6E-01	4.6E-01	4.6E-01	4.6⊑-01	4.6E-01	4.6E-01	4.6E-01		4.8E-01	in a	4.6E-01 P20050	4 GF-01	4.6E-01		4.6E-01		4.6E-01		4.6E-01	4.6E-01		4.6E-01	4.6E-01	4.6E-01
Expression Signal	0.75	0.61	4.37	1.94	1.45	1.8	1.25	1.62	1.62	0.63	0.93	3.52	3.62	1.84		3.62		1 44	0.85	0.9		0.82		2.39		2.39	99.0		0.78	14.65	0.54
ORF SEQ ID NO:	34652	Ì		38052	L			58889	30000			31828	L	32140		32167	0	32480	1			32914		33649			33920	L.	İ	35131	35565
Exan SEQ ID NO:		22352	<u> </u>		L	25281	25361		16997				L	18857		18871	, 1	18873	1.		上	19553		2027	1		ı	ı	- 1	21696	22025
Probe SEQ ID NO:	8049	9278	11084	11340	11658	12401	12529	3837	3837	9899	5535	5588	5588	5663		5677		5685	5783	5850		6386		8069		9069	7379		7906	8515	8946

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8946	22025	35568	26.0	4.6E-01	.6E-01 AA932237.1	EST_HUMAN	oo78b08.s1 NCI_CGAP_Kid5 Homo sapieris cDNA clone IMAGE:1572087 3' sImilar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9501	i	36120	0.93	4.6E-01	8E-01 P56202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEFTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE) CYCLASE)
9501	22557	38121	0.93	4.6E-01	.6E-01 P65202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9866	22806	36490	0.52	4	.6E-01 AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9986	22906	36491	0.52	7	.8E-01 AF162283.1	NT	Glycine max ecetyl-CoA carboxylase (accB;1) gene, complete cds; nuclear gene for chloroplast product
10181			1.15	4	.6E-01 AI915634.1	EST HUMAN	wg73e12.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:2370768 3'
10181	23218	36810	1.15		4.6E-01 AI915834.1	EST_HUMAN	wg73e12.x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
11238	24307				.6E-01 P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (M.)
11248	_		5.06			EST_HUMAN	IL5HT0730-100500-075-g05 HT0730 Hamo sapiens cDNA
11248	24317	2928	5.08	4		EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Hariro sapiens cDNA
11780		37573	4.3	4		NT	Human thiopurine methyltransferase (TPMT) gene, expn 10 and complete cds
11760	23946	37574	4.3	•	.6E-01 AF019369.1	ᅜ	Human thiopurine methyltransferase (TPMT) gene, excn 10 and complete cds
1960	18103	28203	1.15	þ	.5E-01 AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	7	.5E-01 AE001831.1	NT.	Delnococcus radiodurens R1 section 68 of 229 of the complete chromosome 1
2933	16110	29124	4.83	4	.5E-01 AA677085.1	EST_HUMAN	455402.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:454179.3'
3380	16552	29565	99.0	4	.6E-01 AW083761.1	EST HUMAN	xc25c06.x1 NCI_CGAP_Co19 Hamo sapiens cDNA clone IMAGE:2585290 3' sImilar to gb:L07807. DYNAMIN-1 (HUMAN);
3380				4	.8F-01 AW083761.1	EST HUMAN	xc25c06.x1 NCI_CGAP_Co19 Homo septens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
							BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3393	- 1			4	.5E-01 Q05783	SWISSPROI	
3465		29651		4	.5E-01 AF128378.1	¥	Mus musculus DNA polymerese epsilon catalydo subunit (Fole) gene, exons z trrougn 12
4139				4	.5E-01 Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
4186	17336	30329		4	5E-01 AI708908.1	EST_HUMAN	as96e08 x1 Barstead aorta HPLRB6 Homo saplens cDNA clone IMAGE 2333480 3
4292			4.71	4	.5E-01 AW873495.1	EST HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Horno capiens cDNA cione IMAGE:3041810 3
5058				4	.5E-01 BE963445.2	EST HUMAN	601657225R1 NIH_MGC_67 Hamo sepiens cDNA clone IMAGE:3868023 3'
5666		32145		4	5E-01 AW608814.1	EST HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo septens cDNA
6740				*	.5E-01 Q00956	SWISSPROT	COAT PROTEIN
7571	20843	34120	0.91	7	.5E-01 M37038.1	N	Rat nucleolar proteins B23.1 and B23.2

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				. ]			
Proba SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesstan No.	Top Hit Database Source	Top Hit Descriptor
7785	20841	34333	2.39	4.6E-01	.6E-01 AI858849.1	EST_HUMAN	w32e02x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2426618 3' similar to TR:QB2923 Q92923 SW/VSNF COMPLEX 170 KDA SUBUNIT .;
8502			1.11	4.5E-01			D.molenogaster Shaw2 protein mRNA, complete cds
8508	21670	35217	2.87	4.5E-01	.5E-01 A1648596.1	EST_HUMAN	tz59g11.x1 NCI_CGAP_Ov35 Hano sepiens cDNA clane IMAGE:22928443'
				•		<del></del>	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
8766	21835	35376	0.85	4.5E-01	.5E-01 Q52728	SWISSPROT	POLYMERASE)(PHA SYNTHASE)(POLYHYDROXYALKANDIC ACIU SYN I HASE)
8981	1		2.36	4.5E-01	11444786 NT	۲	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mKNA
8200		35817	98.0	4.5E-01	.5E-01 AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10145	1		96'0	4.6E-01	9630816 NT		Bombyx mori nuclear, polyhedrosis virus, complete genome
10713	23746		25.59	4.5E-01	.5E-01 M85006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17
10713	ı		25.59	4.5E-01	5E-01 M86008.1	EST_HUMAN	EST02631 Fetal brain, Stratagene (cat#836206) Homo saplens cDNA clone HFBCY17
11104	L		2.52	4.5E-01	AW 591271.1	EST_HUMAN	xxo14h01.x1 NCL_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW::INT6_MOUSE Q84252 VIRAL INTEGRATION SITE PROTEIN INT-8. [1];
11226	Į.	37835		4	.5E-01 11430789 NT	NT	Homo saplens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11530	24586				4.6E-01 AV719382.1	EST_HUMAN	AV719382 GLC Homo saplens cDNA clone GLCCED12 5
12164	<u> </u>		5.58	4.5E-01	.5E-01 BE871481.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapient cDNA done IMAGE:3852961 5'
12895	25582		1.2	4.5E-01	5E-01 BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183290 5'
12970	25630		12.42	4.5E-01	11422089 NT	LN.	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2002			1.11	4.4E-01	TN 6080503 NT	IN	Mus musculus Integral membrane-associated protein 1 (Itmap1), mRNA
2462	1,4,80	28715	4 18		4 4F-01 P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3390	1				1.4E-01 AF058790.1	۲	Rattus norvegicus SynGAP-b mRNA, complete ods
3300	ı	29576		4.4E-01	.4E-01 AF058790.1	N	Rettus narvegicus SynGAP-b mRNA, compilete cds
3385	L			4.4E-01	.4E-01 BF056726.1	EST_HUMAN	7]91d02y1 NCL_CGAP_Br16 Hamo sepieris cDNA clone IMAGE:3393795 5'
4349	L.			4	1.4E-01 BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clane IMAGE:3606383 5'
5536	18733		131		4.4E-01 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	18733			4	.4E-01 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	32300	1.58	4.4E-01	.4E-01 S05019.1	NT	mucin [rate, Sprague-Dawley, sulfur-dloxide treated tracheal epithelium, mRNA Partial, 390 ntj
5823		32319	1.81	4.4E-01	.4E-01 AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 6
6074		32584	1:12	4	.4E-01 AI198413.1	EST_HUMAN	qi62h11,x1 NCI_CGAP_Brn25 Homo sepiëns cDNA clone IMAGE:1861125 3' similer to TR:Q29168 Q29169 UNKNOWN PROTEIN ;

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Probe SEQ ID S NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	₹	4E-01 A1198413.1	EST_HUMAN	q82h11.x1 NGLCGAP_Brrz5 Homo sapleris cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN :
6370	19539	32899		4	4E-01 AW080795.1	EST HUMAN	xo27e08.x1 NCI_CGAP_Co18 Home septens cDNA clone IMAGE:2585510 3' similar to TR:095154 096154. AFLATOXIN B1-ALDEHYDE REDUCTASE; ;
8458	19625		1.05		4E-01 AA778132.1	EST_HUMAN	ae85d11.s1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7997	20629	34104	1.14	4	4E-01 AE000571.1	TN	Helicobacter pylori 26695 section 48 of 134 of the complete genome
8024	21107		: 12.3	4	4E-01 Z11679.1	NT	S.tuberosum mRNA for Induced stolon tip protein (partial)
8962	22041	35584		<b>†</b>	4E-01 AA056427.1	EST HUMAN	zl68a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
8352	22427	35985	0.78	4	4E-01 AF112540.1	IN	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9386	22460	36023	0.62	4	4E-01 AW612578.1	EST_HUMAN	hh05c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6;
9490	22547	36110	1.13	4	.4E-01 062836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTIEIN
10167	23204	36788	1.95	4	.4E-01 A1268650.1	EST_HUMAN	qo38f09.x1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1910921 3'
10168	23205		2.09	7	.4E-01 P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10302	23337		4.94	4	4E-01 P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23820	37228	1.78	7	4E-01 S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rata, Genomic, 8983 nt, segment 2 of 2]
10585	23620	12278	1.76	7	.4E-01 S76404.1	ΝΤ	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10829	23862	37486	0.46	4	.4E-01 P02716	SWISSPROT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
11522	24578	38226	1.64	4.4E-01	6691408 NT	F	Terebratulina retusa mitochondrion, complete genome
12435	25308	32087	4.23	4	6677874 NT	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12447	26084		13.47	4	4E-01 AL163282.2	NT	Hamo saplens chromosome 21 segment HS 21 C082
13051	25689		1.41	4.4E-01	.4E-01 P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13619		2.42	4	.3E-01 AF155218.1	M	Callithrk Jacchus MW/LW opsin gene, upstream flanking region
424	13819	09992	2.42	4	.3E-01 AF155218.1	NT	Callithrix Jacchus MW/LW opsin gene, upstream flanking region
1633	14785		1,11	4.3E-01	.3E-01 AW866550.1	<b>EST_HUMAN</b>	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2835	16112		1.34		3E-01 AW835269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo saplens cDNA
3127	16303				4.3E-01 AW999477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Hcmo sapiens cDNA
4526	13619		1.27	7	.3E-01 AF165218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4528	13619	26660	1.27	4	.3E-01 AF155218.1	노	Callithrix Jacohus MW/LW opsin gene, upstream flanking region
5071	18199		1.04	4	.3E-01 AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5220	18342		0.94	4	9635250 NT	NT	Xestia c-nigrum granulovirus, complete genome
5480	18679	31693		4	.3E-01 P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
2480	18679		. 0.95	4	.3E-01 P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

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	Top Hit Descriptor	Homo saplens cytochrome c oxidase subunit VIc (COXBC), nuclear gene encoding mitochondrial protein,	Human cytomecalovirus early phosphoprotein p50 mRNA, complete cds	Human cytomeostroyous early phosphographin p50 mRNA, complete cds	NIGRATI & Scarie fetal liver scheen 1NFLS S1 Homo sablens cDNA clone IMAGE:462649 3'	MR3-SN0010-280300-103-h07 SN0010 Homo capiens cDNA	Oryzies latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds	601660352R1 NIH_MGC_71 Hcmo saplens cDNA clone IMAGE:3906085 3'	RC-BT091-210199-142 BT091 Homo saplens cDNA	AV705243 ADB Hamo sapiens cDNA done ADBAHF08 5'	AV705243 ADB Hamo saplens cDNA clone ADBAHF08 5'	PM-BT103-270499-684 BT103 Homo sapiens cDNA	Homo sepiens anaphase-promoting complex subunit 7 (APC7), mRNA	Arabidopsis thallana DNA chromosome 4, contig fregment No. 36	Arebidopsis thallana DNA chromosome 4, contig fragment No. 36	oj94b08.s1 Soeres_NFL_T_GBC_S1 Homo seplens cDNA clone IMAGE:1505943 3'	EST373364 MAGE resequences, MAGG Homo sapiens cDNA	EST373364 MAGE resequences, MAGG Homo saplens cDNA	Rhodocccous sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes		AV747880 NPC Homo saplens cDNA clane NPCBDF10 5'	602166590F1 NIH_MGC_83 Hamo sepiens cDNA clone IMAGE:4297319 5	Mus musculus NIH 3T3 chemckine rantes (Scya5) gene, complete cds	Methenococcus Jannaschill section 77 of 150 of the complete genome	602133261F1 NIH_MGC_81 Hano sepiens cDNA clone IMAGE:4288238 5	Mus musculus signaling intermediate in Toll pethway-evolutionarity conserved (Sitpec-pending), mRNA	Voalave gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for	mitochandrial product	Campylobacter Jejuni NCTC11168 complete genome; segment 3/8	AV649579 GLC Homo saplens cDNA clone GLCBVD12 31	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
	Top Hit Database Source	ţ	Z	Į.	ECT LINAM	EST HUMAN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	INT	NT	NT .	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	NT		EST_HUMAN	EST_HUMAN	. TN	INT	EST_HUMAN	Ę		N	M	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN
.G	Top Hit Acesslon No.	000011	4/ 08039 N	4 DE 04   157424 4	4.XE-01 03/431.1	4.2E-01 AA/05007.1	4.2E-01 AB023489.1	4.2E-01 BE966485.2	4.1E-01 Al905481.1		4.1E-01 AV705243.1	4.1E-01 Al905949.1	7705283 NT	4.1E-01 AL161536.2	4.1E-01 AL181538.2	4.1E-01 AA906344.1	4.1E-01 AW961292.1	4.1E-01 AW961292.1	4.1E-01 AJ249207.1	4.1E-01 AA909257.1	4.1E-01 AV747880.1	4.1E-01 BF681393.1	4.1E-01 U02298.1	4.1E-01 U67535.1	4.1E-01 BF574604.1	8755521 NT		4.1E-01 AF160597.1	4.1E-01 AL139076.2	4.1E-01 AV649579.1	P18584	P18584	4.1E-01 BF349382.1
	Most Similar (Top) Hit BLAST E Value	10,	4.2E-01	20 10 1	10-47-	4 2F-01	4.2E-01	4.2E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01		4.1E-01	4.1E-01	4.1E-01	4.1E-01 P18584	4.1E-01 P18584	4.1E-01
-	Expression Signal		0.72	200	0.0	1 44	1.43	1.87	211	1.46	1.48	1.77	1.48	212	212	0.68	0.73	67.0	3.78	0.99	1.36	4.84	0.65	2.48	1.36	1.51		0.75	1.56	1.15	0.68	0.68	1.14
	ORF SEQ ID NO:		35010	20140		37384	38005	38368	27338	27347	27348	27877	29001	29202	29203	29561	30028	30029	30513		30912	32626	33420	34137	34827	35918				37266			
	Exan SEO ID NO:		21482	2010	-	23212	1_	24678	L		14292	14792	L	١.	16181	$\mathbb{L}_{-}$	L	<u> </u>	17532	17563	17924	19291		20661	21307	22368		227.62	23505	23656	1	l I	23839
	Probe SEO ID NO:		8401		1100	471701	11288	11679	1118	1127	1127	<del>2</del>	2775	3008	3006	3375	3871	3871	4389	4422	4789	9111	6857	7590	8226	9282		9765	10470	10622	10725	10725	10806

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Probe SEQ (D NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No	Top Hit Database Source	Top Hit Descriptor
11078	24153	37790	40.17	4.1E-01	4.1E-01 X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein prixein
11675	L	L		4.1E-01	4.1E-01 Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1)
12810			2.33	4.1E-01	4.1E-01 D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153			1.24	4.1E-01	4.1E-01 AJ131016.1	NT	Homo sapiens SCL gene locus
1084	14229	27288	1.49	4.0E-01	8404656 NT	NT	Laqueus rubellus mitochondrion, complete ganome
1370	14525	27599	1.21	4.0E-01	4.0E-01 AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	L		5.48		6679258 NT	N	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2081	_	28316	1.08		4.0E-01 Z96933.1	NT	Ascobolus immersus masc2 gene
2081			1.08		4.0E-01 Z96933.1	N	Ascobolus immersus masc2 gene
2866			1.11	4.0E-01	E678490 NT	۲	Mus musculus ubiquitin-protein ligase e3 componen n-recognin (Ubr1), mRNA
3033	•		1.18		4.0E-01 AL163280.2	L	Home saplens chromosome 21 segment HS21C080
3033	16203		1.18		4.0E-01 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
	J	<u> </u>					Streptococcus pneumoniae YIC (vilC), YID (vilD), penicilin-bhding protein 2x (pbp2x), and undocapreny- phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete
3786	16947	29955	1.87		4.0E-01 AF068903.1	Z	cds
3932		L	3.21	4.0E-01	4.0E-01 AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	L	L		L	4.0E-01 AJ277811.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4938	L	L	8.59		4.0E-01 Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
158	<u></u>	32535	1.07		4.0E-01 AW970810.1	EST_HUMAN	EST382691 MAGE resequences, MACK Homo sapiens cDNA
	1				2007000	TOGGGGGW	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, IE2 AND E1. A KD PEPTIDE]
9000	- 1				F-21 200	SWISSING TOL	MADA TINITATA ARRON 202-002 TND10 Home seniors CINIA
9113					4.0E-01 BF092634.1	EST HUMAN	IMINATION 10-100300-202-302 1130110 12110 34/14/15 00101
8201					4.0E-01 AB018825.1	N 1	TOTIO SEPTEMBER OF THE Bons, Continued was
2002	_	72855			4.05-01 74020209.1	EST TOWNS	LOTES CONTROL OF Home seniors CDNA clone IMAGE 3828092 5
11869			)Q.	١	4.0E-01 Br030262.1	NEW LOS	Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Contro
12021		1	2.38		4.0E-01 L76080.1	LN.	Synechocystis sp. P.C.C. 9413 transposase gene, complete cus
12463	26978		2.5		4.0E-01 AL163300.2	NT	Hamo sapiens chromosome 21 segment H\$21C100
13027	26116	15	1.38		4.0E-01 Z49301.1	NT	S.cerevisiae chromosome X reading frame ORF YJL026w
12169	28038		12.		4 0F-01 BF432020 1	EST HUMAN	Inab84e05.x1 Sozres_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA done IMAGE: 3' similar to SW:\text{SW:\text{NTCR}} BOV!NO18875 SCDIUM-ANI) CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1;
18222	1		1 28		4.0E-01 Z49301.1	L	S, cerevistae chromosome X reading frame ORF VJL026w
1400	L	27638			3 9E-01 AF206618 1	12	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2707	┸				3.9E-01 AB033019.1	Ž	Homo sapiens mRNA for KIAA1193 protein, partial cds
2770	14885	28994	503		3.9E-01 X82032.1	Į.	H.sapiens B-myb gene
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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3643	16792		76.0	3.8E-01	3.8E-01 AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:2357855 3'
3822	17012			3.8E-01	1,8E-01 BE154080.1	EST_HUMAN	PM0-HT0339-200400-010-G01 HT0339 Homo saplens cDNA
4027	L		99.0	3.8E-01	8754095	NT	Mus musculus general transcription factor IIII (Gt/2i), mRNA
5727	L	L	1,11	3.8E-0:1	3.8E-01 Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6489	19636		0.63	3.8E-01	3.8E-01 S46825.1	NT	prion protein (mink, Genomic, 2448 nt)
6781		33312		3.8E-01	3.8E-01 BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo saplens cDNA
	.l						ta54f11x1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:2047917 3' similar to
6889	20214		4.39	3.8E-01		EST_HUMAN	cartains Alu repetitive element;
707	20132	33549	1.38	3.8E-01	3.8E-01 AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7885	20750		4.27	3.8E-01	3.8E-01 X81597.1	NT	M.musculus gene for kallikrein-binding protein
8493	l	35111	0.54	3.8E-01	3.8E-01 M81385.1	NT	Mouse liver receptor homologous protein (LR'H-1) mRNA, complete cds
8764	21833	35373		3.8E-01	3.8E-01 AB046851.1	IN	Homo sepiens mRNA for KIAA1631 protein, partial cds
8826	L	35444	1.08	3.8E-01	11441264 NT	N	Homo capiens FOS-like antigen-1 (FOSL1), ImRNA
9017	<u> </u>			3.8E-01	3.8E-01 AL163279.2	NT	Homo saplens chromosome 21 segment HS21C079
•							ye43h06.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:120539 5' similar to contains
9761	22699		4.35		3.8E-01 T95413.1	EST_HUMAN	Alu repetitive element contains PTR5 repetitive element;
11034	24113		1.38		3.8E-01 AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens CDNA clone EMFBCE07 5
	L			j			Homo saplens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
							(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin
11699		38388	1.57	3.8E-01	3.8E-01 U82671.2	NT	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
11824	24813		2.87	3.8E-01	3.8E-01 BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Horno sapiens cDNA
11992		38681	2.6	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares Infant brain 1NIB Homo (apiens cDNA clone IMAGE:30289 3'
11992	24977				3.8E-01 R42550.1	EST_HUMAN	y/92h11.s1 Soares Infant brain 1NIB Homo capiens cDNA clone IMAGE:30289 3'
12436					3.8E-01 AE001124.1	TN	Borrella burgdorferi (section 10 of 70) of the complete genome
12689	26082		2	3.8E-01	3.8E-01 U94788.1	IN	Human p53 (TP53) gene, complete cds
12695	1		1.71	3.8E-01	3.8E-01 BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-e05 ET0063 Horino sapiens cDNA
13105	25720		1.48			FZ	Mus musculus apoptosis inhibitar bel-x (bel-x) gene, exon 3 and complete cds
13188	ł	31933			3.8E-01 AF194972.1	N	Mus musculus developmental control protein mRNA, partial cds
2551	15876	28799	12.91	3.7E-01	3.7E-01 AB037831.1	N.	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29726	10.67	3.7E-01	3.7E-01 AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete eds
3974	17131	L	1.09		3.7E-01 AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	L.	30470			3.7E-01 AI218707.1	EST_HUMAN	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_IP_S1 Homo septens cDNA clone IMAGE:1510188 3'
4440	17580	30559			3.7E-01 AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509			2.91		3.7E-01 AE002408.1	NT	Neissena meningitidis serograup B strain MC58 section 50 of 208 of the complete genome

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Single Exon Probee Expressed in Placenta	Top Hit Descriptor	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds	Rattus norvegicus repeat element associated with the Rasgrf1 gene	Human mRNA for KIAA0323 gene, partial cds	P. Irregulare (P3804) gene for actin	RC5-ST0171-181099-011-007 ST0171 Homo saplens cDNA	PROTEIN-L-JSOASPARTATE O-METHYL TRANSFERASE (PROTEIN-BETA-ASPARTATE METHYL TRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYL TRANSFERASE) (L-	ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds	H. sepiens serotonin transporter gene, exons 9 and 10	H.sepiens serotonin transporter gene, exons 9 and 10	RC1-HT0545-150600-014-b12 HT0545 Homo saplens cDNA	Brassica napus mRNA for MAP4K alpha2 protein	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'	MR4-BT0358-270300-005-c10 BT0358 Homo septens cDNA	Homo sapiens lipe gene Intron 5	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3	COMPONENT E)	Homo sapiens PHEX gene	y174a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'	wt72c10.x1 Soares_thymus_NHFTh Homo saplens cDNA clone IMAGE:2513010 3' similar to TR:015117 015117 FYN BINDING PROTEIN. [1] ;	SCO-SPONDIN :	Arabidopsis thaliana DNA chromosome 4, contig fregment No. 79	Human hereditary haemochromatosis region, histone 2A-like protain gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, end sodium phasphate transporter (NPT3) gene, complete ods	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phisphate transporter (NPT3) gene, complete cds	Homo saplens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
e Exon Probe	. Top Hit Database Source	TN	TN	NT	NT	EST_HUMAN		SWISSPROT	N	TN	F	EST_HUMAN	۲	EST_HUMAN	EST_HUMAN	Ę		SWISSPROT	N	EST HUMAN	EST_HUMAN	SWISSPROT	NT.	Ţ	ħ	LΝ	LN
Singl	Top Hit Acessian No.	3.6E-01 AF216207.1	3.6E-01 AF056927.1	3.6E-01 AB002321.1	3.6E-01 X76725.1	3.6E-01 AW812033.1		P2420B	3.6E-01 AF199485.1	3.6E-01 X76758.1	3.6E-01 X76758.1	3.6E-01 BE707883.1	3.6E-01 AJ009609.1	3.6E-01 AW338393.1	3.6E-01 BE067699.1	3.6E-01 AJ006565.1				3.6E-01 R94090.1	3.6E-01 AW027174.1	P98167	3.6E-01 AL161583.2	3.6E-01(U91328.1	3.6E-01 U91328.1	4504956 NT	4504956 NT
	Most Similar (Tcp) Hit BLAST E Value	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01		3.8E-01 P24208	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01		3.6E-01 P16431	3.6E-01	3.6E-01	3.6E-01	3.6E-01 P98167	3.6E-01	3.6E-01	3.6E-01	3.6E-01	3.6E-01
	Expression Signal	6.7	1.15	2.33	2.8	2.66		1.69	8.47	1.98	1.98	1.2	69.0	3.18	0.92	0.64		0.96	1.63	3.85	1.52	0.76	16.45	0.48	0.48	3.04	3.04
	ORF SEQ ID NO:	28263	L			28808		28929		29738		30652		ĺ		31713			33155		33985		35087	35789		35820	36821
	SEQ ID NO:	15147	ı		ı	ı		15814	18475	16723	16723		17996	18249	1	18697	l	18386	19787	20380	20212	l	ı	22257		22281	22281
	Probe SEQ ID NO:	2007	2113	2343	2463	2556		2694	2984	3558	3558	4628	4863	5123	5209	5498	-	6211	2099	7298	7435	8419	8474	9478	9179	8203	9203

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Single Exon Probes Expressed in Pracenta	Ssion Database Source	1,2 NT	NT	NT	- N	SWISSPROT	3.6E-01 BE902380.1   EST_HUMAN		F 838000 1 Y 10 10 0	5.0C-01 AE000650.1	3.6E-01 Y19210.1 INT	3.6E-01 AE000335.1 NT	3.63 3.6E-01   U68888.1   NT   Mus musculus Emr1 mRNA, complete cds	76 100	1.88 3.6E-01 11432588[NI 10 (AF10), MIXIA	1.4 3.6E-01 AW190229.1 EST_HUMAN ALPHA-1 CHAIN (HUMAN);	1.38 3.6E-01 254173.1 NT Pyrococcus sp. pol gene	3.5E-01 6678933 NT	AL161581.2 NT	3.5E-01 7708136 NT	D6136 NT	4,86 3.5E-01 BF129798.1   EST_HUMAN   601811060R1 NIH_MGC_48 Homo sapients cDNA done IMAGE:4053951 3'	1.28 3.5E-01 U35776.1 NT Raftus norvegicus ADP-ribosyletion factor-directed GTP ass activating protein mRNA, complete cds	1.34 3.5E-01 AA223252.1 EST_HUMAN   Z108409.51 Stratagene NT2 neuronal precursor 937230 Homo saplens cDNA clone IMAGE:850872.3"	EST_HUMAN	2.62 3.5E-01 AF071253.1 NT Derio rerio homeobox protein (hoxb6b) genis, complete cds		36.2 NT	SWISSPROT	SWISSPROT	TN	1 3.6E-01 AW 863916.1 EST_HUMAN   PM4-SIN0012-030400-001-e11 SIN0012 Homo septems cDNA
	Mos 1													ŀ																		1 3.0
	ORF SEQ ID NO:	36032		38226	1	36708	37891	38088		2/040	5	1	7		2		5	7 26467		Ì		Н 27033	27905	8 28908	L	30501		9 26376			32146	
:	Exan SEQ ID NO:	3 22468	22864	L	乚	7 23105	24256	24431	1		i	25197	26297	<u> </u>	3 25552	26141	3 25745	<u>L</u>		ı	<u> </u>	13981	14822	16068	L	1		13349	L	Ι.	7 18861	
	Probe SEQ ID NO:	9393	9599	8599	9869	10067	11187	11370		2	12173	12261	12420		12828	13130	13148	214	969	743	743	జై	1670	2671	3795	4378	5048	5323	24 A	5449	586	6367

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	Top Hit Descriptor	zw79f03.r1 Scares_testis_NHT Homo septens cDNA clone IMAGE:782429 5' similar to TR:G1066935 G1066935 F10F2.1;	Bos taurus paptide methionine sulfoxide reductase (msrA) mRNA, complete cds	OLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (GGPD)	S. scrofe mRNA for CD31 protein (PECAM-1)	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA	RC4-ET0024-260600-014-d07 ET0024 Horino saplens cDNA	Rettus norvegicus Ne-K-Cl cotransporter (Nkcc1) mRNA, complete cds	Homo sapiens tyrosine kinase non-receceptor 1 (TNK1), mRNA	VOLTAGE DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-18 SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)	Xiaevis gene for albumin including HP1 enhancer	QV2-HT0577-090400-128-c07 HT0577 Homo saplens cDNA	C.griseus rhodopsin gene for cosh protein	Gallus gallus SPARC gene for osteonectin, promoter and exon 1	Gallus gallus SPARC gene for osteonectin, promoter and exon 1	Human breakpoint cluster region (BCR) gene, complete cds	yz90h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo saplens cDNA clone IMAGE:290375 5'	Human glucokinase (GCK) gene, repeat polymorphism	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA,	complete cds	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-eubunit	Thermotoga maritima section 88 of 138 of the complete genome	Thermotoga maritima section 3 of 136 of the complete genome	ys64f11,r1 Scares retina N2b4HR Homo sepiens cDNA clone IMAGE:219597 5'	ys84f11.r1 Soares retina N2b4HR Homo sepiens cDNA clone IMAGE:219597 5'	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes	isolated from IC4 cervical carcinoma cell line	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene	QV3-HT0281-241199-019-g10 HT0281 Homo saplens cDNA	Azotobactar vinalandii nifA gena for NifA protein (positive regulatory element)	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
	Top Hit Database Source	EST_HUMAN	NT	SWISSPROT	NT	SWISSPROT	SWISSPROT	NT	EST HUMAN	IN	TN	SWISSPROT	F	EST_HUMAN	IN	IN	NT	N	EST_HUMAN	N		Ę	Ę	N	NT	EST_HUMAN	EST_HUMAN		μ	LΝ	EST_HUMAN	NT	۲Z
5	Top Hit Acession No.	3.6E-01 AA431833.1	3,5E-01 U37150.1	024357	X98505.1	P47281		11448042 NT	3.6E-01 BF358871.1	3.5E-01 AF051561.1	4507610 NT	002294	3.5E-01 Z26825.1	3.5E-01 BE174794.1	3.5E-01 X81084.1	3.5E-01 AJ243178.1	3.5E-01 AJ243178.1	3.5E-01 U07000.1	3.5E-01 N77597.1	3.5E-01 L05145.1		3.5E-01 AF297468.1	3.5E-01 X64565.1	3.5E-01 AE001774.1	3.5E-01 AE001691.1	3.5E-01 H80814.1	3.6E-01 H80814.1		3.4E-01 AJ242958.1	3.4E-01 Y09798.2	3.4E-01 AW380120.1	3.4E-01 Y00554.1	3.4E-01 D90909.1
	Most Similar (Top) Hit BLAST E Value	3.6E-01	3.5E-01	3.5E-01 O24357	3.5E-01 X98505.1	3.5E-01 P47281	3.5E-01 P47281	3.5E-01	3.6E-01	3.5E-01	3.5E-01	3.5E-01 Q02294	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01		3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.6E-01		3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01
	Expression Signal	0.79	69.0	6.0	3.38	0.59	0.59	2.12	0.82	0.77	1.17	. 1.75	4.78	1.12	2.62	1.97	1.97	1.33	1.44	1.63		1.51	99.9	2.91	1.5	3.16	3.16		1.78	8.2	2.06	2.35	2.54
.	OŘF SEQ ID NO:	33074							34862		36749	36567			37685	37981		38499	38577	38667						31673				27230			. 28726
	SEQ ID NO:	19701	19742	19958	20066	20778	20778	21344	21347	21742	22206	22976	23128	23209	24052	24342	24342	24800	24880	24065		26209	25249	25348	28472	26026	Ι.		13907	14169		ΙI	15801
	Probe SEQ ID NO:	6538	6580	8803	7201	7713	7713	8262	8265	8662	9127	9937	10090	10172	10972	11274	11274	11810	11892	11980		12271	12344	12507	12710	13198	13196		725	866	1000	1357	2474

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Single Exult Flores Explessed III Flacelina	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C010	Homo capiens chromosome 21 segment HS21C010	Synechocystis sp. PCC6803 complete genoine, 11/27, 1311235-1430418	Canis familiaris rod photoreceptor cGMP-gaied channel alpha-subunit (CNGC1) mRNA, complete cds	Homo saplens pulmonary surfactant protein D, promoter region and exon 1	Methylovorus sp. strain SS1 putetive GrpE (jrpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds	7n94e01.x1 NCI_CGAP_Ov18 Homo sepieris cDNA clone IMAGE:3572232 3' símitar to TR:Q9UJ15 Q9UJ15 DJ18C9.1 ;	no11b10.s1 NCI_CGAP_Phe1 Homo sapleris cDNA clone IMAGE:1100347 3'	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA	aj85c05.x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1867208 3' almitar to containo Alu repetitive element;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90	zn12d11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:5472213'	Echowrus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds	601571811T1 NIH_MGC_55 Hamo sapiens cDNA clone IMAGE:3838826 3	UI-H-BIT-aet-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2719582 3	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5	zb53e12.s1 Soares_fetal_lung_NbHL19W Homo saplens cDNA clone IMAGE:3073423	tm63g05.x1 NOI_CGAP_Brn26 Homo eapiëne cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);	602085283F1 NIH_MGC_83 Hamo sapiens cDNA clone IMAGE:4249365 5	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome	Homo sapiens TCRAV28 gene, allele A4, partial	EST41765 Endometrial tumor Homo sapiens cDNA 5' end	Cricetulus griseus cholesterol 7-alpha-hydroxylase gens, complete cds	Bovine enterovirus strain K2577, complete cenome	INTEGRIN BETA-8 PRECURSOR	INTEGRIN BETA-8 PRECURSOR	Ephydetta fluviatilis mKNA for PLC-gammas, compliate cos	Saccharomyces cerevisiae Mat1p (MAL1) gene, complete cds
EXUIT FIOURS	Top Hit Databasa Source		Ĭ N	NT	<u>5</u>		Meth NT cds	FST HUMAN Q	Г	EST_HUMAN M		NT A	EST_HUMAN   2		EST_HUMAN 6	HUMAN		EST_HUMAN 2	EST_HUMAN L				EST_HUMAN E			SWISSPROT			NT S
Single	Top Hit Acession No.		3.4E-01 AL163210.2	3.4E-01 D90909.1	3.4E-01 U83905.1	7:								3.4E-01 L02971.1	3.4E-01 BE748912.1	3.4E-01 AW204505.1	3.4E-01 AL120544.1	3.4E-01 N95225.1	3.4E-01 AI468082.1			3.4E-01 Y14930.1		3.4E-01 L04690.1	9633624			3.4E-01 AB017510.1	3.4E-01 U19492.1
	Most Similar (Top) Hit BLAST E Value	3.4E-01/	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01/	3.4E-01	3.46-01	3.4年-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01 P26013	3.4E-01 P26013	3.4E-01	3.4E-01
	Expression Signal	0.87	0.87	1.09	6.1	0.78	4.47	1.89	1.48	1.79	6.4	264	4.92	2,17	96.0	1.8	1.71	1.39	1.07	9.0	0.48	0.68	1.38	1.71	1.87	4.12	4.12	0.57	4.68
	ORF SEQ ID NO:	29261	29262	29403	29416	29608	29800			30884	Ì	32285			32676				33604	33480		35044		35380	_		36052		34602
	SEQ ID NO:	16241	1	ı	16404	16593	16784	17049	17313	17802	18194	18992	19118	18309	I_	L	19534	20034	<u> </u>	上	1	1_		21839	l	22487	22487	l	21088
	Prabe SEQ ID NO:	3065	3085	3218	3230	3424	3670	Cogo	4163	4767	5088	5802	5832	6130	6154	6234	6364	6882	7086	7205	8080	8432	9684	8760	9053	9413	9413	9821	9645

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Aœssion No.	Top Hit Database Source	Top Hit Descriptor
9645	21088	34603	4.68	3.4E-01	.4E-01 U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9897	l		0.88	3.4E-01	3.4E-01 U68763.1	TN	Glycine max putative transcription factor SCOF-1 (scof-1) mRNA, complete cds
10083		36735		3.4E-01	.4E-01 AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10695	L			3.4E-01	.4E-01 AE004096.1	NT	Vibrio chalerae chramosome I, section 4 of 251 of the complete chramosome
11267	l		3.28	3.4E-01	.4E-01 AE000881.1	IN.	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 67 of 148) of the complete genome
11307	L	38014	2.1	3.4E-01 P06925	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38088	1.86	3.4E-01	.4E-01 AF045981.1	NT	Rutilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11581	ł	38295	1.91	3.4E-01	3.4E-01 M25858.1	NT	Human von Willebrand factor gene, exons 38 and 37
11561	L.		1.91	3.4E-01		TN	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	1.4E-01 AB035507.1	NT	Rattus norvegicus mRNA for s-gicerin/MUC18, complete cds
11817	24808	38502		ľ	3.4E-01 AL191515.2	NT	Arabidopsis theliana DNA chromocome 4, cantig fragment No. 27
12078	_		1.59	ຶ	.4E-01 BF061948.1	EST_HUMAN	7k89d12x1 NCI_CGAP_GC8 Homo sapients cDNA clone IMAGE:34806463
55,		90700		`	1 AE 04 007848	TORGSSIMS	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE)
12.10	OSDC7			3.45.01	2 4E 04   102804 4	NT SOLVE	Citrus variedation virus putativa replicase gene, partiel cds
12284	1_		1.55	3.4E-01	3.4E-01 Z21621.1	Į.	S.cerevistae RIB5 gene encoding Riboflavin synthase
12387			1.16	3.4E-01	3.4E-01 AF254351.1	Ę	Schizosaccharomyces pombe Cw/8p (cw/8) gene, complete cds
12489	l.		10.71	3.4E-01	3.4E-01 L26339.1	۲	Human autoantigen mRNA, complete cds
							hv42h08.x1 NCI_CGAP_Lu24 Homo saptens cDNA clone INAGE:3176127 3' similær to contains PTR5.t3
12517	25944		2.38	3.4E-01	BE21865	EST_HUMAN	PTR5 repatitive element;
12579	l		1.79	3.4E-01	B838361 NT	F	Beta vulgeris mitochondrion, complete genoine
12700		32023	1.38	3.4E-01	3.4E-01 AJ297131.1	된	Mus musoulus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12954			1.98		3.4E-01 AJ288948.1	된	Clostridium cellulolyticum partial spolVB gerre and spo0A gene, strain ATCC 35319
							Homo septens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
2000	70807		acc	40.0	2 AE 04 AE010412 4	Ę	inguisayassa (CTP21D), complement component C2 (C2) denes:>
2002 4		28283		3.3E.04	3.3E-04 X07990 4	Ę	Rhzoblum leguminosarum sym plasmid pRI.5J1 nodX gene
108	1			3.3E-01	3.3E-01 X07990.1	F	Rhizoblum leguminosarum sym plasmid pRI,5JI nodX gene
46		<u> </u>		3.3E-01	3.3E-01 AL161545.2	Ł	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
650	L	26863	1.97	3.3E-01	7662485 NT	· LN	Homo sepiens KIAA1100 protein (KIAA1100), mRNA
1221	L		2.57		3.3E-01 Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1335	14492				3.3E-01 BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Hama sapiens cDNA clone IMAGE:4300261 3'

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Single Exon Probes Expressed in Placenta	Top Hit Descriptor	Mus musculus disintegrin 5 (Dtgn5), mRNA	Mus musculus kappa B and Rss recognition component (Krc), mRNA	EST36722 Embryo, 8 week I Homo caplens cDNA 5' end	Homo sapiens untiline monophosphate synthistase (orotate phosphoribosy) transferase and orotidino-6-	decarboxylase) (UMPS) mKNA	Bacteriophage phi-YeO3-12 complete genome	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)	Streptomyces argiliaceus mithramycin biosynthedic genes	Homo sapiens MTA1-L1 gene, complete cds	EXODEOXYRIBONUCLEASE V BETA CHAIN	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT   PROTEINASE (HC-PR0); PROTEIN P3	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 10	Hypoxykon fragiforme chitin synthase gene, partial cds	Rattus norvegicus DNA for regucalcin, partial cds	PPBb12.X1 NCI_CGAP_Ut3 Homo septens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766	R.norveglaus mRNA for 3"UTR of ubiquitin-!!ke protein	R.norvegicus mRNA for 3'UTR of ubquittn-like protein	601848090F1 NIH_MGC_55 Hano sapiens cDNA clone IMAGE:4078823 51	601472768T1 NIH_MGC_68 Hcmp sapiens cDNA clone IMACE:38757633	601472768T1 NIH_MGC_68 Hcmo sapiens cDNA clone IMAGE:3875753 3	CIRCUMSPOROZOITE PROTEIN (CS)	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds	Flexibacter Iltoralis gyrB gene for DNA gyrase B subunit, partial cds	Iy84h01.x1 NCI_CGAP_Kid11 Homo sapieris cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element;	tye4h01.x1 NCI_CGAP_Kid11 Homo sapleirs cDNA clone IMAGE:2285809 3' similar to contains Alu renetitus element contains element 11 repetitive element.		J2498F Human fetal heart, Lambda ZAP Express Homo sepiens oDNA clone J2498 6' cimilar to TEGT
e Exon Probe	Top Hit Database Source	ΝĪ	N N	EST_HUMAN		Ę	¥	SWISSPROT	Ŋ	LZ LZ	SWISSPROT	SWISSPROT	Ę	N	L'N	EST_HUMAN	LN LN	TN	NT	TN	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	ΝΤ	EST HUMAN	EST LIMAN	100	EST_HUMAN
Singl	Top Hit Acession No.	6753685 NT	6754477 NT	3.3E-01 AA332734.1		4507834 NT	3.3E-01 AJ251805.1	O02743	3.3E-01 AJ007932.2	3.3E-01 AB012922.1	084645	503602	3.3F-01 At 161498.2	3.3E-01 AF200446.1	D31662.1	3.3E-01 AI539114.1	3.3E-01 M24461.1	3.3E-01 D64003.1	X89819.1	3.3E-01 X89819.1	3.3E-01 BF213873.1	3.3E-01 BE619650.1	3.3E-01 BE619650.1	P05691	3.3E-01 AB034233.1	3.3E-01 AB034233.1	3.3F-01 AIB28131.1	9 0E 04 A1020494 4-	A1020191.1	3.3E-01 N85146.1
	Most Similar (Top) Hit BLAST E Value	3.3E-01	3.3E-01	3.3E-01		3.3E-01	3.3E-01	3.3E-01 002743	3.3E-01	3.3E-01	3.3E-01 084645	9 3F-01 P22602	3.3F-01	3.3E-01	3.3E-01 D31682.1	3.3E-01	3.3E-01	3.3E-01	3.3E-01 X89819.1	3.3E-01	3.3E-01	3.3E-01	3,3E-01	3.3E-01 P05691	3.3E-01	3.3E-01	3.35-01	20.0	9.35-01	
	Expression Signal	1.26	1.43	1.02		6.23	1.61	1.09	0.78	1.04	2.72	. 80	1 19	1.81	2.37	1.81	1.02	1.14	2.55	2.55	0.68	1.37	1.37	1.29	0.59	0.69	4 63	1 83	4.03	1.9
	ORF SEQ ID NO:	27873					29216		29311								30866	L	31617	31618	32411		32677	32684		33681	33588	l.	/9000	34521
	SEQ ID NO:	14788	14828	14926		15604	16190	16256	16297	16749	17070	47080	1722B	17262	17627	17945	17976	18089	18639	18639	19096	19249	19249	18338	ı	1	1	1	20102	21011
	Probe SEQ ID NO:	1636	1674	1771		2477	3014	3080	3121	3584	391	Ş	4072	4108	4487	4812	4843	4980 8980	5430	5439	5907	6067	6067	6162	6932	6932	2020		8337	7961

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					.6		
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesston No.	Top Hit Database	Top Hit Descriptor
8759	21838		23.1	3.3E-01	.3E-01 BF683954.1	EST_HUMAN	802140372F1 NIH_MGC_46 Hcmo sapiens cDNA clone IMAGE:4301800 5
8926	ı		0.73	3.3E-01	.3E-01 BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5
	ì	ŀ					MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 1 (MAPKJERK KINASE KINASE 1) (MEK
9314	22390	35941	0.83	3.3E-01	.3E-01 Q62925	SWISSPROT	KINASE 1) (MEKK 1)
9278	1	36289	1.16	·	.3E-01 BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Hojno saplens cDNA
9278	1	36290	1.16		3.3E-01 BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	E	3.3E-01 N69866.1	EST_HUMAN	za67,h01,s1 Soares_fetal_lung_NbHL19W Homo sepiens cDNA clone IMAGE:2976493
9752	l			e	.3E-01 BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	L		2.08			NT	Homo saplens high-mobility group phosphoprotein (HMGLC) gene, exons 1-3, complete cds
10885	23897		0.74	,	3.3E-01 AE000631.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10960	24041	37675	3.35	,	3.3E-01 X63953.1	NT	D.maunttana Adh gene
10960	ı	L	3.35		3.3E-01 X63953.1	ĹΝ	D.maunitana Adh gene
11279	L		2.1	Ĺ	3.3E-01 BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo squicno cDNA done IMAGE:4213585 5
11507		38242	ľ		3.3E-01 BEZ19351.1	EST_HUMAN	hv31g02.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3176978 3'
					·		GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (38 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN
11626	24706	38339	3.7		3.3E-01 P47953	SWISSPROT	L-29) (CBP30)
12018	L		2.8	ľ	3.3E-01 AA806621.1	EST_HUMAN	OD71802.81 NCI_CGAP_GCB1 Homo sapians cDNA clone IMAGE:1336850 3'
12038				Ü	3.3E-01 X07990.1	TN	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
12250		38357			6598319 NT	TN	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	26686		22.03		3.3E-01 AP000002.1	NT	Pyrococcus horkoshii OT3 genomic DNA, 287001-544000 nt position (2/7)
469	13664		2.6		3.2E-01 AF018261.1	LN	Retus novegicus EH domain binding protein Epsin mRNA, complete cds
738	13918	1	0.76		3.2E-01 AL161561.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03		3.2E-01 AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14467		1.48		3.2E-01 Z50202.1	NT	P.vulgaris arc5-1 gene
1421	14676	l	6.74		3.2E-01 Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1683	L		-	3.2E-01	3.2E-01 AF209730.1	IN	Arabidopsis thaliana cultivar Columbia RPP <sub>1</sub> 13 (RPP13) gene, complete cds
1815	14864	\$ 28057	1.3		3.2E-01 Z36041.1	LN	S.cerevisiae chromosome II reading frame ORF YBR172c
1825	14974	28069	6.42		3.2E-01 AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1825	L	1 28070			3.2E-01 AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1891	L	5 28142			3.2E-01 AL111655.1	TN	Botryils cinerea strain T4 cDNA library under conditions of ritrogen deprivation
2227	15361	28490			BF203817	EST HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5
2606	15729	6	2.83	3.2E-01	TV10079 NT	TN	Mus musculus Pbx/knotted 1 hameobox (Pignox1), mRNA
2774	16889	29000			3.2E-01 AF080588.1	IN	Homo sapiens promyelocytic leukemia zincifinger protein (PLZF) gene, complete cds

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SEQ ID NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO: 0.00   NO:		R =	Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Si	Most Similar (Top) Hit BLAST E Value 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3.2E-01 3	5	Source Source Source Source Source FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN FUNMAN 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10198				3.2E-01	3.2E-01 AF041829.1 3.2E-01 U44914.1	N N	From saptens b-phosphorince—2-kinasomicatosa-2,0-casphosphatase (FFAX) gene, excite 12 and 13 Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
10198	23235	36824	4.33	3.2E-01	U44914.1	CLUMAN	Borrella burgoonen piasmid cp.2-2, et politina erpolgenes, comprete cus, and unividant genes. Propries y NCT CCAP 1 1/24 From saniers CDNA clone IMAGE:3181569 3'
10402				3.2E-01	3.2E-01 BE326230.1	EST_HUMAN	hVB9f06.X1 NCI_CGAP_Lu24 Framo sapiens cuna cone imauer:3161309 3
40848	1			3.2F-01	3 2F-01 AB011399.1	LN	Homo sapiens gene for AF-6, complete cdis
arcor	-		£0.0	3.4E-01	ADV 1 1355.1	-	

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	Top Hit Descriptor	EST04702 Fetal brain, Stratagene (cat#936206) Homo saplens cDNA clone HFBDZ21	Drosophila melanogaster laminin A (Lam-A) inRNA, complete cds	ELONGATION FACTOR TU (EF-TU)	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds	Homo sapiens deoxycytidylate deamlinase gene, complete cds	801275480F1 NIH_MGC_20 Hamo sapiens cDNA done IMAGE:3616746 5	ye90h06.rl Soares fetal liver spleen 1NFLS Homo saptens cDNA clone IMAGE:125051 5' similar to gb:M84241 QM PROTEIN (HUMAN);	Homo saplens KIAA0174 gene product (KIAA0174), mRNA	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA	hi46h08.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:2975391 3'	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6	Daucus carota mRNA for transcription factor E2F (E2F gene)	Xylella fastidiosa, section 130 of 229 of the complete genome	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1	HYPOTHETICAL PROTEIN H11236	S.cerevisiae chromosome XV reeding frame/ORF YOL141w	Mus musculus mRNA for polycystin	Homo saplens filamin 2 (FLN2) gene, exons 10 through 22	RC3-HN0001-310300-011-b04 HN0001 Homo septens cDNA	ql39d01,x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA	601308121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5	Homo sapiens hyaluronan synthase 2 (HAS;), mRNA	yg46f01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'	Mus musculus phosphatidylinositd-4-phosphate 5-khase, type 1 gamma (Plp5K1c), mRNA	602124743F1 NIH_MGC_56 Homo seplens cDNA clone IMAGE:4281611 5'	602124743F1 NIH_MGC_56 Homo saplens; cDNA clone IMAGE:4281611 5'	qi81e11.x1 NOL_CGAP_Kid3 Homo seplens cDNA clone IMAGE:1863980 3' similer to gb:S66700 HYDROXYMETHYLGLUTARYL-COA LYA3E PRECURSOR (HUMAN);	yb47h08.st Stratagene fetal spleen (#837205) Homo saptens cDNA clone IMAGE:74367 3' similar to similar to chemonase mac HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)	SAGESTALL MODES LINE AND SET LINES AND SERVE HANDE SANDERS AND SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SE	00188359ZF1 NIN_MCC_5/ noing septens contactions to the
	Top Hit Database Source	EST_HUMAN	١	SWISSPROT	TN	NT	EST_HUMAN	EST HUMAN	NT		T_HUMAN	NT	NT	NT	NT	SWISSPROT	LN	NT	IN	EST_HUMAN	EST_HUMAN	NT		EST_HUMAN	NT	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	EST HUMAN	MAMILIA TOT		EST_HUMAN
	Top Hit Acession No.	T06813.1	-07288.1	083217	3.2E-01 AF157625.1	139874.1	3.2E-01 BE386776.1	3.1E-01 R18051.1	7661971 NT	7681971 NT	3.1E-01 AW62B038.1	3.1E-01 AB029069.1	3.1E-01 AJ251589.1	3.1E-01 AE003984.1	3.1E-01 AF176111.1	P44132	3.1E-01 Z74883.1	3.1E-01 Y1327B.1	3.1E-01 AF184122.1	3.1E-01 AW983549.1	3.1E-01 AI284458.1	3.1E-01 X71887.1	3.1E-01 AW377354.1	3.1E-01 BE737392.1	4885390 NT	3.1E-01 R45318.1	6679322 NT	BF696639.1	3.1E-01 BF696639.1	3.1E-01 AI244001.1	2 4E 04 TEE30E 4	1 00000	3.1E-01 BF216117.1
	Most Similar (Top) Hit BLAST E Value	3.2E-01 T06813.1	3.2E-01 L07288.1	3.2E-01 083217	3.2E-01	3.2E-01 L39874.1	3.2E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01 P44132	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01		3.15-01	3.15-01	9 10 04	3.15-01	3.1E-01
-	Expression Signal	3.05	3.11	3.26	22	2.07	1.24	3.30	3.77	3.77	1.28	3.51	0.94	7.0	9.24	0.7	0.75	0.83	2.65	1.3	96.0	0.79	0.69	2:32	2.0	0.84	89.0	1.04	1.04	168	o c	08.0	1.84
-	ORF SEQ ID NO:	37620					31546	28967		28986			30181	31177		32205	32206		32390					31491	34416		L						37789
	Exon SEQ ID NO:	23988	26083		L	1	26129		L	1_	L		17173		18780	18910	18911	18922	19080	ı		乚	L	L_	20911		L_		L	1	1	- 1	24151
	Probe SEQ ID NO:	10905	12289	12861	12069	13018	13089	2736	2782	2782	2920	3242	4016	5077	5695	5717	5718	5729	5892	6595	6863	6821	6805	7109	7856	8849	10108	10272	10272	10334	1	Dien	11076

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
11474	24533	l			.1E-01 AW074910.1	EST_HUMAN	xa62g09.x1 NCI_CGAP_HSC2 Homo saplens cDNA clone IMAGE:2571424 3'
11827	Ι.	38507		3.1E-01	T062291 NT	뉟	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
							yg89505.rt Soares infant brain 1NIB Homo sepiens cDNA clone IMAGE:40722 5' similar to contains Alu
11828	24817	38508	1.67	ຕ	.1E-01 R55735.1	EST_HUMAN	repetitive element;
12123	25103		1.3		3.1E-01 AF195953.1	NT	Homo saplens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
							Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene
12418			1.22	3	.1E-01 AF294308.1	NT	for mitochondrial product
12455	25319		1.73		3.1E-01 AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12813			3.73	9	.1E-01 AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
	I.						Homo sepiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,
	_			•		ļ	JMTO protein. A4 differentiation-dependent protein, triple LIM domain protein o, and synaptionnysin genes,
13028	- 1		3.82	°	AF1967	Į.N.	complete cas, and L-type cacium original e
13068	20123		1.22			攴	Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), miklyA
74				3.0E-01	- 6755083 NT	F	Mus musculus protein kinase C, epsilon (Pkce), mRNA
264	L		11.52		3.0E-01 AJ271735.1	NT	Homo saplens Xq pseudoautosomal region; segment 1/2
1251	14410		2.35		3.0E-01 AW300400.1	EST_HUMAN	xs83f08.x1 NCI_CGAP_Kid11 Homo sapieirs cDNA clone IMAGE:2774343 31
1537	14690		5.77	8	.0E-01 AJ008755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1838	14984		1.2	3	3.0E-01 X99082.1	NT	A immersus putative gene encoding integrase, Mars2 (RP)
3069	16245		0.8	}	3.0E-01 AB008677.1	Z	Bos taurus mRNA for UDP-glucuronosytransfarasa, complete cds
3283	L_		1.33		3.0E-01 AB030481.1	NT	Corynebacterium sp. ALY-1 alyFG gene for polyguluronata lyase, complete cds
3968	17128	30129		Ì	3.0E-01 AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo suplens cDNA
4082	17237	30243	1.16	ľ	3.0E-01 AJ271736.1	IN	Homo sepiens Xq pseudoautosomal region; segment 2/2
4636	17772	30752	1.79	ì	3.0E-01 AJ006755.1	NT	Balænoptera physalus gene encoding atrial natriuretic peptide
5258	16849	29665	2.33	,	3.0E-01 P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5467	18667	L	6.1	·	3.0E-01 BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens;cDNA clone IMAGE:3948734 5
							Homo sapiens mannosidase, beta A, tysoscimal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
929	18745	31780	0.64		3.0E-01 AF224669.1	TN	(UBE2D3) genes, complete cds
5552	18749	31785	•	3.0E-01	3.0E-01 AF229247.1	INT	Cantagalo orthopoxyirus hemagglutinin gena, complete cds
5821	18815	31883	4.01		3.0E-01 BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo saplens cDNA
5621	18815	31884	4.01		3.0E-01 BE693575.1	EST HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo cepiens cDNA
5658	18852		3.87		3.0E-01 U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6970			2.82	;	3.0E-01 D16313.1	TN	Mouse cytokeratin 15 gene, complete cds
6669	ı				3.0E-01 U02369.1	LN	Strongy/ocentrotus purpuratus 34/67 kDa kiminin-binding protein mRNA, partial cds
7065		33532	1.15		3.0E-01 AF229247.1	NT	Centagelo orthopoxvirus hemagglutinin gene, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

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Doc	s Expressed in Pracenta	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C006	Mus musculus midnolin (Midn-panding), mRNA	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds	Thermotoga maritima section 67 of 138 of the complete genome	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Cleosfig) mRNA	H.sapiens gene for US snRNP-specific 200kD protein	601339079F1 NIH_MGC_53 Homo sapiens CDNA clone IMAGE:3681594 5'	Streptomyces sulfonofaciens isopenicilin N synthase (pcbC) gene, partial cds	Homo sapiens DKF2P586M0122 protein (DKF2P686M0122), mRNA	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosultransferase gene partial city; and unknown gene	HYPOTHETICAL 59.5 KD PROTEIN IN W.ZA-ASMA INTERGENIC REGIÓN	Synochacystis sp. PCC8803 complete genome, 6/27, 630555-781448	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'	Actinobacilus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadE), and TadG (tadG) genes, complete cds	Actinobacillus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE),	TedF (tedF), and TedG (tedG) genes, complete cds	xe03d10.x1 Soares_NFL_T_GBC_S1 Homis sepiens cDNA clane IMAGE::2606035 3'	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:194107 5	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5	PONTICULIN PRECURSOR	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA	Mus musculus mas proto-oncogene and Igi2r gene for insulin-like growth factor type 2 and L41ps and Au76	pseudoganes	Home sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA	Aquifex aeolicus section 68 of 109 of the complete genome	Chrysodidymus synuroideus mitochandrhan, complete genome	Xenopus lasvis transcription factor E2F mRNA, complete cds
Exan NO: 10 NO: 10 NO	Exon Probe	Top Hit Database Source	NT	IN	LN	NT	Ę	LZ.	EST_HUMAN	N F	TN	<u>F</u>	SWISSPROT	Ę	EST_HUMAN	Ę		닏	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	TN	LN		F	LN	NT	NT	NT
Exan NO:         ORF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Palue         Most Similar (Top) Hit Palue           20353         33806         0.86         3.0E-01           20735         34028         4.3         3.0E-01           20735         34214         1.51         3.0E-01           21736         34214         1.51         3.0E-01           21737         3528         0.48         3.0E-01           22703         36050         1.09         3.0E-01           227151         3628         0.64         3.0E-01           227151         36380         0.82         3.0E-01           227151         36980         0.64         3.0E-01           227151         36992         0.45         3.0E-01           23840         37246         0.64         3.0E-01           23841         37246         0.64         3.0E-01           23642         37246         0.64         3.0E-01           23643         3771         0.76         3.0E-01           25643         38755         2.16         3.0E-01           26042         3.0E-01         3.0E-01           26042         3.0E-01 <td< td=""><td>Singi</td><td>Top Hit Acession No.</td><td>4L163206.2</td><td>10947007</td><td>4F071810.1</td><td>4E001755.1</td><td>9940164</td><td>270200.1</td><td>3E566083.1</td><td>4F141676.1</td><td>7661685</td><td>A E000607 4</td><td>P76389</td><td>D90904.1</td><td>BF5746121</td><td>AF152598.3</td><td></td><td>AF152598.3</td><td>AW118111.1</td><td>AB030231.1</td><td>BF683841.1</td><td>BF683841.1</td><td></td><td></td><td></td><td></td><td>9977799</td><td></td><td>AJ249895.1</td><td>5174502</td><td>AE000736.1</td><td>AF222718.1</td><td>AF078111.1</td></td<>	Singi	Top Hit Acession No.	4L163206.2	10947007	4F071810.1	4E001755.1	9940164	270200.1	3E566083.1	4F141676.1	7661685	A E000607 4	P76389	D90904.1	BF5746121	AF152598.3		AF152598.3	AW118111.1	AB030231.1	BF683841.1	BF683841.1					9977799		AJ249895.1	5174502	AE000736.1	AF222718.1	AF078111.1
Exan NO:         ORF SEQ ID NO:         Express Signa Signa 207353         Express 34214           207353         33806         34214           207353         34214         34713           217363         34214         34713           217371         35286         227103           227103         34606         227103           227103         35649         227103           227103         35692         227103           227103         36902         227103           23261         37246         23260           23381         36902         23266           23381         36902         23266           23381         36902         23266           23381         36902         23266           23663         37271         23663           25048         38756         25048           26042         26042         16020           16020         28340         16450           16427         29445		Similar p) Hit \ST E alue	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	20 E 04	3.0E-01	3.0E-01	3.0E-01	3.05-01		3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01		2.9€-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01
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		ORF SEQ ID NO:	33808												l	36992								ļ									
		Exen SEQ ID NO:	20353	20668	20735	21103	l	_I .	L		l			1		l <u>.</u>			_ }		23663	23683	25048	25048	25324	26062	26121				ı		1
			7270	7481	7670	8111	BERR	8658	8671	9029	9072	9,5	8778	9927	10173	10346		10348	10606	10608	10629	10829	12087	12067	12470	12731	13061		1771	1930	2080	2322	3253

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					26		
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Tap Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
3323	16496	29513		37	IE-01 AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Honio sapiens cDNA
3323	l		2.88	25	3E-01 AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sepiens cDNA
4003	L			55	E-01 AI610836.1	EST HUMAN	fp21a11 x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN),contding cloment L1 repetitive element ;
170		L		l	A1750472 1	EST HIMAN	wj14drj0.x1 NCI_CGAP_Kid12 Homo sapielis cDNA clone IMAQE:2402803 3' strnilar to WP:C34F6.7 CF15678
245	1		0.00		2.9E-01 AB016428.1	N	Cavia porcellus mRNA for glutatrione s-transferase, complete cds
4185					AW002902.1	EST HUMAN	wr02f10.x1 NCI_CGAP_GC8 Homo saplens cDNA clone IMAGE:2480385 3'
					A A 284 488 4	EST HIMAN	2857d12.r1 NCL_CGAP_GCB1 Homo saplens cDNA clone IMAGE:701591 5' similar to contains Aluranditive element
4008	17/40	30124		1	2 9F-01 At 163207 2		Homo seplens chromosome 21 segment HS21C007
7307		31083	65.0			Į.	Mus musculus gene, complete cds, similar to EXLM1
	1_			İ	Γ		wa08f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.t2 L1
5222	18344		0.89		2.9E-01 AI670899.1	EST_HUMAN	repetitive element ;
5320	1	31083				TN	Mus musculus gene, complete cds, similar to EXLM1
6372	ı		1.59			EST_HUMAN	y77e12.s1 Scares Infant brain 1NIB Homo septens cDNA clone IMAGE:28291 3'
5511		33656		<u> </u>		IN	Suaeda maritima subsp. salsa S-adenosymethionine sythetase 2 mRNA, complete cds
	ľ			<u> </u>			B. subtilis levanase operon levD, levE, levF, levC and sacC (partial) genes for fructose phosphotransferase
5884	18073	32381	5.27	2	9E-01 X56098.1	LN	system polypepudes P10,16,26,30 end tevanase
	l				2 00 04 ×40000 1	Ę	B. subtilis (evanase operon levD, levE, levF, levF and sacC (parda) genes for fructose phosphotransferase
800	┙				ACCOSO. I	I-N	Miss misserilis Enh recentor A8 (Enhaß) mRNA
268	40357	32287	1,55	1	AA41814	EST HUMAN	2x97b12.rt Soares, NhHMPu_S1 Homo sapiens cDNA clone IMAGE:787711 5
5	L						we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.f1 L1
6411	19580	32841	1.07		AI797128.1	EST_HUMAN	repetitive element;
6455	ı				U03420.1	N	Bos taurus myosin i mRNA, complete cds
7007			0.71		AF321001.1	LN	Suaeda maritima subsp. selsa S-adenosymethionine sythetase 2 mRNA, complete cds
7128	L				AF142329.1	NT	Mus musculus Filih protein (Filih) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7245				L	2.9E-01 Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR508C
	L			_			Mus musculus major histocompatibility locus class il region; Fas-binding protein Daxx (DAXX) gene, partial
				•			ods, Brig1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-
7310	- 1	1			2.9E-01 AF100956.1	Z	galectosy fransferase (beta1,3-galactosy ti>
8104	1 21186	34705	1,61		BE540422.1	EST HUMAN	601055530-1 NIH MCC. 10 Homo saptents CLON Grote IMMCE. 3452507 5
8104					BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiers clina clore image:3432207 3

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Exan NO: SEQ ID NO: 21424 21424 21424 224424 22524 225311 22563 22440 23440 23440 23440 23440 23440 23440 23440 23440 23440 23440 23440 23440 23440 23440 235519 25519 25519 25519 25519 14452 25519 14452 114452

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(Top) Hit Top Hit Acession Database BLASTE No. Source	Top Hit Descriptor
2.8E-01 U85300.1	Orthogeomys heterodus cytochrome b (cytb)/gene, mitochandrial gene encoding mitochandrial protein, compiete cds
2.8E-01 U05633.1 NT	Marsilea quadrífolla ribulose-1,5-bisphosphate carboxylaso/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cde
2.8E-01 AI346126.1 EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo saplens cDNA clone IMAGE:1926289 3' similar to gb;X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
2.8E-01 AI346126.1 EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
	Homo saplens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
2.8E-01 AA911629.1 EST_HUMAN	of02h05.s1 NCI_CGAP_Co12 Homo saplens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
7.1	802022987F1 NCI_CGAP_Brr67 Homo saplens cDNA clone IMAGE:4138525 5
	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
	Lycopersicon esculentum peroxidase (TPX1) mRNA, complete cds
2.8E-01 AF132728.1 NT	Escherichte coli translocated Intimin receptor Tir (tir) gene, complete cds
	Escherichia coli translocated intimin receptor, Tir (tir) gene, complete cds
2.8E-01 AE001310.1 NT	Chlamydia trachomatis section 37 of 87 of the complete genome
2 BE-01 A F2943G3 1 NT	Rattus nonvegicus glycerot-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
36163	Homo sapiens hypothetical protein (LOC61319), mRNA
2.8E-01 9626164 NT	Fujinami sarcoma virus, complete genome
	1801654822R1 NIH_MGC_57 Homo saptens cDNA clone IMAGE:3839765 3'
	601880794F1 NIH_MGC_55 Hamo saplens cDNA clone IMAGE:4109350 5'
2.8E-01 BF241062.1   EST_HUMAN	601880794F1 NIH_MGC_56 Hamo saptens cDNA clone IMAGE:4109350 5
2.8E-01 BF695970.1   EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5
	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, excns 1 through 7
	and complete cas
	יסטקיפילאוסרן אווא וואופר סט רומווס אבטיפוא כוטופ וואיא חבר אדי ססטט ט
	Pyrococcus abysis complete genome: segment 3/0
2.8E-01 AJ248285.1 NT	Pyrococcus abyssi complete genome; segment 3/6
	Mus musculus DNA for prostaglandin D2 synthase, complete cds
	PM4-HT0606-030400-001-a07 HT0806 Horino sapiens cDNA
BE9001	601673020F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3955996 5'
11433629	Homo sepiens CDC42-binding protein kinasie beta (DMPK-like) (CDC42BPB), mRNA
1.1 1.1 1433629	T HUMAN

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| Top Hit Descriptor                            | Zattus norvegicus CDK104 mRNA                     | ecabrio et Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE: 788827 3' similar to contains Alu repetitive element;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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Acession<br>Veltue<br>Source<br>Source<br>13643         Top Hit Acession<br>Veltue<br>Source<br>13644         Top Hit Acession<br>Veltue<br>Source<br>13644         Top Hit Acession<br>Veltue<br>Source<br>13644         Top Hit Acession<br>Veltue<br>Source<br>13644         NT         NT           14848         27512         2.04         2.7E-01 AB004906.1         NT         NT           14803         3.7E-01 X79815.1         NT         NT         NT | Exon SEQ ID         ORF SEQ ID NO:         Expression Signal LAST E         Top Hit Top Hit Acession Signal No:         Top Hit Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Top Hit Acession No:         Top Hit Acession Signal No:         Top Hit Acession Signal No:         Top Hit Acession No:         Top Hit Acession Signal No:         Top Hit Acession Signal No:         Top Hit Acession Signal No:         Top Hit Acession Signal No:         Top Hit Acession Signal No:         Top Hit Acession Signal No:        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    Top Hit Top Hit Top Hit Acession Source Source Source No.         Top Hit Top Hit Top Hit Acession Source Source Source No.         Top Hit Top Hit Top Hit Top Hit Acession Source Source No.         Top Hit Top Hit Top Hit Top Hit Acession Source Source No.         Top Hit Top Hit Top Hit Top Hit Acession Source Source No.         Top Hit Top Hit Top Hit Top Hit Acession Source Source No.         Top Hit Top Hit Top Hit Acession No.         Top Hit Top Hit Top Hit Acession No.         Top Hit Top Hit Acession No.         Top Hit Top Hit Acession No.         Top Hit Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         Top Hit Acession No.         < | Exan<br>SEQ ID<br>ID NO:         CRF SEQ<br>Signal<br>Signal         Most Similar<br>(Top) Ht<br>Value         Top Hit<br>No.         Top Hit<br>Source           13683         28717         4.34         2.7E-01         Y17324.1         NT           13813         28835         13.64         2.7E-01         A4450061.1         EST HUMAN           14848         27512         2.04         2.7E-01         A8004806.1         NT           14903         1.63         2.7E-01         W58067.1         EST HUMAN           14968         28059         1.46         2.7E-01         W58067.1         EST HUMAN           16657         2.7E-01         M58067.1         EST HUMAN           14868         28059         1.46         2.7E-01         W58067.1         EST HUMAN           16657         2.7E-01         M58067.1        
EST HUMAN           12.7E-01         M58067.1         EST HUMAN           14868         28059         1.46         2.7E-01         W58067.1         EST HUMAN           15057         2.7E-01         M5047676.1         NT | Exam<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal<br>ID NO:         Expression<br>Signal<br>Signal<br>Analysis         Most Similar<br>LASTE<br>Value<br>Analysis         Top Hit<br>No:<br>Signal<br>Value<br>Analysis         Top Hit<br>Detabase<br>Source<br>Analysis           13813         28835         13.64         2.7E-01         Y17324.1         NT           14803         27512         2.04         2.7E-01         AA450061.1         EST_HUMAN           14917         28012         3.16         2.7E-01         W89067.1         EST_HUMAN           14966         28059         1.46         2.7E-01         W89067.1         EST_HUMAN           15057         3.1         2.7E-01         M68067.1         SWISSPROT           16057         3.1         2.7E-01         M68067.1         EST_HUMAN           15383         28510         0.94         2.7E-01         AR5047572.1         EST_HUMAN | Exam<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal<br>ID NO:         Expression<br>Signal<br>Signal<br>ID NO:         Most Similar<br>Signal<br>Value<br>A34         Top Hit Acession<br>Value<br>A450061.1         Top Hit Acession<br>Detabase<br>Source<br>A450061.1         Top Hit Acession<br>Source<br>A450061.1         Top Hit Acession<br>A450061.1         Top Hit Ace | Exan<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>ID NO:         Expression<br>Signal<br>Signal<br>ID NO:         Most Similar<br>Signal<br>Value<br>A:34         Top Hit Acession<br>Value<br>A:34         Top Hit Acession<br>Value<br>A:34         Top Hit Acession<br>Value<br>A:34         Top Hit Acession<br>Value<br>A:34         Top Hit Acession<br>A:34         Database<br>A:3604:1         Database<br>A:3604:1 <t< td=""><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal<br/>Signal         Most Similar<br/>Veltue         Top Hit<br/>No:         Top Hit<br/>Source           13683         26717         4.34         2.7E-01         Y17324.1         NT           13813         28835         13.64         2.7E-01         AA450061.1         EST HUMAN           14448         27512         2.04         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         M58067.1         EST HUMAN           14907         28012         3.16         2.7E-01         W58067.1         EST HUMAN           16057         3.1         2.7E-01         W58067.1         EST HUMAN           16383         28510         0.94         2.7E-01         A8047772.1         EST HUMAN           16581         28611         0.94         2.7E-01         A8047772.1         EST HUMAN           15583         28611         0.94         2.7E-01         A8047772.1         EST HUMAN           15583         28611         0.94         2.7E-01         A80478772.1         EST HUMAN           15583         28611         0.94         2.7E-01         A80488.1         NT           15584         275-01         <t< td=""><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>Top Hit<br/>Veltue         Top Hit<br/>No:         Top Hit<br/>Source           13683         26717         4.34         2.7E-01         Y17324.1         NT           13683         26717         4.34         2.7E-01         A450061.1         EST HUMAN           14448         27512         2.04         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         W58057.1         EST HUMAN           16057         3.16         2.7E-01         W58057.1         EST HUMAN           1638         28510         0.94         2.7E-01         A80577.1         EST HUMAN           16581         28611         0.94         2.7E-01         A1372772.1         EST HUMAN           15563         28615         0.94         2.7E-01         A1372772.1         EST HUMAN           15563         28615         0.94         2.7E-01         A1372772.1         EST HUMAN           16561         28615         0.94         2.7E-01         A1310868.1         NT           16562         27E-01         A1310868.1</td><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>Frop) Hit<br/>PLASTE         Top Hit<br/>No:         Top Hit<br/>Postates         Top Hit<br/>Postates           13683         26717         4.34         2.7E-01         Most Similar<br/>Netton         13.64         2.7E-01         Most Similar<br/>No:         NT           14448         27512         2.04         2.7E-01         A85004906.1         NT           14803         1.63         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         Most Simple Not Not Not Not Not Not Not Not Not Not</td><td>Exam<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>ID NO:         Most Similar<br/>Signal<br/>Value<br/>IASS         Top Hit Acession<br/>Value<br/>IASS         Top Hit Acession<br/>IASS         Top Hit</td><td>Exam<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Appression<br/>Signal<br/>Signal<br/>ID NO:         Most Similar<br/>Signal<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>IAA48         Top Hit Acession<br/>IAA480         Top Hit Acession<br/>IAA480</td><td>Exam<br/>NO:<br/>13813         ORF SEQ<br/>201D<br/>200.         Expression<br/>Signal<br/>200.         Most Similar<br/>Frop Hit<br/>Value<br/>3.16         Top Hit Acession<br/>Value<br/>2.7E-01         Top Hit Acession<br/>No.<br/>2.7E-01         Top Hit Acession<br/>No.<br/>2.7</td><td>Exam<br/>NO:<br/>13813         ORF SEQ<br/>201D<br/>201D<br/>20222         Expression<br/>Signal<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D</td><td>Exam<br/>NO:<br/>13683         ORF SEQ<br/>2801D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>200</td><td>Exan<br/>NO:<br/>13883         ORF SEQ<br/>250 ID<br/>10 NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID
NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID 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      14803         2.8012         3.16         2.7E-01         AF047675.1         NT           14804         2.8012         3.16         2.7E-01         AF047675.1         NT           14805         2.8050         1.46         2.7E-01         AF047675.1         NT           15383         2.8611         0.94         2.7E-01         AF047675.1         NT           16533         2.8650         7.07         2.7E-01         AF047677.1         NT           16533         2.8650         7.07         2.7E-01         AF216214.1         NT           17286</td><td>Exan<br/>NO:<br/>13813         ORF SEQ<br/>201D<br/>201D<br/>20271         Expression<br/>Signal<br/>Annual         Most Similar<br/>Fraction         Top Hit Acession<br/>Value<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Detabase<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Annual         Top Hit Acession<br/>Annu</td><td>Exam<br/>NO:<br/>13813         ORF SEQ<br/>2010<br/>2010<br/>2010<br/>2010<br/>2010<br/>2010<br/>2010<br/>201</td><td>Exan ORF SEQ Fignal SEQ ID NO:         CRP SEQ Expression Signal ID NO:         CTop Hit Top Hit Top Hit Acession Patabase Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Native Native         Top Hit Top Hit Top Hit Acession Native Native         Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Native Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Nati</td><td>Exan<br/>SEQ ID<br/>ID NO:         CRF SEQ<br/>Signal<br/>I3813         Expression<br/>Signal<br/>Signal<br/>I3813         Top Hit Acession<br/>Signal<br/>Value<br/>I3813         Top Hit Acession<br/>Signal<br/>I3813         Top Hit Acession<br/>Value<br/>I3813         Top Hit Acession<br/>Value<br/>I3813         Top Hit Acession<br/>I3813         Top</td><td>Expn<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Value<br/>Signal<br/>Value         (Top) Hit<br/>Top Hit Acession<br/>Value         Top Hit Acession<br/>Value<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit<br/>Source           13813         28835         13.64         2.7E-01         M732A-1         NT           14486         27512         2.04         2.7E-01         A4450061-1         EST HUMAN           14907         28012         3.16         2.7E-01         M80567-1         EST HUMAN           14907         28012         3.16         2.7E-01         M80667-1         EST HUMAN           16583         28651         0.84         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A137280-1         NT           16583         28655         7.07         2.7E-01         A137280-1         NT           16583         28655         7.07         2.7E-01         A1310858-1         NT</td><td>Exan<br/>SEQ ID<br/>ID NO:<br/>13813         CRF SEQ<br/>Signal<br/>260 ID NO:<br/>13813         Expression<br/>261 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2137 ID NO:<br/>2137 ID NO:<br/>2138 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID 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ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2</td><td>Exan<br/>NO:         CRF SEQ<br/>ID NO:         Expression<br/>Signal<br/>Signal         (Top) Hit<br/>Value         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           138813         26835         13.64         2.7E-01         2.7E-01         Y17324.1         NT           14448         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.052         2.04         2.7E-01         W58056.1         EST_HUMAN           14907         28012         3.16         2.7E-01         W58057.1         EST_HUMAN           14908         2.8056         1.46         2.7E-01         W58057.1         EST_HUMAN           16533         28610         0.84         2.7E-01         M58057.1         EST_HUMAN           16533         28651         0.94         2.7E-01         M58057.1         EST_HUMAN           16533         286547         0.66         2.7E-01         M58058.1         MT           17226         30281         0.84         2.7E-01         M58058.1         MT           17226         30281         0.86         2.7E-01         M58058.1         MT           17226         30281         0.86         2.7E-01         M78058.1<td>Exan<br/>NO:         CRF SEQ<br/>ID NO:         Expression<br/>Signal<br/>Public         (Top) Hit<br/>Value         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           13883         26177         4.34         2.7E-01         Y17324.1         NT           14480         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.0612         3.16         2.7E-01         W58067.1         EST_HUMAN           14906         2.8059         1.46         2.7E-01         W58067.1         EST_HUMAN           16533         22811         0.84         2.7E-01         M58067.1         EST_HUMAN           16533         228510         0.94         2.7E-01         M79067.1         EST_HUMAN           16533         228511         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.56         2.7E-01         M7372772.1         EST_HUMAN           17226         30281         0.66         2.7E-01         M7516214</td></td></t<></td></t<> | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal<br>Signal         Most Similar<br>Veltue         Top Hit<br>No:         Top Hit<br>Source           13683         26717         4.34         2.7E-01         Y17324.1         NT           13813         28835         13.64         2.7E-01         AA450061.1         EST HUMAN           14448         27512         2.04         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         M58067.1         EST HUMAN           14907         28012         3.16         2.7E-01         W58067.1         EST HUMAN           16057         3.1         2.7E-01         W58067.1         EST HUMAN           16383         28510         0.94         2.7E-01         A8047772.1         EST HUMAN           16581         28611         0.94         2.7E-01         A8047772.1         EST HUMAN           15583         28611         0.94         2.7E-01         A8047772.1         EST HUMAN           15583         28611         0.94         2.7E-01         A80478772.1         EST HUMAN           15583         28611         0.94         2.7E-01         A80488.1         NT           15584         275-01 <t< td=""><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>Top Hit<br/>Veltue         Top Hit<br/>No:         Top Hit<br/>Source           13683         26717         4.34         2.7E-01         Y17324.1         NT           13683         26717         4.34         2.7E-01         A450061.1         EST HUMAN           14448         27512         2.04         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         W58057.1         EST HUMAN           16057         3.16         2.7E-01         W58057.1         EST HUMAN           1638         28510         0.94         2.7E-01         A80577.1         EST HUMAN           16581         28611         0.94         2.7E-01         A1372772.1         EST HUMAN           15563         28615         0.94         2.7E-01         A1372772.1         EST HUMAN           15563         28615         0.94         2.7E-01         A1372772.1         EST HUMAN           16561         28615         0.94         2.7E-01         A1310868.1         NT           16562         27E-01         A1310868.1</td><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>Frop) Hit<br/>PLASTE         Top Hit<br/>No:         Top Hit<br/>Postates         Top Hit<br/>Postates           13683         26717         4.34         2.7E-01         Most Similar<br/>Netton         13.64         2.7E-01         Most Similar<br/>No:         NT           14448         27512         2.04         2.7E-01         A85004906.1         NT           14803         1.63         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         Most Simple Not Not Not Not Not Not Not Not Not Not</td><td>Exam<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>ID NO:         Most Similar<br/>Signal<br/>Value<br/>IASS         Top Hit Acession<br/>Value<br/>IASS         Top Hit Acession<br/>IASS         Top Hit</td><td>Exam<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Appression<br/>Signal<br/>Signal<br/>ID NO:         Most Similar<br/>Signal<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>Value<br/>IAA48         Top Hit Acession<br/>IAA48         Top Hit Acession<br/>IAA480         Top Hit Acession<br/>IAA480</td><td>Exam<br/>NO:<br/>13813         ORF SEQ<br/>201D<br/>200.         Expression<br/>Signal<br/>200.         Most Similar<br/>Frop Hit<br/>Value<br/>3.16         Top Hit Acession<br/>Value<br/>2.7E-01         Top Hit Acession<br/>No.<br/>2.7E-01         Top Hit Acession<br/>No.<br/>2.7</td><td>Exam<br/>NO:<br/>13813         ORF SEQ<br/>201D<br/>201D<br/>20222         Expression<br/>Signal<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D<br/>201D</td><td>Exam<br/>NO:<br/>13683         ORF
SEQ<br/>2801D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>2001D<br/>200</td><td>Exan<br/>NO:<br/>13883         ORF SEQ<br/>250 ID<br/>10 NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID NO:<br/>219 ID 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2.7E-01         Y17324.1         NT           1448B         27512         2.04         2.7E-01         AA450061.1         EST_HUMAN           14803         1.63         2.7E-01         AB004906.1         NT           14803         2.8012         3.16         2.7E-01         AB004906.1         NT           14803         2.8012         3.16         2.7E-01         AA50061.1         EST_HUMAN           14803         2.8012         3.16         2.7E-01         AF047675.1         NT           14804         2.8012         3.16         2.7E-01         AF047675.1         NT           14805         2.8050         1.46         2.7E-01         AF047675.1         NT           15383         2.8611         0.94         2.7E-01         AF047675.1         NT           16533         2.8650         7.07         2.7E-01         AF047677.1         NT           16533         2.8650         7.07         2.7E-01         AF216214.1         NT           17286</td><td>Exan<br/>NO:<br/>13813         ORF SEQ<br/>201D<br/>201D<br/>20271         Expression<br/>Signal<br/>Annual         Most Similar<br/>Fraction         Top Hit Acession<br/>Value<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Detabase<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Annual         Top Hit Acession<br/>Source<br/>Annual         Top Hit Acession<br/>Annual         Top Hit Acession<br/>Annu</td><td>Exam<br/>NO:<br/>13813         ORF SEQ<br/>2010<br/>2010<br/>2010<br/>2010<br/>2010<br/>2010<br/>2010<br/>201</td><td>Exan ORF SEQ Fignal SEQ ID NO:         CRP SEQ Expression Signal ID NO:         CTop Hit Top Hit Top Hit Acession Patabase Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Native Native         Top Hit Top Hit Top Hit Acession Native Native         Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Native Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Nati</td><td>Exan<br/>SEQ ID<br/>ID NO:         CRF SEQ<br/>Signal<br/>I3813         Expression<br/>Signal<br/>Signal<br/>I3813     
   Top Hit Acession<br/>Signal<br/>Value<br/>I3813         Top Hit Acession<br/>Signal<br/>I3813         Top Hit Acession<br/>Value<br/>I3813         Top Hit Acession<br/>Value<br/>I3813         Top Hit Acession<br/>I3813         Top</td><td>Expn<br/>SEQ ID<br/>ID NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Value<br/>Signal<br/>Value         (Top) Hit<br/>Top Hit Acession<br/>Value         Top Hit Acession<br/>Value<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit<br/>Source           13813         28835         13.64         2.7E-01         M732A-1         NT           14486         27512         2.04         2.7E-01         A4450061-1         EST HUMAN           14907         28012         3.16         2.7E-01         M80567-1         EST HUMAN           14907         28012         3.16         2.7E-01         M80667-1         EST HUMAN           16583         28651         0.84         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A137280-1         NT           16583         28655         7.07         2.7E-01         A137280-1         NT           16583         28655         7.07         2.7E-01         A1310858-1         NT</td><td>Exan<br/>SEQ ID<br/>ID NO:<br/>13813         CRF SEQ<br/>Signal<br/>260 ID NO:<br/>13813         Expression<br/>261 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2136 ID NO:<br/>2137 ID NO:<br/>2137 ID NO:<br/>2138 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID 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NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2139 ID NO:<br/>2</td><td>Exan<br/>NO:         CRF SEQ<br/>ID NO:         Expression<br/>Signal<br/>Signal         (Top) Hit<br/>Value         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           138813         26835         13.64         2.7E-01         2.7E-01         Y17324.1         NT           14448         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.052         2.04         2.7E-01         W58056.1         EST_HUMAN           14907         28012         3.16         2.7E-01         W58057.1         EST_HUMAN           14908         2.8056         1.46         2.7E-01         W58057.1         EST_HUMAN           16533         28610         0.84         2.7E-01         M58057.1         EST_HUMAN           16533         28651         0.94         2.7E-01         M58057.1         EST_HUMAN           16533         286547         0.66         2.7E-01         M58058.1         MT           17226         30281         0.84         2.7E-01         M58058.1         MT           17226         30281         0.86         2.7E-01         M58058.1         MT           17226         30281         0.86         2.7E-01         M78058.1<td>Exan<br/>NO:         CRF SEQ<br/>ID NO:         Expression<br/>Signal<br/>Public         (Top) Hit<br/>Value         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           13883         26177         4.34         2.7E-01         Y17324.1         NT           14480         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.0612         3.16         2.7E-01         W58067.1         EST_HUMAN           14906         2.8059         1.46         2.7E-01         W58067.1         EST_HUMAN           16533         22811         0.84         2.7E-01         M58067.1         EST_HUMAN           16533         228510         0.94         2.7E-01         M79067.1         EST_HUMAN           16533         228511         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.56         2.7E-01         M7372772.1         EST_HUMAN           17226         30281         0.66         2.7E-01         M7516214</td></td></t<> | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>Top Hit<br>Veltue         Top Hit<br>No:         Top Hit<br>Source           13683         26717         4.34         2.7E-01         Y17324.1         NT           13683         26717         4.34         2.7E-01         A450061.1         EST HUMAN           14448         27512         2.04         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         W58057.1         EST HUMAN           16057         3.16         2.7E-01         W58057.1         EST HUMAN           1638         28510         0.94         2.7E-01         A80577.1         EST HUMAN           16581         28611         0.94         2.7E-01         A1372772.1         EST HUMAN           15563         28615         0.94         2.7E-01         A1372772.1         EST HUMAN           15563         28615         0.94         2.7E-01         A1372772.1         EST HUMAN           16561         28615         0.94         2.7E-01         A1310868.1         NT           16562         27E-01         A1310868.1 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>Frop) Hit<br>PLASTE         Top Hit<br>No:         Top Hit<br>Postates         Top Hit<br>Postates           13683         26717         4.34         2.7E-01         Most Similar<br>Netton         13.64         2.7E-01         Most Similar<br>No:         NT           14448         27512         2.04         2.7E-01         A85004906.1         NT           14803         1.63         2.7E-01         A8004906.1         NT           14803         1.63         2.7E-01         Most Simple Not Not Not Not Not Not Not Not Not Not | Exam<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal<br>ID NO:         Expression<br>Signal<br>Signal<br>Signal<br>ID NO:         Most Similar<br>Signal<br>Value<br>IASS         Top Hit Acession<br>Value<br>IASS         Top Hit Acession<br>IASS         Top Hit | Exam<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal<br>ID NO:         Appression<br>Signal<br>Signal<br>ID NO:         Most Similar<br>Signal<br>Value<br>IAA48         Top Hit Acession<br>Value<br>IAA48         Top Hit Acession<br>Value<br>IAA48         Top Hit Acession<br>Value<br>IAA48         Top Hit Acession<br>Value<br>IAA48         Top Hit Acession<br>IAA48         Top Hit Acession<br>IAA480         Top Hit Acession<br>IAA480 | Exam<br>NO:<br>13813         ORF SEQ<br>201D<br>200.         Expression<br>Signal<br>200.         Most Similar<br>Frop Hit<br>Value<br>3.16         Top Hit Acession<br>Value<br>2.7E-01         Top Hit Acession<br>No.<br>2.7E-01         Top Hit Acession<br>No.<br>2.7 | Exam<br>NO:<br>13813         ORF SEQ<br>201D<br>201D<br>20222         Expression<br>Signal<br>201D<br>201D<br>201D<br>201D<br>201D<br>201D<br>201D<br>201D | Exam<br>NO:<br>13683         ORF
SEQ<br>2801D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>2001D<br>200 | Exan<br>NO:<br>13883         ORF SEQ<br>250 ID<br>10 NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID NO:<br>219 ID 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   AB004906.1         NT           14803         2.8012         3.16         2.7E-01         AB004906.1         NT           14803         2.8012         3.16         2.7E-01         AA50061.1         EST_HUMAN           14803         2.8012         3.16         2.7E-01         AF047675.1         NT           14804         2.8012         3.16         2.7E-01         AF047675.1         NT           14805         2.8050         1.46         2.7E-01         AF047675.1         NT           15383         2.8611         0.94         2.7E-01         AF047675.1         NT           16533         2.8650         7.07         2.7E-01         AF047677.1         NT           16533         2.8650         7.07         2.7E-01         AF216214.1         NT           17286 | Exan<br>NO:<br>13813         ORF SEQ<br>201D<br>201D<br>20271         Expression<br>Signal<br>Annual         Most Similar<br>Fraction         Top Hit Acession<br>Value<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Detabase<br>Source<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Annual         Top Hit Acession<br>Source<br>Annual         Top Hit Acession<br>Annual         Top Hit Acession<br>Annu | Exam<br>NO:<br>13813         ORF SEQ<br>2010<br>2010<br>2010<br>2010<br>2010<br>2010<br>2010<br>201                                          | Exan ORF SEQ Fignal SEQ ID NO:         CRP SEQ Expression Signal ID NO:         CTop Hit Top Hit Top Hit Acession Patabase Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Database Source Native         Top Hit Top Hit Top Hit Acession Native Native         Top Hit Top Hit Top Hit Acession Native Native         Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Top Hit Acession Native         Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Hit Top Hit Top Hit Top Hit Top Native         Top Hit Top Native Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Hit Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Native         Top Nati | Exan<br>SEQ ID<br>ID NO:         CRF SEQ<br>Signal<br>I3813         Expression<br>Signal<br>Signal<br>I3813         Top Hit Acession<br>Signal<br>Value<br>I3813         Top Hit Acession<br>Signal<br>I3813         Top Hit Acession<br>Value<br>I3813         Top Hit Acession<br>Value<br>I3813         Top Hit Acession<br>I3813         Top | Expn<br>SEQ ID<br>ID NO:         ORF SEQ<br>Signal<br>Signal<br>ID NO:         Expression<br>Signal<br>Value<br>Signal<br>Value         (Top) Hit<br>Top Hit Acession<br>Value         Top Hit Acession<br>Value<br>Source         Top Hit Acession<br>Source         Top Hit Acession<br>Source         Top Hit Acession<br>Source         Top
Hit<br>Source           13813         28835         13.64         2.7E-01         M732A-1         NT           14486         27512         2.04         2.7E-01         A4450061-1         EST HUMAN           14907         28012         3.16         2.7E-01         M80567-1         EST HUMAN           14907         28012         3.16         2.7E-01         M80667-1         EST HUMAN           16583         28651         0.84         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A1372772-1         EST HUMAN           16583         28655         7.07         2.7E-01         A137280-1         NT           16583         28655         7.07         2.7E-01         A137280-1         NT           16583         28655         7.07         2.7E-01         A1310858-1         NT | Exan<br>SEQ ID<br>ID NO:<br>13813         CRF SEQ<br>Signal<br>260 ID NO:<br>13813         Expression<br>261 ID NO:<br>2136 ID NO:<br>2136 ID NO:<br>2136 ID NO:<br>2136 ID NO:<br>2136 ID NO:<br>2136 ID NO:<br>2136 ID NO:<br>2137 ID NO:<br>2137 ID NO:<br>2138 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2139 ID NO:<br>2 | Exan<br>NO:         CRF SEQ<br>ID NO:         Expression<br>Signal<br>Signal         (Top) Hit<br>Value         Top Hit Acession<br>Value         Top Hit Acession<br>Source         Top Hit Acession<br>Source           138813         26835         13.64         2.7E-01         2.7E-01         Y17324.1         NT           14448         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.052         2.04         2.7E-01         W58056.1         EST_HUMAN           14907         28012         3.16         2.7E-01         W58057.1         EST_HUMAN           14908         2.8056         1.46         2.7E-01         W58057.1         EST_HUMAN           16533         28610         0.84         2.7E-01         M58057.1         EST_HUMAN           16533         28651         0.94         2.7E-01         M58057.1         EST_HUMAN           16533         286547         0.66         2.7E-01         M58058.1         MT           17226         30281         0.84         2.7E-01         M58058.1         MT           17226         30281         0.86         2.7E-01         M58058.1         MT           17226         30281         0.86         2.7E-01         M78058.1 <td>Exan<br/>NO:         CRF SEQ<br/>ID NO:         Expression<br/>Signal<br/>Public         (Top) Hit<br/>Value         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           13883         26177         4.34         2.7E-01         Y17324.1         NT           14480         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.0612         3.16         2.7E-01         W58067.1         EST_HUMAN           14906         2.8059         1.46         2.7E-01         W58067.1         EST_HUMAN           16533         22811         0.84         2.7E-01         M58067.1         EST_HUMAN           16533         228510         0.94         2.7E-01         M79067.1         EST_HUMAN           16533         228511         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.56         2.7E-01         M7372772.1         EST_HUMAN           17226         30281         0.66         2.7E-01         M7516214</td> | Exan<br>NO:         CRF SEQ<br>ID NO:         Expression<br>Signal<br>Public         (Top) Hit<br>Value         Top Hit Acession<br>Value         Top Hit Acession<br>Source         Top Hit Acession<br>Source           13883         26177         4.34         2.7E-01         Y17324.1         NT           14480         27512         2.04         2.7E-01         Y17324.1         NT           14803         2.0612         3.16         2.7E-01         W58067.1         EST_HUMAN           14906         2.8059         1.46         2.7E-01         W58067.1         EST_HUMAN           16533         22811         0.84         2.7E-01         M58067.1         EST_HUMAN           16533         228510         0.94         2.7E-01         M79067.1         EST_HUMAN           16533         228511         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.94         2.7E-01         M7372772.1         EST_HUMAN           16533         22851         0.56         2.7E-01         M7372772.1         EST_HUMAN           17226         30281         0.66         2.7E-01         M7516214 |

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			٠		Signific	ממטון ומשכן	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795		0.87		2.7E-01 Q01168	SWISSPROT	NITROGEN REGULATORY FROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	2.7E-01 Q01168	SWISSPROT	NITROGEN REGULATORY FROTEIN NUIT
7865	20919	34425	2.1	,	2.7E-01 AF248054.1	FN	Boo tauruo mioromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7865		34428	2.1	2.7E-01	2.7E-01 AF248054.1	LN	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	ı				2.7E-01 AA351121.1	EST_HUMAN	EST58740 Infant brain Homo seplens cDNA 5' end similar to similar to myosin-binding protein H
7917				,	2.7E-01 AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA, 5' end similar to similar to myosin-binding protein H
7976	21026				2.7E-01 L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosytransferase (UGT2B13) mRNA, complete cds
8048		34651	99'0		2.7E-01 AA013147.1	EST_HUMAN	ze35b11.s1 Soares retina N2b4HR Homo scipiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element;
8330	21412				2.7E-01 AW868503.1	EST_HUMAN	MR1-SN0062-100500-002-409 SN0062 Homo saplens cDNA
8380	1				2.7E-01 R39257.1	EST_HUMAN	yc91h06.s1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:23511 3'
8486	21567				2.7E-01 AL161552.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8928	1	L			2.7E-01 Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MV.P) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22599		10.58	,	2.7E-01   O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
8534	ı	36172			2.7E-01 O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9537	22602		2.68		2.7E-01 P37928	SWISSPROT	FIMBRIAE W PROTEIN
							Ratus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 8, 7, 8, 9, 10, 11,12, 13, 14, 15, 16, 17
10005	23043	36638	0.8		2.7E-01 D89660.1	. L	and complete cds
10286	23321	36923	6.0	,	2.7E-01 AF091848.1	NT	Oryctolegus ouniculus calgranulin C mRNA; partial ods
10323	23358	36968	2.06		2.7E-01 AF087434.1	LN	Mus musculus transcription factor NF-ATc isoform a (NF-ATca) mRNA, complete cds
10455					2.7E-01 AF156539.1	TN	Homo saplens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	J				2.7E-01 AF156539.1	TN.	Homo sapiens xeroderma pigmentosum coniplementation group C (XPC) gene, intron 9
10749	23782		0.51		2.7E-01 AB011679.1	Į,	Rattus novegicus mRNA for class I beta-tubulin, complete cds
10785	23798	37418	0.58		2.7E-01 AF281074.1	LN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10785	J_	37419	0.58		2.7E-01 AF281074.1	LN	Homo sapiens neuropilin 2 (NRP2) gans, complete cds, alternatively spliced
11050	L				2.7E-01 AV705043.1	EST_HUMAN	AV705043 ADB Homo saplens cDNA clone ADBCOD05 5
11050		37762			2.7E-01 AV705043.1	<b>EST_HUMAN</b>	AV705043 ADB Hamo saplens cDNA clone ADBCOD05 5
70077		<u> </u>			2 75 04 6 1482250 4	F	Homo sapiane caveolin-1/-2 locus, Contig1, D7S522, ganes CAV2 (exons 1, 2s, and 2b), CAV1 (exons 1 and
3	_]_	31116			A DODG 700 4		Andridamais theolisma mDNA for sulfide transferre commission of
12816	$\perp$		1.49		2.7E-01 AB008/82.1	Z	A ablaphys italiana inna ita aurate u aliane u angara a a a a a a a a a a a a a a a a a a
13034			2		2.7E-01 AF217491.1	LN.	Homo sapiens fragile 16D oxdo reductase (FOK) gene, exon 6
482	16013	26710	2.8		2.6E-01 P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

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					6		
Probs SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database · Source	Top Hit Descriptor
8	13688		1.94	2.6E-01	2.6E-01 D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	l.	27651	1.77	2.6E-01		EST_HUMAN	601510838F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3912345 5
1468	ı	L	1.09	2.6E-01		NT	Glycine max pseudogene for Bd 30K
1945	ł	28188	7.69	2.6E-01		NT	Arabidopsis thaliana DNA chromosome 4, contig fregment No. 2
1946	15088		7.69	2.6E-01	.6E-01 AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:lM14689_cds1 Mouse surfeit locus surfeit 3 protein gene
2159			10.39	2.6E-01		EST_HUMAN	(MOUSE);
2220	15354	28485	1.13	2.6E-01		NT	Human prealbumin gene, complete cds
2611			11.66		2.6E-01 BE272440.1	EST HUMAN	501126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5
3161	16336		1.11	2.6E-01	2.6E-01 AW974531.1	EST_HUMAN	EST386635 MAGE resequences, MAGM Homo sapiens cDNA
3671	16834	29845	0.84	2.6E-01	.6E-01 M22342.1	L	Bacteriphage T2 DNA-(adenine-N6)methyltreinsferase (dam) gene, complete cds
3733	1	ŀ		2.6E-01	.6E-01 AF229118.1	Ę	Homo sepiens eactycholineoterase collagen-ilke tall subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4215	17384	30352	0.79	2.6E-01	2.6E-01 AW959510.1	EST_HUMAN	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4270	ı			2.6E-01	.6E-01 BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-eC3 BT0630 Horrio sapiens cDNA
	į .	l				Ŀ	Enterococcus faecium strain N97-330 vanD giycopeptide resistance gene cluster, complete cds, and
4478				^	.8E-01 AF1 / 5283.1	Z	מושק אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אייסיוניים אוויסיוניים אוויסיוניים אוויסיים אוויסיים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיוניים אוויסיים איטיים אוויסיים אוויסיים איטיים אוויסיים איטייטיים אוויסייטיים אוויסייטיים אוויסייטיים אוויסייטיים אוויסייטיים אוויסייטיים אוויסייטיים אוויסייטיים אוויסייט
4817		30735			.6E-01 AB021180.1	¥	Gallus gallus mRNA for skeletal myosin hearly chain, complete das
4617			69'0		2.6E-01 AB021180.1	٤	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4870		l		7	.6E-01 AA457617.1	EST_HUMAN	as89d07.r1 Stratagene fetal refina 937202 Homo sapiens cDNA cione IMAGE:638477 5
4770	17905	30887	2.25	2	.6E-01 U01103.1	Ä	Arabidopsis thaliana PSI type III chlorophyli a⁄b-binding protein (Lhca3*1) mRNA, complete cos
4837			1.15	N	.BE-01 AF142703.1	FN	Ophrestia radicosa maturase-like protein (matk) gene, complete cds; chloroplast gene for chloroplast product
5086	1	L	3.63		2.6E-01 H04858.1	EST_HUMAN	
5165	ı		0.61	2	.6E-01 AA884625.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Horito sapiens cDNA clone IMAGE::1468605 31
5457			1.29	2	.6E-01 AB035972.1	NT	Peramecium caudatum gene for PAP, complete cds
5565	18762	31802	0.67	2	.6E-01 M96060.1	Į,	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds
302	Į.	┨		·	A 19622308 4	PAN I	Idd6a03.x1 NCI_CGAP_Co16 F.omo capiens cDNA clone IMAGE:2075788 3' similar to contains element. MFR35 repetitive element
FROG O	18885		Š.	1	AIQ02330.1		professor of section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section
7002	40083	33304	78		6F-01 AF207550.1	<u> </u>	Homo septiens protein translocase, JMZ6 protein, UDr-galactose translocator, plint∠ protocatozygere fromougy plim-Zh, and shal-type polassium channel genes, complete cds, JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g>
2000	1	1			1000000		

Page 84 of 550 Table 4 Single Exon Probes Expressed in Placenta

		•			in in	A EAULY FILLIANS	Single Excit Flores Expressed in Fracting
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
6196	26211		2.57	2.6E-01	2.6E-01 AE001811.1	N	Thermotoga maritima section 123 of 138 of the complete genome
0889	19501	32859	1.96		2.6E-01 AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo septens cDNA clone IMAGE:2227438 3' stmilar to SW:NDF1_RAT QQ4289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive clonent;
6330	1 .	32860	1.96	2.6E-01	2.6E-01 A1582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo septens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element;
8552	1			2.8E-01	2.6E-01 AL162757.2	NT	Neisseria meningitidis serogroup A strain 22/91 complete genome; segment 6/7
2080	1	١.		2.6E-01	2.6E-01 BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5
2089	1				2.6E-01 BE792052.1	<b>EST_HUMAN</b>	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938156 5
218	1		1.04		2.6E-01 Al914380.1	EST_HUMAN	wd48c04.x1 Scares_NFL_T_GBC_S1 Homé sapiens cDNA clone IMAGE:2331363 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	ı		0.7		26E-01 BE148961.1	EST_HUMAN	CM0-HT0245-031189-085-f04 HT0245 Homo sapiens cDNA
7587	ı		96'0		2.6E-01 AL.139077.2	L	Campylobacter Jejuni NCTC11168 complete genome; segment 4/6
7626	}		0.78		2.6E-01 AA196149.1	EST_HUMAN	zp92e01.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA done IMAGE:627872 5
7918		34478			26E-01 R10365.1	EST HUMAN	ytg7a03.s1 Soares fatal iver spleen 1NFLS Homo saplens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8033					2.6E-01 R02411.1	EST_HUMAN	ye82g07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212.5'
8888					2.6E-01 BE144331.1	EST_HUMAN	MR0-HT0166-181199-003-412 HT0166 Homo capiens cDNA
8529	1		2.97		2.6E-01 BF343588.1	EST_HUMAN	602014422F1 NC _CGAP_Bm64 Homo squiens cDNA clone IMAGE:4150398 5
8605		35223	1.74		2.6E-01 Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8892	ı		4.06		2.6E-01 BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo saplens cDNA
8892	_		4.06		2.6E-01 BE830339.1	EST HUMAN	IRCS-ET0082-310500-021-F10 ET0082 Homo capiens cDNA
2996	l	36200	0.92		26E-01 X17604.1	NT	S, occidentalls INV gene for invertase (EC 3.2.1.26)
	l _				, , , , , , , ,	Į.	Lontra canadensis cytochrome b (cytb) gene, mitochondriai gene encoding mitochondrial protein, complete
0 <del>7</del> 68		١			Z.6E-01 AF05/121.1	TO COUNTY	COBESA SENSITIVE OBSINICEDEN CONE PHOTORECEPTOR PICMENTY (KFH.G.)
10072					2.6E-01 P87366	SWISSPROI	GREEN-SCINOLINE OF SIN (GREEN CONE FIGURE OF TOTAL CONE OF TOTAL CONE OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OF THE OPEN CHARACTER OPEN CHARACTER OF THE OPEN CHARACTER OPEN CHARACTER OPEN CHARA
10072	23110	36714			2.6E-01 P8/368	SWISSPRO	GREEN-SCHOOL (GALERY CONT. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907) (CA. 1907)
10393	23428		0.63		2.6E-01 Q28295	SWISSPROT	VON WILLEBRAND FACIOR PRECURSOR (VWF)
10727	23760		1.09		2.6E-01 Y10196.1	NT	Home sepiens PHEX gene
10840	23873		0.48		2.6E-01 Y15874.2	NT	Danio rerio mRNA for RPTP-elpha protein
11815	L		31.14	1	2.6E-01 X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	1		4.14	$ig _{-}$	2.6E-01 BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 51
12635	25365	32069	3.88		2.6E-01 AF316896.1	TN	Home sapiens Nafk-ATPase gamma suburiti (FXYD2) gene, complete cds, alternatively spliced

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				8	221111100	Oligie Lyon Flores Lypessed III Flacolina
Probe Ex SEQ ID SEG NO: N	Exen ORF SEQ ID NO: NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslan No.	Top Hit Database Source	Top Hit Descriptor
	25607	2.04	2.6E-01		NT	Cavia cobaya mRNA for serine/threoine kinase, complete cds
13007 25	5663	1.78			L	Thermotoga maritima section 25 of 136 of the complete genome
	25692	2.36	L	2.6E-01 AF141325.2	ᅜ	Homo sapiens inosital polyphosphate 1-phosphatase (INPP1) gene, complete cds
L	15735	1.43			EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5
L	25722	2.04	L	2.6E-01 P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
	25748	2.4			NT	Arabidopsis thallana floral homeotic (AP3) gene, promoter region and partial cds
<u>.                                    </u>					!	Homo septens ATP synthese, H+ trensporting, miltochondrial F1 complex, delta subunit (ATP6D), nuclear
251 13	13472 28503	1.87	2.5E-01	4502288 NT	Z	gene encoding mitochondrial protein, mRNA
	13472 28503	1,7		4502296 NT	Ę	Homo sepiens ATP synitesse, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
265 13	13484	2.51	2.6E-01	2.6E-01 M28501.1	NT	Starfish (P.ochraceus) cytoplasmic actin gene, complete cds
L	14032 27093	1.23			ΤΛ	Mus musculus ICR/Swiss glyceraldehyde 3-jhosphata dehydrogenase (Gapd-S) gene, complete cds
L					F	Ureaplasma urealyticum section 57 of 59 of the complete genome
	14310 27367	5.45		2.5E-01 T89837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#937210) Homo saplens cDNA clone IMAGE:117468 5'
	14916	4.63		4885406 NT	LΝ	Homo sapiens hyperpolarization activated cycilc nucleotide-gated potassium channel 4 (HCN4) mRNA
	15608	11.21	2.5E-01		TN	Aquifex aeolious section 7 of 109 of the complete genome
	15688 28814	1.22		6679218 NT	TN	Mus musculus protein-L-isoaspertate (D-aspartate) O-methyltransferase 1 (Pcmt1), mRNA
2585 16		i		2.5E-01 AA251987.1	EST_HUMAN	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
ł	15820 28936	3 . 1	2.5E-01		NT	B.taurus mRNA for D-aspartate oxidase
	L	3.34			EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
		5 7.18			NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
l	17108 30106	1.25		AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3950 17	17108 30106	1.25		AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'
4438 17	17578	0.88		Q03314	SWISSPROT	RHIB PROTEIN
						Mus musculus neuronal apoptosts inhibitory protein 6 (Naip6) gene, complete cds, and Naip3 gene, exons 2-9
	17872 30855	5 0.7		AF242431.1	NT	and 11-16
4871 18	18004	1.13		Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
L	18009 30993	e		2.6E-01 AF007768.1	М	Choristoneura fumiferana diapausa associated protein 2 (DAP2) mRNA, complete cds
		3 2.3		AE004416.1	NT	Vibrio chalerae chromosome II, section 73 of 93 of the complete chromosome
1	-					Mus musculus annexin V gene, intron 4 segment containing 5 LTR and gag portion of MuERV-L (murine
				2.5E-01 AJ230113.1		endogenous retrovirus) element
4954 18	18084 31060	0 0.8		BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Hcmo septens; cDNA clone IMAGE:3922600 5

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Probe SEQ ID NO:	SEO ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
4894	18123	31101	0.61	2.5E-01	SE-01 U83656.1	NT	Rattus norvegicus NF-KB gene, promotor region
5212	ı		0.62	2.5E-01	.5E-01 P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	ı		0.62	2.5E-01	SE-01 P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
	ı						zr35a05.r1 Scares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755000 5' similar to gb:M88279
6337	18450		1.08	2.5E-01	SE-01 AA419208.1	EST_HUMAN	P59 PROTEIN (HUMAN);
5441	L		12.21	2.6E-01		Ā	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nf]
9090	19262	32591	9.0	2.6E-01	.6E-01 AJ006345.1	LΝ	Homo sepiens KVLQT1 gene
6081			0.81	2.6E-01	:6E-01 AL163207.2	٦	Homo saplans chromosoms 21 segment HS21C007
6762			0.82	2.6E-01	.6E-01 AJ251973.1	NT	Homo sapiens partial stearin-1 gene
7180	20055	33465	0.64	2.5E-01	8394138 NT		Rattus norvegicus rabin 3 (RABINS), mRNA
	L.						Feine calicivirus CFI/68 RNA helicase/cyste/ne protease/RNA-dependent RNA polymerase polyprotein
7607	20581	34064	0.71	2.5E-01	.5E-01 U13992.1	님	precursor and capsid protein precursor, genes, complete cds; and unknown gene
7536	ı		1.13	2.5E-01	.5E-01 AF134119.1	Ā	Mus musculus SKD1 (Skd1) gene, complete cds
77.70	1	34319		2.5E-01	2.5E-01 AL161508.2	۲	Arabidopais thaliana DNA chromosome 4, contig fragment No. 18
7814	1			2.5E-01	.5E-01 AL183282.2	NT	Homo sapiens chromosoma 21 segment HS21C082
8028	1	34630		2.6E-01	.5E-01 BF109040.1	EST_HUMAN	7157a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8039		L		2.5E-01	.5E-01 BE980712.1		601653391R2 NIH_MGC_58 Homo saptens cDNA clone IMAGE:3826198 3'
8421	1		1.9	2.5E-01	.5E-01 BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_68 Hamo sapiens cDNA clone IMAGE:3862809 5'
8591	l		0.8	2.6E-01	.5E-01 P04492		E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8837	21918			2.5E-01	.5E-01 H53236.1	I_HUMAN	yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
9076	ı	35699			2.5E-01 M88828.1	NT	Mause testis-specific protein (TPX-1) gene, exon 10
9716	ı				2.6E-01 U89651.2	NT	Homo sapiens matrix metalloproteinase MMi <sup>2</sup> Rasi-1 gene, promoter region
9716	1		16.85	7	2.5E-01 U89651.2	NT	Homo seplens matrix metalloproteinase MMIP Rasi-1 gene, promoter region
9772	l		2.44	2.5E-01	2.5E-01 AF085164.1	¥	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9772	22769			2.6E-01	2.5E-01 AF085164.1	N.	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10303				2.5E-01	2.5E-01 AW 581997.1	997.1 EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10860		37193		2.5E-01	11465652	LN.	Porphyra purpurea chloroplast, complete genome
							xg40c10.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive
10783	23786	37418	1,4		2.5E-01 AW152246.1	EST_HUMAN	element;contains element MSR1 repetitive element ;
10767		L	19.1	2.55-01	2.5E-01 X58491.1	NT	Mouse L1Md LINE DNA
11332	l_	L	2.98		2.5E-01 D50914.1	FN	Human mRNA for KIAA0124 gene, partial cits
12204	1	38834			2.5E-01 AF200528.1	L	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
12233	26167		6.12		25E-01 AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

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Onligie Evoli Floues Expressed in Facelina	Top Hit Descriptor	Della brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial	product on70404.91 Sogres NFL T GBC S1 Homb saplens cDNA done IMAGE:1562023 3"	802132442F1 NIH_MGC_81 Hamo sapiens cDNA clone IMAGE:4271578 6	Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens FLI-1 gene, partial	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds	Zaccys dhumnades fructose-1,6-bisphoaphatase mRNA, complete cds	wg76d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:080287 080287 KIAA0512 PROTEIN.;	Homo sapiens serine palmitoyi transferase, subunit II gene, complete cds; and unknown genes	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)	Aquifex aedicus section 12 of 109 of the complete genome	D.discoideum (Ax3-K) ponA gene	S.pombe swi6 gene	Bovine adenovirus 3 complete gename	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds	H.sapiens AGT gene, Pstl fragment of introin 4	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome	Raftus norvegicus mRNA for aphaB crystallin-related protein, complete cds	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA done IMAGE:2576618 3	xb18a02.x1 NCI_CGAP_Kid13 Homo septens cDNA clone IMAGE:2576618 3'	Bacillus firmus hypothetical 34.0 kDa protelin, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thioculfate sulfurtransferase, hypothetical 16.1 kDa transcriptional	regulator and hypothetical 18.2 kDa>	Hamo saplens gene for TU12B1-TY, exon 13	Homo saplens gene for TU12B1-TY, exon 13	wo33405x1 NCL CGAP_Gas4 Homo capions oDNA clone IMAGE:2457129 3'	wc33d05x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2467129 3'	Glycine max mRNA for mitotic cyclin b1-type, complete cds	Mus musculus Wm protein (Wm) gene, complete cds	Mus musculus Wrn protein (Wrn) gene, complete cds
S EXOII LIONES	Top Hit Database Source		FST HUMAN	Ī		-			, IN	EST_HUMAN	¥	SWISSPROT	Ę		LN.	IN	Ę	F		LN	EST HUMAN	EST_HUMAN :		- L	IN	IN	EST_HUMAN	EST_HUMAN	NT		N
ignio.	Top Hit Acession No.		2.5E-01 AF325363.1	2.4E-01 BF576124.1	2.4E-01 AJ289880.1	2.4E-01 AJ289880.1	2.4E-01 Y17293.1	2.4E-01 AF287753.1	2.4E-01 AF251708.1	2.4E-01 AI742958.1	2.4E-01 AF111168.2	P45384	2.4E-01 AE000680.1	2.4E-01 236534.1	2.4E-01 X71783.1	2.4E-01 AF030154.1	2.4E-01 U72726.1	2.4E-01 X74209.1	2.4E-01 AE000312.1	2.4E-01 D29960.1	24E-01 AW078598.1	2.4E-01 AW078598.1		2.4E-01 U89914.1	2.4E-01 AB032785.1	2.4E-01 AB032785.1	2.4E-01 AI925707.1	2.4E-01 AI925707.1	2.4E-01 D50871.1	2.4E-01 AF091216.1	2.4E-01 AF091216.1
	Most Similar (Top) Hit BLAST E Value		2.5E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01 P45384	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	24E-01	245-01	2.4E-01		2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01
	Expression Signal		1.22	4.4	16.83	16.83	76.0	29.78	1.43	1.64	1.17	1.25	2.29	3.13	2.22	6.27	3.03	1.51	0.97	0.65	0.65	0.65		1.89	1.46	1.48	6.0	0.9	0.59		
	ORF SEQ ID NO:		78783	27/13	27667	27558	27842		28183	28353	28467		28602	28845	29045	29069		29402			31268	31267		31415	31416				31847	32266	
	SEQ ID		13750	14047	14489	14489	ı	16041		ł	1	.l	ı	i		15960	l		L	17280	18303	18303		18447	L	<u> </u>	1_		18797	H	18964
	Probe SEQ ID NO:		13024	874	1332	1332	1415	1898	1949	2091	2200	2237	2338	2602	2820	2846	3202	3217	3856	4141	5181	5181		5334	5335	5335	6578	5678	5602	5772	5772

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Probe SEQ ID	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9800	18990		7.0	2.4E-01	.4E-01 M83377.1	TN	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	26815		26.0	2.4E-01	.4E-01 AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulih 2 (caM2 gene)
							7154004.x1 NC_CGAP_Br16 Homo septent; cDNA clone IMAGE:3338503 3' similær to SW :3FR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
6016	19200	32517	2.54	2.4E-01	.4E-01 BF592338.1	EST_HUMAN	
6106	19286	32620		2.4E-01	2.4E-01 AF035546.1	NT	Drosophila malanogaster p38a MAP kinase jena, complete cds
6215	19390	32738			7661801 NT	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6269	19443	32792	<b>76'0</b>	,	2.4E-01 AV733787.1	EST_HUMAN	AV733787 oda Homo sepiens cDNA clone cdAADE11 5'
6516	19681	33051	0.87	2.4E-01	.4E-01 AA398672.1	<b>EST_HUMAN</b>	z/70d02.s1 Soares_bestis_NHT Homo sepiens cDNA clone IMAGE:727683 3'
6965	19824	33212	1.59	2	.4E-01 AI698989.1	EST_HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sspiejns cDNA clone IMAGE:2323220 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(1) CHAIN PRECURSOR (HUMAN);
7498	20673	34046		<u> </u>	2.4E-01 L43001.1	N	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7802	20954	34461		2	.4E-01 AF229644.1	NT	Mus museulus DXimx48e protein (DXimx48e) mRNA, complete cds
8271	21353		0.5	~	2.4E-01 X97252.1	NT	M.musculus pah gene and promotor
8271	21353	34869	9.0	``	.4E-01 X97252.1	NT	M.musculus pah gene and promotor
8392	21473		1.48		2.4E-01 AJ006397.1	NT	Streptococcus pneumonlae rr08 and hk08 genes; two component system 08
8392	21473	35000	1.48	7	.4E-01 AJ006397.1	NT	Streptococcus pneumoniae m08 and hk08 genes; two component system 08
8544	21825				.4E-01 AJ012585.1	NT	Tetrahymana thermophlia macronuclear gane encoding ribosomal protein L3, exons 1-2
8798	21877		1.18	2	.4E-01 BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4106298 5'
9332	22408		89.0		2.4E-01 AL138077.2	TN	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9332	22408	35962	0.58		2.4E-01 AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9783	2701	36267	8.39		2.4E-01 A1693515.1	EST HUMAN	wd43e02xf Soares_NFL_T_GBC_Sf Horio saplens cDNA clone IMAGE:2330908 3' similar to contains MER22.b1 TAR1 repetitive element;
3005	22945		0.68	Ľ	3.4E-01 AF220067.1	K	Drosophila melanogaster SKPB gene, complete cds
9008	22845				2.4E-01 AF220067.1	NT	Drosophila melanogaster SKPB gene, compilete cds
10654	23688	37297	1.8	<u> </u>	2.4E-01 Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11008	24085		7	"	2.4E-01 AL181494.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11074	24149				2.4E-01 AF030199.1	TA.	Mus musculus type 1 sigma receptor gene, complete cds
11447	24608				2.4E-01 BE296917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508		1.8	``	2.4E-01 BE296917.1	EST HUMAN	601176416F1 NIH_MGC_17 Homo capiens cDNA clone IMAGE:3531843 5'
11478	24537		8.04		2.4E-01 Z21847.1	NT	P.aslatica mosaic virus genomic RNA
12159	25127	28827			2.4E-01 AF217491.1	NT	Homo sapiens fragile 18D codo reductase (FOR) gene, exon 6
12289	25932		1.35	"	2.4E-01 AF004213.1	FZ	Arabidopsis thallana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12360	25258		1.62		2.4E-01 AJZ78191.1	N	Mus musculus mRNA for putative mc7 protein (mc7 gene)

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Table 4

Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Gallus gallus gene coding for a-actin	RC3-CT0413-100800-023-b06 CT0413 Honto saplens cDNA	Homo sapiens mRNA for bradykinin B1 receptor (B1BKR gene)	Homo sapiens chromosome 21 segment HS21C081	aromatase [Poephlla guttata≂zebra finches, ovary, mRNA, 3188 nt]	Mycoplasma genitalium section 35 of 51 of the complete genome	Methanococcus jannaschil secilon 138 of 150 of the complete genome	601142073F1 NIH_MGC_14 Hcmo saplens cDNA clone IMAGE:3505818 5	Brassica napus sig gene for S-tocus glycoprotein, cultivar T2	Mus musculus odh5 gene, exon 1, partial	Homo saplens partial intron 3 of the wild type AF-4/FEL gene	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'	Human erythropoletin gene, complete cds	Marinilabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957	no16d06.s1 NCI_CGAP_Phe1 Homo sapleris cDNA clane IMAGE:1100843 3' similar to contains Alu	repetitive element; contains element THR repetitive element;	yh21b07.s1 Soares placenta Nb2HP Homo capiens cDNA clone IMAGE:130357.3'	yr97h10.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:213283 5'	GSTA5-glutatrione S-transferase Ye2 subtinit (5' region, Intron 1) (rats, Morris hepatoma cell line, Genomic,	2212 nt, segment 1 of 3]	Horno sapiens KIAA0450 gene product (KIAA0450), mRNA	y17f01.r1 Soares placenta Nb2HP Homo sciplens cDNA clone IMAGE:149017 5	Mus musculus renin (Ren-1c) gene, promoter region	Synschocyetis sp. PCC6803 complete genome, 1/27, 1-133859	Homo saplens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Mus musculus tulip 1 mRNA, complete cds,	Human namma-R-crystallin (namma 1-2) and parima-C-crystallin (parima 2-1) genes. complete eds	602132210F1 NIH MGC 81 Homo sapiani cDNA done IMAGE:4271547 5	Homo saniens, mRNA for KIAA1512 protein, partial ods	TOTAL OCCUPANT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY	7K30b08.X1 NCI_CGAP_OV18 Homo sapiens CDNA cione INAGE:34 (6689 3 SIMIRATIO 3W 34AG_SWDAY P03330 GAG POLYPROTEIN [CONTAINS]; CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];
and How	Top Hit Database Source	NT	EST_HUMAN	NT	TN TN	TN	NT	NT	EST_HUMAN	NT	NT	IN	EST_HUMAN	LN.	Z		EST_HUMAN	EST_HUMAN	EST_HUMAN		NT	LN	EST_HUMAN	TN	NT	NT	۲N	IN	12	EST HIMAN	PA PA		EST HUMAN
e e e e e e e e e e e e e e e e e e e	Top Hit Acessian No.		2.4E-01 BF229975.1						2.3E-01 BE311893.1	2.3E-01 AJ245480.1		2.3E-01 AJ235353.1	2.3E-01 BE297718.1		3.1		2.3E-01 AA601379.1	321732.1	169836.1			7662133 NT	382252.1		2.3E-01 D90899.1	2.3E-01 AF092535.1	5031984 NT	2.3E-01 AB032400.1	225 04 140064 4	2 9E A4 BE574904 4	2.3E 04 ABOADOAR 1	4DC#68#3.1	23F-01 BF058381.1
	Most Similar (Top) Hit BLAST E Value	2.4E-01 V01507.1	2.4E-01	2.4E-01	2.4E-01	2.3E-01 S75898.1	2.3E-01 U39713.1	2.3E-01 U67596.1	2.3E-01	2.3E-01	2.3E-01 Y10887.2	2.3E-01	2.3E-01	2.3E-01 M11319.1	2.3E-01		2.35-01	2.3E-01 R21732.1	2.3E-01 H69836.1		2.3E-01 S82821.1	2,35-01	2.3E-01 R82252.1	2.3E-01 L78789.1	2.3E-01	23E-01	23E-01	23E-01	20 00	2 3 5 0 0	2000	2.3E-01	2.3F-01
	Expression Signal	1.95	1.37	1.4	4.16	1.39	5.53	29.31	3.57	1.11	1.72	1.78	1.85	0.98	1.5		1.08	7.06	1.32		0.98	5.15	98.0	1.91	1.12	2.78	5.65	0.87		98.0	200	7.71	2.03
	ORF SEQ ID NO:					26633		26900	27188				28764	28945	L		28227		29644		30100		30588			30728		31246		31210			34776
	Exon SEQ ID NO:	25914	28151	25701	25718	13597	L	ı	14130	14786	14813	16242	15643	15835	14573		16204	16328	1	l	17103	1	17610	1	17710	17748		18281	ı	2 6	Т	200	18742
	Probe SEQ ID NO:	12588	12839	13072	13102	8	884	684	957	1634	1881	2103	2517	2717	2885		3028	3153	3486		3944	4046	4470	4520	4573	4611	4678	5169	000	300	2000	8	55.65

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Г		Т	٦	Т	$\overline{}$					П	Т	Т	Т	٦	Т	Т	Т	Т	T	$\neg \neg$	1	-	T	Т	Т	Т	П	Т	
Single Exon Probes Expressed in Placenta	Top Hit Descriptor	C.familiaris rom1 gene	Vittaforma corneum small subunit ribosormal RNA gene	23S rRNA [Leuconostoc camosum, Genomic, 2868 nt]	as27e12.x1 Barstead sorta HPLRB6 Homo/sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);	es27e12.x1 Barsbad aoria HPLRB6 Homo sapiens cDNA clone iMAGE::23184463' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);	Oryctologus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product	es42f12.x1 Berstead aorta HPLRB6 Homo saplens oDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA	Secale cereale omega secalin gene, complete cds	Glycine max resistance protein LM17 precursor RNA, partial cds	AV719681 GLC Homo seplens cDNA clone GLCDGB08 5	AV719681 GLC Homo sapiens cDNA clone GLCDGB08 5	Mus musculus myosin XV (Myo15), mRNA	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE::282358 5	Homo sapiens protocadherin alpha oluster (LOC63960), mRNA	Homo saplens protocadharin alpha duster (LOC83960), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds	Mus musculus prosaposin (psap\SGP-1) gene, complete cds	xc90e06.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591554 3	EST376533 MAGE resequences, MAGH Homo sapiens cDNA	EST84061 Rhabdomyosarcama Homo saplans cDNA 5' end similar to DnaJ homdog (GB:X63368)	EST84061 Rhabdomyosarcoma Homo saplens cDNA 5' end strillar to DnaJ homolog (GB:X63358)	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3od), mRNA	601120110F1 NIH_MGC_20 Homo sapien's cDNA clone IMAGE:2966739 5	EST376533 MAGE resequences, MAGH Homo saplens cDNA	Heemophilus influenzae genes for Hincil restriction-modification system (Hincil methyltransferase (EC [2.1.1.72) and Hincil endonuclease (EC 3.1.21.4))
Exon Probes	Top Hit Database Source	NT	LN	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	LN	NT.	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT
Single	Top Hit Acessian No.			2.3E-01 S60371.1	2.3E-01 AJ708840.1	2.3E-01 AI708840.1	_	2.3E-01 AI718148.1	23323	2.3E-01 AF000227.1			2.3E-01 AV719681.1	6754779 NT	1.1	2.3E-01 N80983.1	11416821 NT	11416821 NT	2.3E-01 AL161558.2	M68931.1	2.3E-01 U57999.1	2.3E-01 AW090541.1	2.3E-01 AW864460.1	2.3E-01 AA372164.1	2.3E-01 AA372164.1	6679318 NT	2.3E-01 BE277860.1	2.3E-01 AW984460.1	2.3E-01 X52124.1
	Most Similar (Top) Hit BLAST E Value	2.3E-01 X96587.1	23E-01 L39112.1	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01
	Expression	5.25	66.0	1.32	86.1	1.98	0.68	4.63	0.86	0.76	2.54	5.37	5.37	4.26	1.56	2.8	0.71	0.71	0.52	1.73	0.62	0.58	0.52	0.64	0.64	0.5	0.53	0.81	1.57
	ORF SEQ ID NO:	32122		32367	32569				١				34126		34338		34530		34637	34788	35300	35594	35715		35971	36398		36616	38875
	SEQ ID NO:	18841	18858	19060	19244	19244	19949	20153		20517	1	1	ŀ	20840	1		21018	21018	21118	21265	_	<u> </u>	L	乚	22417	22820	ı	23024	23075
	Probe SEQ ID NO:	5647	6788	5870	. 6062	6062	6794	7017	7260	7440	7573	7576	7576	7784	7789	7831	7968	7,068	8036	8183	8690	8972	5808	9341	8341	9780	9930	9885	10037

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Oligie Lycii Fronce Lypiessed II Fracellia	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C085	Mus musculus ATP-binding cassette protein (Abcbs) mRNA, partial cds	Mus musculus breastlovarian cancer susceptibility protein (BRCA1) mRNA, complete cds	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds	Mus musculus mixed lineage kinase 3 (MIk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds	Human scRNA (BC200 beta) pseudogene	Human scRNA (BC200 beta) pseudogene	Human beta-cytoplasmic actin (ACTBP9) pseudogene	zq87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'	Mus musculus vinculin gane, exon 3	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens CONA	Homo sapiens diaphanous (Drosophila, hornolog) 2 (DIAPH2), transoript variant 156, mRNA	Synachocyclis sp. PCC6803 complete genome, 19/27, 2392729-2538999	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds	Homo saplens gene for fukutin, complete cits	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'	Streptococcus pyogenes phosphotidyglyce/ophosphate synthase (pgsA) and ABC transporter ATP-binding prolein (stpA) genes, complete cds; and unknown genes	Streptococous pyogenes phosphotidylglyceiophosphate synthase (pgsA) and ABC transporter ATP-binding inclient streA) arenes complete ads and unknown genes.	Himan discondard B dena extra 4	Human alycophorin B gene axon 4	Myconlesma nneumoniae M129 section 45 of 63 of the complete genome	Homo saplens homeobox B7 (HOXB7) gene, partial cds; and homeobox B8 (HOXB8), homeobox B5	(HOXB5), homeobox B4 (HOXB4), and horneobox B3 (HOXB3) genes, complete cds	Bacilius halodurans DNA, complets and partial cds, strain:C-125	Mus musculus nm23-M1 gene, promoter region	E.coll sepA and sepB genes	Pan troglodytas MeCP2 gene 3UTR	Mouse HD protein mRNA, complete cds
Excii riones E	Top Hit Datebase Source		IN	NT	NT DI		N			NT H	Ī	EST_HUMAN   29		T_HUMAN						EST_HUMAN A	S TN	N.					두			NT		N F
Billio	Top Hit Acession No.		2.2E-01 AF213391.1	.2E-01 U68174.1	.2E-01 AF119102.1	2.2E-01 AF155142.1		1.1	2.2E-01 U01307.1	2.2E-01 U01307.1	2.2E-01 D50604.1	2.2E-01 AA211216.1	2.2E-01 L13299.1	5.1	5803002	2.2E-01 D64000.1	2.2E-01 U67087.1	2.2E-01 U67087.1	2.2E-01 AB038490.1		2.2E-01 AF082738.1	2 2E 04 AE082748 4			];	Τ	2.2E-01 AF287967.1	2.2E-01 AB024553.1	2.2E-01 AF155143.1		8.1	2.2E-01 [_23312.1
	Most Similar (Top) Hit BLAST E Value	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	l``	,			2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	10,50	2 25 24	2000	2 25 0	2.2.2	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01
	Expression Signal	0.62	0.69	9.0	1.07	8	2.74	2.74	1.07	1.07	1.08	2.2	1.57	1.34	1.89	3.75	0.78	0.78	0.77	10.63	1.61	ā	90.0	2.30	200	2000	0.88	0.71	2.45	2.68	0.81	0.52
	ORF SEQ ID NO:					30480		30603				31058			32360		32640		33405		33815	200	ı	l			34436	34463				35705
ĺ	SEQ ID NO:	17008	17360	17388	17471	17478		17522	17615	17615	18077	18082		١	19053	19064	19301	19301	19998	L	20362	L	L	20210	L		20930	20957	21292	1		22162
	Probe SEQ ID NO:	3848	4211	4242	4328	4335	4379	4379	4475	4475	4947	4952	5156	5226	5863	6874	6122	6122	6845	7166	7279	0,0	8/7/	7447	714/	000/	7878	7905	8210	8280	8748	9083

Page 93 of 550 Table 4 Single Exon Probes Expressed in Placenta

					ignic	EXUII FIODE	Single Extri Flobes Expressed in Fracetika
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6083	22162				2.2E-01 L23312.1	NT	Mouse HD protein mRNA, complete cds
2608	22176	35720	4.58		AE001713.1	NT	Thermotoga martima section 25 of 136 of the complete genome
0117	22196	35740	0.48		2.2E-01 U08964.1	IN	Mus musculus ICR/Swiss glyceraldehyde 3/phosphate dehydrogenase (Gapd-S) geno, complote odo
9224			2.88		AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0283 Homo saplens cDNA
8315		35942			2.2E-01 8393247 NT	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
8389	1	36039	1.13		2.2E-01 BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9489	ı	36109	1.42		W02988.1	EST_HUMAN	za04f08.rf Soares melanocyte 2NbHM Honio sapiens cDNA clone IMAGE:291591 51
8507	ı		15.08		P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	,	36187			AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
858	1	ļ			7657428 NT	NT	Mus musculus esteoblast specific factor 2 (OSF-2), mRNA
9578	ı	l _			M89643.1	IN	Brachydanio rerio ependymin beta and gamina chains (Epd) gene, complete cds
	ı				00000	TOGGGGGG	OYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG
DZ88	22860	30441	co.u	1	ZE-U1 (28080)	SWISSTAG	Ginarda historometrics chloroplaset Joseff and the standard contain (CPs.HSP21) mBNA complete cds:
10020	23058	36654	3.84		2.2E-01 AF197941.1	K	nuclear gene for chloroplast product
10159	1_				2E-01 BF206507.1	EST HUMAN	601869724F1 NIH_MGC_19 Homo sapients cDNA clone IMAGE:4100189 5'
10380	23415	37024	-	7	9625671 NT	N N	Human herpesvirus 5, complete genome
10540	I_			2	.2E-01 T59472.1	EST HUMAN	y683408.r1 Stratagene ovary (#937217) Homo saplens cDNA clone IMAGE:75855 5
10540	Ł		0.65	2	ZE-01 T59472.1	EST_HUMAN	yb63d08.r1 Stratagene ovary (#937217) Hojmo sapiens cDNA clone IMAGE:75855 5'
	L						Pseudomonas aeruginosa quinoprotein ethenol dehydrogenase (exaA) gene, partial cds; cytochrome c550
						ŀ	precursor (exaB), NAD+ dependent acetaldehyde dehydrogenese (exaC), and pyrrologuinoline quinone
10580	23615	3/220	0.0		2.2E-01 AFU08264.1	z E	Mus musculus PHR1 (Phr1) gene, bardal cds
10033		27244			2.2E-01 AF001562 1	I-N	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	L	l	0.67	L	2 2F-01 AF001562 1	LN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10853	1	l			2F-01 AF049720 1	LN	Homo saplens neuronal nitric codde synthase (NOS1) gene, alternative exons 11 and AS
11380	١.				2E-01 AF257772.1	LN.	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	L				2E-01 X01918.1	Z	Drosophila 68C glue gene cluster
11748	1	L		7	7706215 NT	NT	Homo sapiens H-2K binding factor-2 (LOCi31580), mRNA
12207	25161			2	BE87095	EST HUMAN	601448957F1 NIH_MGC_65 Homo septens cDNA clone IMAGE:3850670 67
3,	ļ				05-04   (82874.0	F <sub>N</sub>	Homo sapiens chromosome Xq28 metanoma antigen family A2a (MAGEA2A), metanoma antigen family A12 (MAGEA12), metanoma entigen family A2b (MAGEA2B), metanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenaso-like protein (NSDHL), end Ll>
8107	-		20.		2000		

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Single Exon Probes Expressed in Fracelika		П					Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16	Chlamydia muridarum, section 45 of 85 of the complete genome	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA	Mus musculus mas proto-oncogene and lgf2r gene for Insulin-like growth factor type 2 and L41ps and Au76 pseudogenes		Γ	Homo sapiens potasstum voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA	AN Ing90b10.s1 NCI_CGAP_Co9 Homo septents oDNA clone IMAGE:1159579 3'	Beta vulgaris mitochondrion, complete genome					Home sapiens pshsp47 gene, complete cdg	P.falciparum mRNA for small GTPase rab11	_		Doto fragilis mitochondrial 16S rRNA gene, partial			_	Archaeoglobus fulgidus section 135 of 172 of the complete genome	Canis familiaris karatin (KRT9) gene, complete cds	Glycine max malate dehydrogenzase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
e Exon Pic	Top Hit Database Source	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMA	NT	NT	IN	NT	ŁZ	EST HUMAN	EST_HUMAN	N	EST_HUMAN	NT	TN	SWISSPROT	SWISSPROT	NT	뉟	Ę	NT	EST_HUMAN	NT	NT	SWISSPROT	SWISSPROT	NT	ΤN	TN
iguio	Top Hit Acession Na	2.2E-01 AF188843.1	2.2E-01 AW361098.1	2.2E-01 AW661922.1		2.1E-01 AA569289.1	2.1E-01 AL181504.2	2.1E-01 AE002314.2	6754299 NT	6754299 NT	2.1E-01 AJ249895.1	2.1E-01/AA906824.1	2.1E-01 BF695073.1	6912445 NT	2.1E-01 AA639482.1	9838361 NT	2.1E-01 AE001793.1				2.1E-01 AB010273.1	2.1E-01 X83161.1	2.1E-01 D13567.1	2.1E-01 BF672695.1	2.1E-01 AJ223392.1	2.1E-01 U04642.1	2.1E-01 Q01956	2.1E-01 Q01958	2.1E-01 AE000972.1	2.1E-01 AF000949.1	2.1E-01 AF068687.1
	Most Similar (Top) Hit BLAST E Value	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01 P11675	2.1E-01 P11675	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01
	Expression Signal	3.24	1.86	1.47	3.08	1.88	0.72	2.43	1.45	1.45	4.29	2.15	3.55	2.52	6.1	6.81	29.0	1.57	1.57	1.83	1.82	0.93	0.7	6.31	1.05	1.8	7.00	77.0	1.88	1.64	1.38
	ORF SEQ.		31531			27228			27446	27447	27774			29183	L			30310	30311		30819	30871	31228	31692	33585	33508	34111	34112		34441	34488
	Exan SEQ ID NO:	25286	18492	25353	28148	14166	14167	14312	14385	14385	14692		15358	16167	16698	17067	17279	17315	17315	17635	17834	17892	18261		L	ı	l _	20636		l	20980
	Probe SEQ ID NO:	12407	12518	12519	13115	88	988	1148	1225	1225	656	1963	2224	7884	3533	3908	4126	4165	4165	4495	4689	4757	5138	5416	7027	7038	7564	7564	7576	7883	7930

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					JE STEEL	EXUIT FILLINGS	Single Exoli Flobes Explessed in Flagorica
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7830	20980	34489	1.38	2.1E-01	.1E-01 AF068687.1		Glycine max melate dehydrogenace (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	上			2.1E-01	7305030 NT		Mus musculus erythrocyte protein band 4.1 Hike 3 (Epb4.113), mRNA
							Haamophiluo Influenzae hmcD, putative harmocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmc) genes, complete
8700	21780	36313	4.76	2.1E-01			cds
8997			16.0	2.1E-01	2.1E-01 AL040537.1	7	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA cione DNFZp434H0614 o
8897	22078	35616	<b>ι</b> σο	2.1E-01	2.1E-01 AL040537.1	HUMAN	DKFZp434H0614_r1 434 (synonym: ntess) Homo sapiens culvin cione Dirizpasativo 14 3
9159	22237	L	0.5		2.1E-01 AB022524.1	NT	Homo saplens APCL gene, exon 9
9237	L	35856	6.7	2.1E-01	2.1E-01 235786.1	- 1	S.cerevisiae chromosome II reading frame URF YBLUZ3W
9704	1		0.66		2.1E-01 N42536.1		lyd 1e10.r1 Soares melanocyte 2NbHM Homo sapiens clovA done IMAGE.270934 5
9704	Ι.	36324	99.0		2.1E-01 N42536.1	L_HUMAN	ly/1610.r1 Soares melanocyte 2NbHM Homo sapiens cDINA Gone IMAGE: 270934 3
9713	ı		2.72		2.1E-01 X97378.1	NT	A.thailana mRNA for AlRanBP1b protein
9817	ı		1.02		2.1E-01 AB036529.1	NT	Homo saplens p53R2 gene for ribonucleotide reductase, exon 6
10535					2.1E-01 Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1 beta
	L_	_			000	TOGGGGGIA	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DEL!A)  An KO DIACYLGI YOFRO! KINASE)
10569		1			2.1E-01 P02024	EST HIMAN	A02131427E1 NIH MGC 81 Homo saplens cDNA clone IMAGE:4270831 5
10576		37218			2.15-01 6F3/4234.1	NAMOU ICE	Accessed of Sames fatal heart NHM10W Home seriens CDNA clone IMAGE:16917513
11778			1.34		A11418,	ESI_HUMAN	quotional sociales letter from from the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second seco
11882	2 24850		1.68		11036847 NT	Į.	Homo sapiens paricipate Mayepude & Lington 1
11879	3 24867	38565	2.6		2.1E-01 BE180422.1	EST HUMAN	RC3-H106ZZ-04050U-013-011 H100ZZ Figino Sapiens CONA
12688	3 25459		1.92		١	뉟	Homo sapiens fragile 1bD oxido reductase (FUN) gents, exclis o, s, and paner us.
12994	4 25646	12	1.39			EST_HUMAN	601440712F1 NIH MGC 72 Homo eaptens adulty diene introcal 307 de
13158	3 25763	31928	1.19			¥	Mus musculus genomic fregment, Z/8 No. criticanoscine /
88	5 13428	3 26460	1.92		AB01743	Ę	Gallus gallus mKNA tor avena, complete cos
क्र	L.		1.97		7705601 NT	NT	Homo caplens CGI-18 protein (LOC51008), mKNA
2	L	26937			2.0E-01 M77088.1	NT	O.cumiculus germline IgH heavy chain V-H pseudogene, allotype VHaZ
833	L				AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
186	1	L	1.83		2.0E-01 D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1149	L	L	2.81		2.0E-01 AL163213.2	NT	Homo saplens chromosome 21 segment HS21C013
1283	L				2.0E-01 AJ132695.5	NT	Homo sapiens rac1 gene
1336	L	L	1.99	L	2.0E-01 AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT042Z Homo saptens cUNA
161	1		22.4	L	4503408 NT	NT	Homo sapiens dystrobrevin, alpha (DTNA)) mRNA
4582	1				2.0E-01 AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
3	1						

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Most Similar Top Hit Acession (Top) Hit Descriptor	ID NO: Signal BLASTE No. Source	27821 3.48 2.0E-01 AF260700.1 NT	27273 0 98 2.0E-01 U22346.1 NT	2.58 2.0E-01 AF111170.3 NT	3.87 2.0E-01 U67525.1 NT	28185 1.46 2.0E-01 8922238 NT	1.9 2.0E-01 X82877.1 NT	0.79 2.0E-01 AF074990.1 NT	20E-01 P46607 SWISSPROT	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SWISSPROT	2,000 2,000 0.00 0.00 0.00 0.00 0.00 0.0	8 71 2.0E-01 BE828165.1 EST HUMAN	31243 6.41 2.0E-01 8922080 NT	29963 0.6 2.0E-01 P34641 SWISSPROT	31797 2.55 2.0E-01 X66600.1 NT	32355 2.08 2.0E-01 11432540 NT	32464 0.82 2.0E-01 X91856.1 NT	32709 5.99 2.0E-01 U15300.1 NT	0.74 2.0E-01/M76967.1 NT	33098 47.65 2.0E-01 X61033.1 NT	33206 3.74 2.0E-01 AW360865.1 EST_HUMAN	33995 1.41 2.0E-01 AF250371:1 NT	34147 0.83 2.0E-01 P54422 SWISSPROT	6.16 2.0E-01 AF028028.1 NT	35003 3.12 2.0E-01 X91151.1 NT	0.48 2.0E-01 BE562247.1 EST_HUMAN	36186 1.17 2.0E-01 U82511.1 NT	36215 0.82 2.0E-01 U71122.1 NT	5.42 2.0E-01 AE001278.1 NT	36579 0.52 2.0E-01 P11420 SWISSPROT	36580 0.62 2.0E-01 P11420 SWISSPROT	2.24 2.0E-01 AF146692.1
		27821	27973	213		28185			29758		60000	78803		31243	29963	31797	32355	32464	32709		33098			34147		L				L			
Exon	NON ON ON	14740	L		L	L	L	L			$oldsymbol{\perp}$	100 C	┸	L	上	L	L	L	<u> </u>	L.		L	5 20522	3 20673	9 21221	5 21476	L	Ļ	Ļ	上	L	1	
Probe	S S S S	1588	4792	1755	1708	1044	2423	2955	3578		8	80/E	1880	5152	5243	559	5859	5983	6185	8303	6559	8859	7445	7603	8139	8395	8921	9551	8280	9756	8947	9947	10095

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Most Similar (Top) Hit Top Hit Acession Database BLASTE No. Source	1.89 Z0E-01 AF086907.1 NT Arabidopsis thallana root gravitopism control protein (PIN2) gene, complete cds	1.89 2.0E-01 AF086907.1 NT Arabidopsis thetiana root gravitropism control protein (PINZ) gene, complete cds	2.0E-01 AF157814.1 NT	0.67 2.0E-01 AF157814.1 NT Homo septems CAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12	NT	NT	NT	2.0E-01 D89088.1 NT	2.0E-01 7524759 NT	4759 NT	INT	2.0E-01 AF302773.1 NT	2.0E-01 AW975297.1 EST HUMAN	2.0E-01 A1023592.1 EST_HUMAN		4.89 1.9E-01 7549743 NT Rettus norvegious Aryl hydrocarbon receptor nuclear translocator 1 (Amit1), mrkNA	5.58 1.9E-01/AF004353.1 NT Mus musculus pale ear (ep) gene, wild type allele, 3 region, partial cds	1.9E-01 U32581.2 NT		1.9E-01 BE070801.1 EST_HUMAN	BE070801.1 EST_HUMAN	1.72 1.9E-01 7305190 NT Mue musculus interleukin 2 receptor, gamma chain (IlZrg), mRNA	r HUMAN	1.9E-01 AF081282.1 NT		3922533 NT	1.8E-01 U66066.1 NT	1.9E-01 J00922.1	1.9E-01 D13197.1 NT	1.9E-01 R16467.1 EST_HUMAN	1.9E-01 AF264017.1 NT	3.68 1.9E-01 AB008784.1 NT Schizosaccharomyces pombe DNA for cycloplasmic dynein heavy chain, compiete cds	1.9E-01 AW754106.1 EST HUMAN	1.31 1.9E-01 AE01912.1 NT Deinococcus radiodurans R1 section 49 of 229 of the compasse chromosome i
	1 AF086907.	1 AF086907.	1 AF157814.	1 AF157814.	1 X78388.1	1 X97121.1	1 D89088.1	1 D89088.1			1 AF206637.	1 AF302773.	1 AW975297	1 A1023592.1	1 AF078164.		1 AF004353.	1 U32581.2	1 U32581.2	1 BE070801	BE07080		1 AA358813	11 AF081282	11 AF184623.	11	1 U66066.1	1 J00922.1	1 D13197.1	N R16467.1	M AF264017	11 AB008784	01 AW75410	01 AE001912
Most Simila (Top) Hit BLAST E Value		Ľ		2.0E-0	Ï	,	,	"	<u> </u>										L															
Expression Signal	1.89	1.89	0.67	0.67	9.0	0.88	2.12	2.12	1.33			1.84	1.63			4.89																		1.31
ORF SEQ ID NO:	36878	36879				37259				38588			31851				26604				L		27349	27629		28711			29666	L				
Exan SEQ ID NO:	23282	23282	23406	23406	١	<u> </u>	L	24154	L	L	L			L	L				L		L		14293	14656			L		L			┸	ı	17397
Probe SEQ ID NO:	10247	10247	18371	10371	10419	10616	11079	11079	11908	11908	12666	12899	12012	12952	12977	113	362	673	673	980	681	1010	1128	1401	1466	2456	2989	3004	3482	3569	3907	4100	4193	4251

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				Mare Circlian			
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4346	17489		0.89		.9E-01 BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Hcmo saplens cDNA
4592	L	30711		Ĺ	1.9E-01 AL161493.2	NT	Arabidopsis thaliana DNA chrcmosome 4, contig fragment No. 5
6124	L	l			.9E-01 AF223642.1	TN	Rettus norvegicus chemokine receptor CXCR3 mRNA, complete cds
	<u>L</u>		1			1444	X28407 XI NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
5721					1.9E-01 AW 130149.1	ESI HUMAN	MOID RECEIT ON ALTHAN (Library).
5761		╻┃			1.9E-01 AF127937.1	I N	Tromg sagretis CNA polytica asserption catalytic descriptions.
5962	19148	32463	1.08	·	1.9E-01 AF091218.1	L	Mus musculus Wrn protein (Wrn) gans, complete cas
9009	19181		2.45		1.8E-01 AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA ctone N   ZRP4001328 5
6457	19824	32987	1.03		1.9E-01 AI762391.1	EST_HUMAN	wi64h02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394089 3
6518	i i		1.1		1.9E-01 AW148452.1	EST_HUMAN	x14c08.x1 NCI_CGAP_KId8 Homo sepiens cDNA clone IMAGE:2618030 3' similer to gb:X03559 A1P SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
	1						yg09a12.s1 Sogres Infant brain 1NIB Home sapiens cDNA clone IMAGE:31663 3' similar to contains MER13
7112	18538		1.54		1.9E-01 R43212.1	EST_HUMAN	repetitive element;
7138	ı		0.74		1.9E-01 AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7138	l	Ì		,	1.9E-01 AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7409	ı				1.9E-01 U73846.1	IN	Drosophila melanogastar testis-specific RNA-binding protein (bruno) mRNA, complete cds
	_			L			Staphylococcus aureus toxic shock syndroine toxin-1 (tst), enteroloxin (ent), and integrase (int) genes,
7638	3 20707	34186	0.78		1.9E-01 U9368B.1	LΝ	complete cds
7661	ı	34204	1.38		1.9E-01 U80922.1	L	Arabidopsis thalians serine/threonine protein phosphatase type one (10PPS) gene, complete cas
7708	1_				1.9E-01 AF072724.1	LΝ	Zea mays starch branching enzyme I (sba1) gene, complete.cds
8174	L		1.83		1.9E-01 AL161657.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8885	L			Ŀ	1.9E-01 AB033024.1	NT	Home capiens mRNA for KIAA1198 protein, partial cds
9146	1				1.9E-01 M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9146	1				1.9E-01 M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
							ol96g10.61 NCL_CGAP_PNS1 Homo saplens cDNA clone IMAGE:1537506 3' similar to contains Alu
10079	23117	36719	0.77		1.9E-01 AA912486.1	EST_HUMAN	repetitive element
5	L		0.81	L	1.9E-01 BE830353.1	EST_HUMAN	RCS-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10447	1	37091		L	1.9E-01 BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10880	1	l			1.9E-01 AL161503.2	۲	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880	1	l			1.9E-01 AL161503.2	5	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 15
	L						Homo sapiens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
10892	24071	37704	2.18		1.9E-01 AF223391.1	TN	policed
12025	1				1.9E-01 AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	7 25028				1.9E-01 L07344.1	ᅜ	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5 end
	J						

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-		_		_	_													_	-			$\overline{}$	_		_	_	_		_
	Top Hit Descriptor	Mus musculus p116Rip mRNA, complete cds	Mus musculus Cotg gene for chaperonin containing TCP-1 gamma subunit, partial cds	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated	products	Oryzias latipes gene for membrana guanylyl cyclase OIGC1, complete cds	wd71f02x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'	Dictyostelium discoideum plasmid Ddp5, complete genome	Yersinia pestis plasmid pCD1	Mus musculus guanyate nucleotide binding protein 1 (Gbp1), mRNA	Mus musculus guanyate rucleotide binding protein 1 (Gbp1), mRNA	gg22d10.x5 NCI_CGAP_Kid3 Homo sapleris cDNA clone IMAGE:1761811 3' similar to TR:075936 075936 GAMMA BUTYROBETAINE HYDROXYLASE;	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small Inducible cytokine A6 precursor, small	Inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds	QV3-DT0018-081299-036-g04 DT0018 Hcmo sapiens cDNA	Jonopsidium acaule LEAFY protein (LEAFY'2) gene, partial cds	X/41a03.x1 Soares_NFL_T_GBC_S1 Homo caplens cDNA clone IMAGE:2659756 3'	QV0-BN0041-070300-147-c04 BN0041 Hcmo sapiens cDNA	601809723R1 NIH_MGC_18 Homo seplens cDNA clone IMAGE:4040821 3'	y/45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element,	y/45e01.s1 Soares placenta Nb2HP Home sapiens cDNA clone IMAGE:161704 3' similar to contains Alu renefitive element:	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds	Arabidopsis thallana DNA chromosome 4, contig fragment No. 56	Mus musculus Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds	N.tabacum mRNA pNLA-36	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA	Mesocricetus auratus Na-taurocholate cotrensporting polypeptide mRNA, partial cds	ti57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'	M.barkeri mtaC and mtaB genes
	Top Hit Database Source	F	뉟		TN	TN	EST_HUMAN	۲	TN	TN	LN.	EST_HUMAN		NT	EST_HUMAN	ΤN	<b>EST_HUMAN</b>	<b>EST_HUMAN</b>	EST_HUMAN	EST HUMAN	TAN I	N-L	NT	Ę	NT	EST_HUMAN	TN	EST_HUMAN	۲
Significant	Top Hit Acession No.	1.8E-01 U73200.1	1.8E-01 AB022090.1		4502532 NT	1.8E-01 AB021490.2	1.8E-01 AI912212.1	1.8E-01 AF000580.1	1.8E-01 AL117189.1	6753947 NT	6753947 NT	1.8E-01 AI733708.1		1.8E-01 AB051897.1	1.8E-01 AW935728.1	1.8E-01 AF184589.1	1.8E-01 AW182300.1	1.8E-01 AW995178.1	1.8E-01 BF183582.1	1.8E-01 H03369.1	7000	1.8E-01 D37954.1	1.8E-01 AL181556.2	1.8E-01 AB051897.1	1.8E-01 X79794.1	1.8E-01 AW814270.1	1.8E-01 AF181258.1	1.8E-01 Al439881.1	1.8E-01 Y08310.1
	Most Similar (Top) Hit BLAST E Value	1.8E-01	1.8E-01		1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01		1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	200	1.85.01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01
	Expression Signal	1.85	1.47		1.9	0.78	1.8	2.14	6.87	1.49	1.49	1.91		2.28	3.34	2.3	1.18	1.61	77.0	0.87	600	0.92	5.61	2.68	0.65	1.79	2.55	68.0	1.2
	ORF SEQ ID NO:	26274					27235		L	L	L			28208	L		29163		229638				30801	31011	L	L	L	31313	
	Exan SEQ ID NO:	13270	ı	1	13589	13946	1			14686	14688	15058	l	15108	Ĺ	ı	16144	16369			i i	L	L	18025	L	<u> </u>	18327	18340	ı
	Probe SEQ ID NO:	32	270		38	766	1003	1115	1317	1533	1633	1915		1965	2756	2963	8967	3194	3452	3712	25.6	4453	4678	4895	5129	5158	5206	5218	5291

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Exan O SEQ ID O NO. NO. NO. NO. NO. NO. NO. NO. NO. N		SEB - CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF 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THE SECOND CONTRACTOR OF THE SECOND CONTRACTOR OF T	Top Hit.Acession No. No. BE082626.1 AL 161684.2 N28629.1 G678428 G678428 G678428 G678428 D302\714 N2863.1 N2863.1 N2863.1 N2863.1 N2863.1 N2863.1 N2268.1 N2268.1 N2268.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 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N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N2269.1 N226	Top Hit Detabase Source Source Source ST_HUMAN T_HUMAN	RCG-BT0841-300300-011-H03 BT064 i Homo saplens cDNA Arabidopsis thaliana DNA chromosome 4, config fragment No. 90 yo28108.17 Scares melanocyte 2NBHM Homo explens cDNA clone IMAGE:294063 5: Wuss musculus Tri receptor-essociated factor of (Traff), mRNA Muss musculus Tri receptor-essociated factor of (Traff), mRNA Muss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus Tri receptor-essociated factor of (Traff), mRNA Miss musculus mRNA for weats, complete cds Coltulus lanatus mRNA for weats, complete cds Stoffulus lanatus mRNA for weats, complete cds Miss musculus mRNA for Dieperplate decarboxylase (URA1) gene, complete cds Amp NUCLE OSIDASE Aduatius amplus cytochrome coddase subunit I (COI) gene, partial cds; mitochondrial Minusculus mRNA for P19-problain tycosile phosphatese Homo sapiers mRNA for P19-problain tycosile phosphatese Homo sapiers mRNA for P19-problain tycosile phosphatese Homo sapiers mRNA for P19-problain tycosile phosphatese Homo sapiers mRNA for P10-problain tycosile phosphatese Homo sapiers mRNA for P10-problain tycosile phosphatese Homo sapiers mRNA for ribonucleotide reductiose P2  Bactariophage 14 interrase remeasor makin for No. All mrn.  Bactariophage 14 interrase remeasor makin for No. All mrn.  Bactariophage 14 interrase remeasor makin for No. All mrn.
	3 3.05	1.8E-01 A	<u> </u>		exocurprises in integratise, repressor projein (mo), dUTPase, holin and lysin genes, complete cds Citralius lanatus mRNA for weas, complete cds
24338		1.8E-01 AF019107	$\prod$		Citrulius lanatus mRNA for weus, complete cds Dictycstellum discoideum unknown (DG10ệ1) gene, complete cds
Ш		1.8E-01 A	3.1	EST_HUMAN x	Human carcinoembryonic entigen (CEA) giane, excn 4 xp40h10 x1 NCI CGAP HN11 Home sepiens cDNA chine INA CE-2220eps or

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Oingie Exon Probes Expressed in Fracence	Top Hit Descriptor	B.taurus mRNA for potassium channel	Rattus norvegicus Thromboxane receptor (Tbxa2n), mRNA	cp2798.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'	Bovine ephemeral fever virus, complete genome	602019928F1 NCL_CGAP_Bm57 Homo sapiens cDNA clone IMAGE:4155318 5/	Yersinia pestis plasmid pCD1	DNA TERMINAL PROTEIN (BELLETT PROTEIN)	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5	E.dispar mRNA for hexokinase (hxk1)	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcoce), mKNA	601274604F1 NIH_MGC_20 Homo saptens cDNA clone IMAGE:3613736 3	P. dumerilii histone gene cluster for core histones M24, M25, M3 and M4	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMEN I LIGHT) PULTPET TIDE) (NF4.)	Lymantria dispar nucleopolyhedrovirus, complete genome	Lymantria dispar nucleopolyhedrovirus, complete genome	Arabidopsis thaliana DNA chromosome 4, contig tragment No. 69	Homo sepiens BNIP3H (BNIF3H) gene, complete cds; rucieer gene for mitochondrial product	Vibrio cholerae hypoxanthine phosphoribos/ytransferase (hpt) gene, partial ods, hemagglutinin/protease requiatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial ods		Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds	EST41651 Endometrial tumor Homo saplens cDNA 5' end	Naja naja atra ctx-1 gene, exons 1-3	Naja naja atra otx-1 gene, exons 1-3	Taxus canadensis gerany/gerany/ diphosphate synthase mRNA, complete ods	J2346F Human fetal heart, Lembda ZAP Express Homo saplans cDNA clone J2346 5	Anabasna sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE	gene and adpF gene	Homo septens derivative 11 breakpoint fragment, partial intron 10 of the ALL-1/MLL/HRX gene rused to introl in the ALL-1/MLL/HRX gene rused to introl	5 of the Ar-4/ret gene	Schistocerca gregaria appra repeative Livin	MO sepiens fregile 160 oxago reduciase (FOR) yerre, exuits o, e, airu parizar oue
Exon Propes C	Top Hit Database Source	NT B.t		EST_HUMAN CP		EST HUMAN 60		SWISSPROT DN				EST_HUMAN 60		ISSPROT		NT Ly		NT Ho	10A		NT P	EST_HUMAN ES	NL	Ž LN	T/S	EST HUMAN J2		NT			X :	
Single	Top Hit Aæsslon No.	.8E-01 X57033.1	8394421 NT	.8E-01 AA095094.1	10086561 NT	.8E-01 BF348623.1	.8E-01 AL117189.1	.8E-01 Q96682	.8E-01 R24494.1	.8E-01 Y11114.1	9506952	.7E-01 BE385164.1	1	.7E-01 P35616	.7E-01 AF081810.1			.7E-01 AF255051.1	7F.01 AF000718 1	100010	1.7E-01 AF000716.1	1.7E-01 AA336909.1	1.7E-01 AJ238738.1	1.7E-01 AJ238738.1	1.7E-01 AF081514.1	1.7E-01 N55763.1		1.7E-01 AJ269505.1		1.7E-01 AJ236377.1	1.7E-01 X52936.1	1.7E-01 AF217490.1
	Most Similar (Top) Hit BLAST E Value	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	175.01	10-17-1	1.7E-01	1.7E-01	1.7E-01			1.7E-01		1.7E-01				
	Expression Signal	8.94	3.48	1.77	1.79	1.26	1.18	3.28	20.8	4.98	1.7	8.4	3.18	1.79	0.89	0.89	244	3.23	c 5	217	2.13	1.47	1.09	1.09	1.65	0.81		1.52				0.59
	ORF SEQ ID NO:	37563	38751	38808		32103					31548	28801			27306				25.0		20113				l	l	L	29710		30215		30838
	Exon SEQ ID NO:	23938	ı		L	i_	l	1		25643	ì	l	L		14249	14249	15008	L			16100	L	L	16237		ı	1	16699			1	18014
	Probe SEQ ID NO:	11750	12081	12124	12239	12306	12719	12811	12942	12988	13035	591	828	983	1083	1083	1880	2038	2	7787	2000	2993	3061	38	3174	3451		3634		4048	4681	4884

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					)		
Probe SEQ ID 8	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hil Descriptor
4961	18090	31066	1.3	1.7E-01	1.7E-01 AI247635.1	EST_HUMAN	dh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similer to contains OFR.b1 OFR repetitive element;
5231	18353		1.07	1.7E-01		NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
6272	18301	31350	. 0.72	1.7E-01	.7E-01 BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_38 Homo sapierjs cDNA clone IMAGE:3827197 5'
5312	18429	31399	PG.0	1.7E-01	.7E-01 D37961.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc Intron binding protein 1), complete cds
5524	18721	31737	88.	1.7E-01	.7E-01 AA470886.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	88.	1.7E-01		EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapleits cDNA clone IMAGE:881088 3' similar to go:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18903	32198	0.820	1.7E-01	1.7E-01 U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6469	19626	32988		1.7E-01	.7E-01 H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6517	19682	33052	0.72	1.7E-01	1.7E-01 Al370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Home sapiens cDNA clone IMAGE:20454923'
6517	19682	33053		1.7E-01	.7E-01 AI370976.1	EST_HUMAN	ta29c11.x1 Sogres_fetal_lung_NbHL18W Home sepions eDNA clone IMAGE:20454923'
6992	18511	31503	0.75	1.7E-01		EST_HUMAN	600944087T1 NIH_MGC_17 Homo sapiens cDNA done IMAGE:2960248 3'
7019	20155			1.7E-01	.3	ΙN	Mesocricetus auratus oviduciin precursor (OVI) gene, complete cds
7140	20275		0.69	1.7E-01	1.7E-01 Z92910.1	IN	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	1.7E-01 AP000422.1	NT	Escherichia coli 0157:H7 genomic DNA, Sakal-VT2 prophege inserted region
7448	20525	33398		1.7E-01	1.7E-01 BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo saplens cDNA done IMAGE:3843964 5'
7849	20718	34195	1.21	1.7E-01	1.7E-01 P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN ULS6 (HFLF0 PROTEIN)
7666	25850	34208		1.7E-01		SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8046	21128	34648	1.26	1.7E-01	1.7E-01 AF000573.1	LΝ	Homo sapiens homogentisate 1,2-dloxygenase gene, complete cds
8150	21232	34752	0.75	1.7E-01	1.7E-01 AF150669.1	IN	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8472	21553	35083				۲	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8472	21553	35084	<u> </u>	1.7E-01	7706426 NT	L	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8892	21974	35511	0.5		1.7E-01 AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.93	1.7E-01	1.7E-01 D00384.1	TN	Rat (SHR strain) SX1 gene
9045	22124		0.94	1.7E-01	1.7E-01 AF217413.1	TN	Homo saplens neuroligin 3 isoform gene, complete cds, alternatively spiloed
9045	22124		0.94	١.	1.7E-01 AF217413.1	ᅜ	Homo sapiens neuroligin 3 lscform gene, complete cds, alternatively spliced
9198	22276	35814	0.51	1.7E-01	1.7E-01 R77002.1	EST_HUMAN	y/66g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5
6988	22444	36005		1.7E-01	1.7E-01 BE253142.1	EST_HUMAN	601118672F1 NIH_MGC_16 Homo sapienis cDNA clone IMAGE:3357184 5'
6988	22444	36006		1.7E-01	1.7E-01 BE253142.1	EST_HUMAN	601115672F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3357184 5
9789	22829				1.7E-01 AP001508.1	뒫	Bacilius halodurans genomic DNA, section/2/14
6686	22939	36524	0.54		1.7E-01 AW977455.1	EST_HUMAN	EST389564 MAGE resequences, MAGO Homo sepiens cDNA
6686	22939	36526			1.7E-01 AW977455.1	EST_HUMAN	EST389564 MAGE resequences, MAGO Homo septens cDNA

Page 103 of 550 Table 4 Single Exon Probes Expressed in Placenta

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| Top Hit Descriptor                            | Human class IV alcohol dehydrogenase (AI)H7) gene, exon 3                 | Human immunodeficiency virus type 1 (B7.05) env gene (partial)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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                                                                                                                         | Homo sapiens chromosome 21 segment HS21C084                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Homo sapiene solute cerrier family 7 (callonic amino acid transporter, y+ cystem), member 2 (SLC7A2),<br>mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | rq50e07.s1 NCI_CGAP_Co9 Homo septens cDNA clone IMAGE:1148292.3' sImiler to gb:L25081<br>TRANSFORMING PROTEIN RHOC (HUMAN);                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IWAGE:3813258 6'                                                                                                                                                                                                                                                                           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subunit (CACNA1), mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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sapiens cDNA clone IMAGE:135599 5'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Homo sapiens homeobox protein OTX2 gene, complete cds                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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|                                               | Exon ORF SEQ Expression (Top) Hit Acession Signal BLASTE No. Signal Value | Exan         ORF SEQ ID NO:         Expression Signal         (Top) Hit Acession No:         Top Hit Acession No.         Top Hit Acession No. | Expn         ORF SEQ ID NO:         Expression Signal 23831         Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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(B7.35<br>Aces (B1) Accorded to Source         Human class IV alcohol dehydrogenase (AJ)-<br>Human immunodeficiency virus type 1 (B7.35<br>Aces (B1) Accorded to Source         Human immunodeficiency virus type 1 (B7.35<br>Aces (B1) Accorded to Source           23031         36845         0.93         1.7E-01 A.251749.1         NT         Human immunodeficiency virus type 1 (B7.35<br>Accorded to Source | Expn<br>Signal         Most Similar<br>Crop) Hit<br>BLASTE         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Signal         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source<br>No.         Top Hit Acession<br>Source<br>No.           220531         36621         0.47         1.7E-01 (234608.1)         NT           220541         36642         0.93         1.7E-01 (AL163284.2)         NT           22473         2277         1.7E-01 (AL163284.2)         NT | Expn<br>SEQ ID<br>NO:         ORF SEQ<br>Signal         Expression<br>Figure         Top Hit<br>Top Hit<br>No.         Top Hit<br>Signal         Top Hit<br>BLASTE         Top Hit<br>No.         Top Hit<br>Source           22856         36543         2.08         1.7E-01         U16288.1         NT           23031         36622         0.47         1.7E-01         Z34508.1         NT           23053         36645         0.93         1.7E-01         Z34508.1         NT           23473         1.56         1.7E-01         AJ251749.1         NT           23673         2.77         1.7E-01         AJ251749.1         NT           23473         1.56         1.7E-01         AL163284.2         NT | Expn<br>SEQ ID         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>PLASTE         Top Hit Acession<br>No.         Top Hit Acession<br>No.         Top Hit Acession<br>Source           22866         36543         2.08         1.7E-01 U16288.1         NT           23031         38621         0.47         1.7E-01 U16288.1         NT           23053         36622         0.47         1.7E-01 Z34508.1         NT           23054         36645         0.93         1.7E-01 AJ51748.1         NT           23673         2.77         1.7E-01 AJ51748.1         NT           23673         37247         1.56         1.7E-01 AL63284.2         NT | Expn<br>SEQ ID<br>NO:         ORF 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| Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>PLASTE<br>Plane         Top Hit Acession<br>NO:         Top Hit Acession<br>Plane         Top Hit Acession<br>Plane         Top Hit Acession<br>Source<br>No:         Top Hit Acession<br>Source<br>Nature               220531             36622             0.47             1.7E-01             234608.1             NT               230541             36645             0.93             1.7E-01             A.251749.1             NT               23673             37247             1.5E-01             1.7E-01             A.163284.2             NT               23639             37247             1.66             1.7E-01             A.1427203             NT               2402             37636             9.54             1.7E-01             A.17E-01             EST_HUMAN               24122             37766             2.12             1.7E-01             AA62797.1             EST_HUMAN               24122             37766             2.12             1.7E-01             AA62797.1             EST_HUMAN | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>PLASTE<br>PLASTE<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>Source<br>No:         Top Hit Acession<br>NO:         Top Hit Acession<br>Source<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>Source<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>Source<br>NO:         Top Hit Acession<br>Source<br>NO:         Top Hit Acession<br>NO:         Top Hit Acession<br>NO:< | Expn<br>NO:         ORF
SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>PLASTE<br>PLASTE<br>NO:         Top Hit<br>NO:         Top Hit<br>Source<br>Value         Top Hit<br>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         36621         0.47         1.7E-01         U16288.1         NT           23051         36645         0.47         1.7E-01         Z34608.1         NT           23473         37247         1.7E-01         AJ251749.1         NT           23639         37247         1.56         1.7E-01         AL163284.2         NT           23639         37249         1.66         1.7E-01         AL163284.2         NT           24022         37636         9.54         1.7E-01         AA62792.1         EST_HUMAN           24122         37766         2.12         1.7E-01         AR844617.1         EST_HUMAN           24434         38090         6.81         1.7E-01         A706300 NT           24434         38091         6.81         1.7E-01         A706300 NT | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>BLASTE<br>Value         Top Hit<br>No.         Top Hit<br>Source<br>Value         Top Hit<br>Source           228E6         36543         2.08         1.7E-01         1.7E-01         1.16288.1         NT           23031         36622         0.47         1.7E-01         234608.1         NT         Source           23051         36645         0.63         1.7E-01         234608.1         NT         NT           23473         37247         1.56         1.7E-01         AL163284.2         NT         NT           24432         36645         0.93         1.7E-01         AL2631749.1         NT         NT           23473         1.56         1.7E-01         AL163284.2         NT         NT           24434         37249         1.66         1.7E-01         AL163284.2         NT           24434         36090         6.81         1.7E-01         AR814817.1         EST_HUMAN           24736         36091         6.81         1.7E-01         AR814817.1         EST_HUMAN           24736         38427         1.71         1.7E-01         AR883375.1         EST_HUMAN | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>Top) Hit<br>Velue         Top Hit Acession<br>No.         Top Hit<br>Source           228E6         36543         2.08         1.7E-01         U16228.1         NT         H           22031         36621         0.47         1.7E-01         U16228.1         NT         H           23031         36622         0.47         1.7E-01         234508.1         NT         H           23051         36645         0.93         1.7E-01         A251748.1         NT         H           23473         2.77         1.7E-01         AL163284.2         NT         H         I           23639         37247         1.56         1.7E-01         AL163284.2         NT         H           24002         37766         1.7E-01         AA627972.1         EST_HUMAN         EST_HUMAN           24434         38090         6.81         1.7E-01         AA814617.1         EST_HUMAN           24434         38091         6.81         1.7E-01         AA8433375.1         EST_HUMAN           24366         38427         1.71         1.7E-01         AA8433375.1         EST_HUMAN           24686         1.75         1.7E-01 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal<br>Signal         Most Similar<br>ID NO:         Top Hit Acession<br>Signal<br>Velue         Top Hit Acession<br>No:         Top Hit Acession<br>Source         Top Hit Acession<br>No:         Top Hit Acession<br>Source           22866         36543         2.08         1.7E-01         1.7E-01         1.7E-01         1.7E-01         NT         H           23031         38622         0.47         1.7E-01         2.24608.1         NT         H           23053         36645         0.93         1.7E-01         2.24608.1         NT         H           23054         36645         0.93         1.7E-01         AL251748.1         NT         H           23054         36645         0.93         1.7E-01         AL251748.1         NT         H           23057         1.7E-01         AL251748.1         NT         H         H           23639         37247         1.56         1.7E-01         AL427203         NT         H           24022         37636         9.54         1.7E-01         AR4814617.1         EST_HUMAN         L           24434         36091         6.81         1.7E-01         AA814617.1         EST_HUMAN         L           24434 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>ID NO:         Top Hit<br>Signal         Top Hit<br>ID NO:         Top Hit<br>Signal         Top Hit<br>ID NO:         Top Hit<br>Signal         Top Hit<br>ID NO:         Top Hit<br>Source         Top Hit<br>Source           228656         36543         2.08         1.7E-01         1.06288.1         NIT         Hit<br>Source           23031         36621         0.47         1.7E-01         234608.1         NIT         Hit<br>Source           23051         36645         0.93         1.7E-01         234608.1         NIT         Hit<br>Source           23053         36645         0.93         1.7E-01         AL251749.1         NIT         Hit<br>NIT         Hit<br>NIT | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>Top Hit<br>Value         Top Hit<br>No:         Top Hit<br>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT         H           22031         36621         0.47         1.7E-01         U26288.1         NT         H           23051         36622         0.47         1.7E-01         234608.1         NT         H           23051         36645         0.93         1.7E-01         A251749.1         NT         H           23053         37247         1.56         1.7E-01         A163284.2         NT         H           23054         37249         1.66         1.7E-01         A1463284.2         NT         H           23054         37247         1.56         1.7E-01         A1463284.2         NT         H           2402         37636         9.54         1.7E-01         A1427203         NT         H           24434         38090         6.81         1.7E-01         A4814617.1         EST HUMAN         C           24434         38090         6.81         1.7E-01         A4883375.1         EST HUMAN         C           24566 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Top Hit<br>Top) Hit<br>Palue         Top Hit<br>No:         Top Hit<br>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           22031         36621         0.47         1.7E-01         U16288.1         NT           23031         36622         0.47         1.7E-01         234608.1         NT           23051         36645         0.93         1.7E-01         A25608.1         NT           23473         37249         1.56         1.7E-01         A153149.1         NT           24402         37636         9.54         1.7E-01         A1427203         NT           24434         38090         6.81         1.7E-01         A2627972.1         EST_HUMAN           24736         9.54         1.7E-01         A883375.1         EST_HUMAN           24736         9.81         1.7E-01         A4883375.1         EST_HUMAN           24736         9.81         1.7E-01         A4883375.1         EST_HUMAN           24736         9.82         1.7E-01         A4883375.1         EST_HUMAN           24696         1.77         1.7E-01         A4883375.1         EST_HUMAN </td <td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         (Top) Hit<br/>Top Hit Top Hit Acession<br/>Velue         Top Hit Acession<br/>No:         Top Hit<br/>Source           228E6         36543         2.08         1.7E-01 U16288.1         NT         H           220531         36622         0.47         1.7E-01 Z34508.1         NT         H           220551         36645         0.93         1.7E-01 Z34508.1         NT         H           22057         37247         1.7E-01 Z34508.1         NT         H           22473         37249         1.66         1.7E-01 Z34508.1         NT         H           24424         37766         2.17         1.7E-01 Z4508.1         NT         H           24434         38091         6.81         1.7E-01 Z481467.1         EST HUMAN         I           24434         38091         6.81         1.7E-01 Z481467.1         EST HUMAN         I           24628         38427         1.71         1.7E-01 Z48147.1         EST HUMAN         I           25023         38728         1.87         1.7E-01 Z4883375.1         EST HUMAN         I           25023         38728         1.87         1.7E-01 Z48899         SWISSPROT         I           25027<!--</td--><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Kpest Similar<br/>Signal         Most Similar<br/>Velue         Top Hit<br/>No:         Top Hit<br/>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT           220631         36622         0.47         1.7E-01         Z34608.1         NT           220541         36622         0.47         1.7E-01         Z34608.1         NT           220543         36624         0.93         1.7E-01         Z34608.1         NT           220541         37249         1.56         1.7E-01         AL251748.1         NT           24473         37636         2.77         1.7E-01         AL63284.2         NT           24434         38090         6.81         1.7E-01         AA627972.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA8483375.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA883375.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA883375.1         EST_HUMAN 
         25023         38728         1.5         1.7E-01         P56899         SWISSPROT           25023         38</td><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expnession<br/>Signal         Most Similar<br/>(Top) Hit<br/>PLASTE         Top Hit<br/>No.         Top Hit<br/>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         A251748.1         NT           220632         36624         0.03         1.7E-01         A2608.1         NT           220643         36627         0.47         1.7E-01         A2608.1         NT           224632         37247         1.56         1.7E-01         A2627912.1         EST_HUMAN           24433         38090         6.81         1.7E-01         A4627912.1         EST_HUMAN           24434         38091         8.81         1.7E-01         A4883375.1         EST_HUMAN           24668         38727         1.71         1.7E-01         A66899         SWISSPROT           25623         3872</td><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>Top) Hit<br/>PLASTE         Top Hit<br/>No:         Top Hit<br/>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         38622         0.47         1.7E-01         Z34608.1         NT           23053         38622         0.47         1.7E-01         Z34608.1         NT           23054         36645         0.93         1.7E-01         AL251748.1         NT           23057         36645         0.93         1.7E-01         AL251748.1         NT           23057         37247         1.5E-01         AL251748.1         NT         NT           24432         37636         9.54         1.7E-01         AL251748.1         NT           24434         36091         8.81         1.7E-01         AA8214617.1         EST_HUMAN           24434         36091         8.81         1.7E-01         AA883375.1         EST_HUMAN           24568         38727         1.7E-01         AA883375.1         EST_HUMAN           25023         38727         1.67         1.7E-01         P56899         SWISSPROT           25023         38728         1.8</td><td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>(Top) Hit<br/>PLASTE         Top Hit<br/>No:         Top Hit<br/>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         38622         0.47         1.7E-01         Z34608.1         NT           23053         38622         0.47         1.7E-01         Z34608.1         NT           23054         36645         0.93         1.7E-01         A1551748.1         NT           23053         36645         0.93         1.7E-01         A1551748.1         NT           23054         36645         0.93         1.7E-01         A1551748.1         NT           23057         1.7E-01         A163284.2         NT         NT           24434         37636         9.54         1.7E-01         A1427203         NT           24434         38090         6.81         1.7E-01         A4814617.1         EST_HUMAN           24434         38090         6.81         1.7E-01         A4883378.1         EST_HUMAN           24696         6.81         1.7E-01         A4883378.2         SWISSPROT           25023         38726         1.87         1.7E-01<td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Pub.         Top Hit Acession<br/>Pub.         Top Hit Ace</td><td>Exan<br/>ORF SEQ<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>PLASTE         Top Hit Acession<br/>No:         Top Hit Acession<br/>Signal         Top Hit Acession<br/>Top Hit Top Hit Acession<br/>No:         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           2265G         36543         2.08         1.7E-01 U16238.1         NT         Dafabase<br/>Source           23031         3662I         0.47         1.7E-01 Z34608.1         NT         NT           23051         3662S         0.63         1.7E-01 Z34608.1         NT         NT           23053         3664S         0.63         1.7E-01 Z34608.1         NT         NT           23054         3662Z         0.47         1.7E-01 Z34608.1         NT         NT           23053         3662F         0.53         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37766         2.12         1.7E-01 AL63284.2         NT         NT           24022         37786         2.12         1.7E-01 AL63284.2         NT         NT</td><td>Even SEQ ID         ORF SEQ Expression Signal ID NO:         Signal PLASTE Source Source Signal ID NO:         Most Similar Top Hit Acession Source Source Source Adults         Top Hit Acession Top Hit Acession Source Source Source ID NO:         Top Hit Acession Source Source ID NO:         Top Hit Acession ID Database Source Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID ID NO:         Top Hit Acession ID ID Hit Acession ID ID ID ID ID ID ID ID ID ID ID ID ID</td><td>Expn<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>ID NO:         (Top) Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>ID NO:         T</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal<br/>DINO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>Signal<br/>Signal<br/>Signal<br/>DINO:         (Top) Hit<br/>Signal<br/>Value<br/>DIABBSB         Top Hit Acession<br/>No:         Top Hit Acession<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Source<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Databas</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Pub.         Top Hit Acession<br/>Value         Top Hit
Acession<br/>Source         Top Hit Acession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Acc</td></td></td> | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         (Top) Hit<br>Top Hit Top Hit Acession<br>Velue         Top Hit Acession<br>No:         Top Hit<br>Source           228E6         36543         2.08         1.7E-01 U16288.1         NT         H           220531         36622         0.47         1.7E-01 Z34508.1         NT         H           220551         36645         0.93         1.7E-01 Z34508.1         NT         H           22057         37247         1.7E-01 Z34508.1         NT         H           22473         37249         1.66         1.7E-01 Z34508.1         NT         H           24424         37766         2.17         1.7E-01 Z4508.1         NT         H           24434         38091         6.81         1.7E-01 Z481467.1         EST HUMAN         I           24434         38091         6.81         1.7E-01 Z481467.1         EST HUMAN         I           24628         38427         1.71         1.7E-01 Z48147.1         EST HUMAN         I           25023         38728         1.87         1.7E-01 Z4883375.1         EST HUMAN         I           25023         38728         1.87         1.7E-01 Z48899         SWISSPROT         I           25027 </td <td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Kpest Similar<br/>Signal         Most Similar<br/>Velue         Top Hit<br/>No:         Top Hit<br/>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT           220631         36622         0.47         1.7E-01         Z34608.1         NT           220541         36622         0.47         1.7E-01         Z34608.1         NT           220543         36624         0.93         1.7E-01         Z34608.1         NT           220541         37249         1.56         1.7E-01         AL251748.1         NT           24473         37636         2.77         1.7E-01         AL63284.2         NT           24434         38090         6.81         1.7E-01         AA627972.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA8483375.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA883375.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA883375.1         EST_HUMAN           25023         38728         1.5         1.7E-01         P56899         SWISSPROT           25023         38</td> <td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expnession<br/>Signal         Most Similar<br/>(Top) Hit<br/>PLASTE         Top Hit<br/>No.         Top Hit<br/>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         A251748.1         NT           220632         36624         0.03         1.7E-01         A2608.1         NT           220643         36627         0.47         1.7E-01         A2608.1         NT           224632         37247         1.56         1.7E-01         A2627912.1         EST_HUMAN           24433         38090         6.81         1.7E-01         A4627912.1         EST_HUMAN           24434         38091         8.81         1.7E-01         A4883375.1         EST_HUMAN           24668         38727         1.71         1.7E-01         A66899         SWISSPROT           25623         3872</td> <td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>Top) Hit<br/>PLASTE         Top Hit<br/>No:         Top Hit<br/>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         38622         0.47         1.7E-01         Z34608.1         NT           23053         38622         0.47         1.7E-01         Z34608.1         NT           23054         36645         0.93         1.7E-01         AL251748.1         NT           23057         36645         0.93         1.7E-01         AL251748.1         NT           23057         37247         1.5E-01         AL251748.1         NT         NT           24432         37636         9.54         1.7E-01         AL251748.1         NT           24434         36091         8.81         1.7E-01         AA8214617.1         EST_HUMAN           24434         36091         8.81         1.7E-01         AA883375.1         EST_HUMAN           24568         38727         1.7E-01         AA883375.1         EST_HUMAN           25023         38727         1.67         1.7E-01         P56899         SWISSPROT           25023         38728         1.8</td> <td>Expn<br/>NO:         ORF SEQ<br/>ID NO:         Expression<br/>Signal         Most Similar<br/>(Top) Hit<br/>PLASTE         Top Hit<br/>No:         Top Hit<br/>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         38622         0.47         1.7E-01         Z34608.1         NT           23053         38622         0.47         1.7E-01         Z34608.1         NT           23054         36645         0.93         1.7E-01         A1551748.1         NT           23053         36645         0.93         1.7E-01         A1551748.1         NT           23054         36645         0.93         1.7E-01         A1551748.1         NT           23057         1.7E-01         A163284.2         NT         NT           24434         37636         9.54         1.7E-01         A1427203         NT           24434         38090         6.81         1.7E-01         A4814617.1         EST_HUMAN           24434         38090         6.81         1.7E-01         A4883378.1         EST_HUMAN           24696         6.81         1.7E-01         A4883378.2         SWISSPROT           25023         38726         1.87         1.7E-01<td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Pub.         Top Hit Acession<br/>Pub.         Top Hit Ace</td><td>Exan<br/>ORF SEQ<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>PLASTE         Top Hit Acession<br/>No:         Top Hit Acession<br/>Signal         Top Hit Acession<br/>Top Hit Top Hit Acession<br/>No:         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           2265G         36543         2.08         1.7E-01 U16238.1         NT         Dafabase<br/>Source           23031         3662I         0.47         1.7E-01 Z34608.1         NT         NT           23051         3662S         0.63         1.7E-01 Z34608.1         NT         NT           23053         3664S         0.63         1.7E-01 Z34608.1         NT         NT           23054         3662Z         0.47         1.7E-01 Z34608.1         NT         NT           23053         3662F         0.53         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37766         2.12         1.7E-01 AL63284.2         NT         NT           24022         37786         2.12         1.7E-01 AL63284.2         NT         NT</td><td>Even SEQ ID         ORF SEQ Expression Signal ID NO:         Signal PLASTE Source Source Signal ID NO:         Most Similar Top Hit Acession Source Source Source Adults         Top Hit Acession Top Hit Acession Source Source Source ID NO:         Top Hit Acession Source Source ID NO:         Top Hit Acession ID Database Source Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID ID NO:         Top Hit Acession ID ID Hit Acession ID ID ID ID ID ID ID ID ID ID ID ID ID</td><td>Expn<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>ID NO:         (Top) Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID
NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>ID NO:         T</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal<br/>DINO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>Signal<br/>Signal<br/>Signal<br/>DINO:         (Top) Hit<br/>Signal<br/>Value<br/>DIABBSB         Top Hit Acession<br/>No:         Top Hit Acession<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Source<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Databas</td><td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Pub.         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Acc</td></td> | Expn<br>NO:         ORF SEQ<br>ID NO:         Kpest Similar<br>Signal         Most Similar<br>Velue         Top Hit<br>No:         Top Hit<br>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT           220631         36622         0.47         1.7E-01         Z34608.1         NT           220541         36622         0.47         1.7E-01         Z34608.1         NT           220543         36624         0.93         1.7E-01         Z34608.1         NT           220541         37249         1.56         1.7E-01         AL251748.1         NT           24473         37636         2.77         1.7E-01         AL63284.2         NT           24434         38090         6.81         1.7E-01         AA627972.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA8483375.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA883375.1         EST_HUMAN           24736         38091         6.81         1.7E-01         AA883375.1         EST_HUMAN           25023         38728         1.5         1.7E-01         P56899         SWISSPROT           25023         38 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expnession<br>Signal         Most Similar<br>(Top) Hit<br>PLASTE         Top Hit<br>No.         Top Hit<br>Source           228E6         36543         2.08         1.7E-01         U16288.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         234608.1         NT           220631         36622         0.47         1.7E-01         A251748.1         NT           220632         36624         0.03         1.7E-01         A2608.1         NT           220643         36627         0.47         1.7E-01         A2608.1         NT           224632         37247         1.56         1.7E-01         A2627912.1         EST_HUMAN           24433         38090         6.81         1.7E-01         A4627912.1         EST_HUMAN           24434         38091         8.81         1.7E-01         A4883375.1         EST_HUMAN           24668         38727         1.71         1.7E-01         A66899         SWISSPROT           25623         3872 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>Top) Hit<br>PLASTE         Top Hit<br>No:         Top Hit<br>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         38622         0.47         1.7E-01         Z34608.1         NT           23053         38622         0.47         1.7E-01         Z34608.1         NT           23054         36645         0.93         1.7E-01         AL251748.1         NT           23057         36645         0.93         1.7E-01         AL251748.1         NT           23057         37247         1.5E-01         AL251748.1         NT         NT           24432         37636         9.54         1.7E-01         AL251748.1         NT           24434         36091         8.81         1.7E-01         AA8214617.1         EST_HUMAN           24434         36091         8.81         1.7E-01         AA883375.1         EST_HUMAN           24568         38727         1.7E-01         AA883375.1         EST_HUMAN           25023         38727         1.67         1.7E-01         P56899         SWISSPROT           25023         38728         1.8 | Expn<br>NO:         ORF SEQ<br>ID NO:         Expression<br>Signal         Most Similar<br>(Top) Hit<br>PLASTE         Top Hit<br>No:         Top Hit<br>Source           22866         36543         2.08         1.7E-01         U16288.1         NT           23031         38622         0.47         1.7E-01         Z34608.1         NT           23053         38622         0.47         1.7E-01         Z34608.1         NT           23054         36645         0.93         1.7E-01         A1551748.1         NT           23053         36645         0.93         1.7E-01         A1551748.1         NT           23054         36645         0.93         1.7E-01         A1551748.1         NT           23057         1.7E-01         A163284.2         NT         NT           24434         37636         9.54         1.7E-01         A1427203         NT           24434         38090         6.81         1.7E-01         A4814617.1         EST_HUMAN           24434         38090         6.81         1.7E-01         A4883378.1         EST_HUMAN           24696         6.81         1.7E-01         A4883378.2         SWISSPROT           25023         38726         1.87         1.7E-01 <td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>Pub.         Top Hit Acession<br/>Pub.         Top Hit Ace</td> <td>Exan<br/>ORF SEQ<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>(Top) Hit<br/>PLASTE         Top Hit Acession<br/>No:         Top Hit Acession<br/>Signal         Top Hit Acession<br/>Top Hit Top Hit Acession<br/>No:         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source         Top Hit Acession<br/>Source           2265G         36543         2.08         1.7E-01 U16238.1         NT         Dafabase<br/>Source           23031         3662I         0.47         1.7E-01 Z34608.1         NT         NT           23051         3662S         0.63         1.7E-01 Z34608.1         NT         NT           23053         3664S         0.63         1.7E-01 Z34608.1         NT         NT           23054         3662Z         0.47         1.7E-01 Z34608.1     
   NT         NT           23053         3662F         0.53         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37766         2.12         1.7E-01 AL63284.2         NT         NT           24022         37786         2.12         1.7E-01 AL63284.2         NT         NT</td> <td>Even SEQ ID         ORF SEQ Expression Signal ID NO:         Signal PLASTE Source Source Signal ID NO:         Most Similar Top Hit Acession Source Source Source Adults         Top Hit Acession Top Hit Acession Source Source Source ID NO:         Top Hit Acession Source Source ID NO:         Top Hit Acession ID Database Source Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID ID NO:         Top Hit Acession ID ID Hit Acession ID ID ID ID ID ID ID ID ID ID ID ID ID</td> <td>Expn<br/>SEQ ID<br/>NO:         ORF SEQ<br/>Signal<br/>Signal<br/>ID NO:         Expression<br/>Signal<br/>Signal<br/>Signal<br/>ID NO:         (Top) Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top Hit<br/>Signal<br/>ID NO:         Top 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Acession<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Source<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Database<br/>Source<br/>Database<br/>Source<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Database<br/>Databas</td> <td>Expn<br/>NO:         ORF SEQ<br/>Signal         Expression<br/>Signal         (Top) Hit<br/>Pub.         Top Hit Acession<br/>Value         Top Hit Acession<br/>Source         Top Hit Acession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Accession<br/>Acc</td> | Expn<br>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>Pub.         Top Hit Acession<br>Pub.         Top Hit Ace | Exan<br>ORF SEQ<br>NO:         ORF SEQ<br>Signal         Expression<br>(Top) Hit<br>PLASTE         Top Hit Acession<br>No:         Top Hit Acession<br>Signal         Top Hit Acession<br>Top Hit Top Hit Acession<br>No:         Top Hit Acession<br>Source         Top Hit Acession<br>Source         Top Hit Acession<br>Source           2265G         36543         2.08         1.7E-01 U16238.1         NT         Dafabase<br>Source           23031         3662I         0.47         1.7E-01 Z34608.1         NT         NT           23051         3662S         0.63         1.7E-01 Z34608.1         NT         NT           23053         3664S         0.63         1.7E-01 Z34608.1         NT         NT           23054         3662Z         0.47         1.7E-01 Z34608.1         NT         NT           23053         3662F         0.53         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37636         6.81         1.7E-01 AL63284.2         NT         NT           24022         37766         2.12         1.7E-01 AL63284.2         NT         NT           24022         37786         2.12         1.7E-01 AL63284.2         NT         NT | Even SEQ ID         ORF SEQ Expression Signal ID NO:         Signal PLASTE Source Source Signal ID NO:         Most Similar Top Hit Acession Source Source Source Adults         Top Hit Acession Top Hit Acession Source Source Source ID NO:         Top Hit Acession Source Source ID NO:         Top Hit Acession ID Database Source Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID NO:         Top Hit Acession ID Database Source ID ID NO:         Top Hit Acession ID ID Hit Acession ID ID ID ID ID ID ID ID ID ID ID ID ID | Expn<br>SEQ ID<br>NO:         ORF SEQ<br>Signal<br>Signal<br>ID NO:         Expression<br>Signal<br>Signal<br>Signal<br>ID NO:         (Top) Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>ID NO:         Top Hit<br>Signal<br>ID NO:         Top Hit<br>ID NO:         T | Expn<br>NO:         ORF SEQ<br>Signal<br>DINO:         Expression<br>Signal<br>Signal<br>Signal<br>Signal<br>Signal<br>Signal<br>DINO:         (Top) Hit<br>Signal<br>Value<br>DIABBSB         Top Hit Acession<br>No:         Top Hit
Acession<br>Source<br>Database<br>Source<br>Database<br>Source<br>Source<br>Database<br>Source<br>Database<br>Source<br>Source<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Source<br>Database<br>Database<br>Source<br>Database<br>Source<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Database<br>Databas | Expn<br>NO:         ORF SEQ<br>Signal         Expression<br>Signal         (Top) Hit<br>Pub.         Top Hit Acession<br>Value         Top Hit Acession<br>Source         Top Hit Acession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Accession<br>Acc |

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					igno	EXUIT FIUDE	Single Exon Flobes Expressed in Flacelita
Prabe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Shriler (Top) Hit BLAST E Value	Top Hit Acession Na	Top Hit Database Source	Top Hit Descriptar
3723	16884		1.23	1.6E-01	.6E-01 AJ003165.1	IN	Populus trichocarpa cv. Trichobel ABI3 gene
3723		L		1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3872	17031	30030			.6E-01 AE000982.1	NT	Archeeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8		1.6E-01 AE004413.1	NT.	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4144	17296	30288		l	.6E-01 AF084456.1	NT	Grithidia fasciculata tryparedoxin I (bril) gene, complete cds
4448	17688		10.91		.6E-01 AF179680.1	LN	Homo sapiens apelin gene, complete cds
4578	17715		2.49		.6E-01 AW968601.1	EST_HUMAN	EST380877 MAGE resequences, MAGJ Homo sepiens cDNA
4586	17723		4.39	1.65-01	TN 6155319	TN	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5080	18188	31162	1.39	ļ	.6E-01 AA088343.1	EST HUMAN	z84h09.s1 Stratagene colon (#S37204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955    E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
5083	ı					LN	Lycopersicon esculentum Rsal fragment 2, satellite region
5083	1		1.8	ľ	1.6E-01 A.1008356.1	TN	Lycopersicon esculentum Rsal fragment 2, satellite region
5345			0.93	ľ	1.6E-01 AF045283.1	LN FN	Gallus gallus smooth muscle/non-muscle niyosin light chain kinase gene, exon 29
6503	•	31719		٦	.6E-01 L40608.1	LN LN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31909	2.9		.6E-01 AW 197496.1	EST HUMAN	xm43f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE.2888969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN
5639	1				.8E-01 AW 197498.1	EST HUMAN	xm43f01.x1 NCI_CGAP_GC6 Homo expleins cDNA clone IMAGE:2886969 3' similar to TR:O78984 O76984 HYPOTHETICAL 127.6 KD PROTEIN
5651						IN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6152	19328		0.73		.6E-01 BE925803.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Hcmo sepiens cDNA
6558	19720		2.08		1.6E-01 AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8229	19720	33097	2.06	1	.6E-01 AL161588.2	INT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 84
6639	20262	33688				LN	Homo sepiens mRNA for KIAA1566 protein, partial cds
6985			99'0			EST_HUMAN	602139855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301004 5'
7103	18530	31485			1.6E-01 AW291215.1	EST_HUMAN	UI-H-BI2-agi-b-06-0-UI.st NCI_CGAP_Sub4 Homo saplens cDNA clone IMAGE:27244183'
7451	20528	34001	0.71	1:6E-01	1:6E-01 Z49632.1	TN	S.cerevisiae chromosome X reading frame ORF YJR132w
7965	21005		1.63		1.6E-01 AW246359.1	EST_HUMAN	2822248.6prime NIH_MGC_7 Hamo cepieris aDNA olone IMAGE:2822248 6'
7982	21031	34544		1.6E-01	TN 782837 NT	NT	Mus musculus Ca<2+>dependent activator protein for secretion (Cadps), mRNA
7986	21035				1.6E-01 AU136525.1	EST_HUMAN	AU136526 PLACE1 Hamo saplens cDNA clane PLACE1004466 5'
8063	21136	34657	1.62		1.6E-01 L49349.1	NT	Gorilla gorilla androgen receptor gene, partiti exon
ROTE	21307		0.53		6F-01 BF244087 1	FST HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baykor-HGSC project≔TCBA Homo sapiens idDNA clone TCBAP0607
	ı					ľ	Bacteroides wilgatus beta-lactamase (cfxA) gene, complete cds and mobilization protein (mobA) gene,
8310	21382	34916	0.77		1.6E-01 U38243.1	NT	complete cds

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13985 27037 1.38 1.5E-01 AL163284.2 NT 14281 27337 1.44 1.5E-01 AJ009735.1 NT 44384 27344 2.7 1.5E-01 AJ051885.1 NT		Eou ID ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100. ID NO: 100.	Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Si	Mosts BLASS BLASS ALL 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Top Hit Ace No. 299119.1 1249501.1 249501.1 249501.1 249501.1 111 249501.1 111 8E1559649. AF106964. AF106964. AF287344. BE257894. BE257894. BE257898. BE257898. BE257898. BE257898. BE277898. BE277898.	TOP HII Detabase Source Source T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN	Top Hill  Delabase Source  NIT  EST HUMAN  RCG-ST0200-04189-0118-0418-0418-0418-0418-0418-0418-0418
14298 27241 27 4 5E-01 A 12518851 NT	L.L	Ш		-	AL163284.2 A In09735.1	TN	Homo sapiens chromosome 21 segment HS210084 Cyprhus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
14302 27463 2.37 1.5E-01 (2.59125) 1 14400 27463 2.37 1.5E-01 (2.4400) 17400 27463 2.37 1.5E-01 (2.4400) 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 17400 174		111			AJ251885.1 : L36125.1 : AW195518.1	T HUMAN	Opposition of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Con

Page 106 of 550 Table 4 Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1304	14480	27526		1.6E-01	1.5E-01 D26535.1	LΝ	Human gene for dihydrolipoamide succinyttransferase, complete cds (exon 1-15)
1304	L		322	1.5E-01		NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1511	14684			1.5E-01	1.5E-01 AF117340.1	NT	Mus musculus MAP kinase kinase kinase ( (Mekkt) mRNA, complete cds
1857	15100	28200	96'0	1.6E-01	1.6E-01 AW 444451.1	EST_HUMAN	UI-H-BI3-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Hamo sepiens cDNA done IMAGE:2733541 3
2980	l		6.0	1.5E-01	1.5E-01 AW572516.1	EST_HUMAN	xw56a02.22 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1 THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3100	<u> </u>	29290		1.5E-01	1.5E-01 M81441.1	NT	Bos baurus factor V varient 2 (factor V) mRNA, complete cds
3118	1	29308	0.62	1.5E-01 078687	078687	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3433	16601	28620	6.78	1.5E-01	1.5E-01 AA835049.1	EST_HUMAN	occado 5.1 NCI_CGAP_GC4 Homo saplens cDNA clone IMAGE:1571337 3' similar to gb:M11433 RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3454	١.			1.6E-01	1.6E-01 Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3454	ł_			1.5E-01	1.5E-01 Z23104.1	NT	L. stagnalis mRNA for G. protsin-coupled receptor
3851	L _		2.35	1.5E-01	1.5E-01 U09984.1	NT	Mus musculus ICR/Swiss glyceraldehyde 2-phosphate dehydrogenase (Gapd-S) gene, complete cds
	<u> </u>			1	114 OH COOT F	. <u>L</u>	Homo expiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial
3867				1.55-01	occont.	Į.	Modelly Illivery
3881				1.5E-01	1.5E-01 M97882.1	N. FOL	ATINA, ITRITIONING CONTROL AND THE DAY OF THE WAS CHOSEN AND WAS CHOSEN AND THE TABLE OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF T
3970					1.5E-01 AW 665983.1	ESI_HUMAN	iljulious societa in the societa in the societa contraction in the societa contraction in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the societa in the so
3987					1.5E-01 AJ003165.1	٤	Populus tranocarpa cv. I ranoca Abis garia
3987	14141		0.68		1.6E-01 AJ003165.1	ᅜ	Populus trichocarpa cv. Trichoba Abi's gene
4161	17312		1.16		1.5E-01 AW368659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 H10149 Hcmo sapiens CLINA
4210	17359				1.5E-01 Z12628.1	뉟	Buspus mitochondrion DNA for OKF158
4289	17442	30428	9.85		1.5E-01 AL163284.2	뒫	Homo sapiens chromosome 21 segment HS21C084
4847	17980	L		1.5E-01	1.5E-01 BF687665.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo seplens cDNA clone IMAGE:4086223 5
4874	L	L	2.33	1.5E-01	1.5E-01 BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4247537 5
5114	乚	L			30.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 60
6370	L	L	1.91	1.5E-01	1.5E-01 P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5399	L				52.1	N	Caiman crocodilus MHC class Il beta chalri (hcilbeta) gene, complete cds
	40040		20		1 EC.01 P15108	TORGESIME	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ISBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5665	4	32434			1.5E-01 AW850754.1	EST HUMAN	IL3-CT0219-160200-064-F10 CT0219 Horino sapiens cDNA
209	ı	Ĺ		L	4 5E-04 1 185018 1	LN	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5507	1	1			1 5F-01 (165016.1	TN	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
and a	ı				TMORRADA	F	Homo seniens sodium channel, voltage gated, type VI, atcha polypeptide (SCN6A) mRNA
80	19212	32532	2 0.82			2	

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					)	20 - 1   1   2   2   5   1   1   1   2   2   2   2   2   2   2	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acassion No.	Top Hit Database Source	Top Hit Descriptor
6128	19307	32847	1.71	1.5E-01	6753659 NT	ΤN	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6128	L.,	1	1.71	1.5E-01	6753659 NT	LN	Mus musculus DNA methyltransferase 2 (Chmt2), mRNA
6168	L	l	2.19	1.5E-01	.5E-01 AJZ76505.1	. IN	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19496	32862		1.5E-01	.5E-01 BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3833981 5
6376			1,88	1.6E-01	4608396 NT	ΝΤ	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	L	33002		1.5E-01	.5E-01 AF134807.1	LN	Influenza B virus (B/Nanchang/480/94) NB; protein gene, complete cds; and neuraminidase gene, partial ods
6831	L			1.6E-01		TN	Archaeoglobus fulgidus section 68 of 172 of the complete genome
8861	L	33207	57.4	1.5E-01	11417236 NT	LN	Homo saplens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6672	1			1.5E-01	.5E-01 P48508	SWISSPROT	GLUTAMATE—CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876			1.5E-01	.5E-01 Q28462	SWISSPROT	AMELOGENIN
6823				ľ	.5E-01 AA714760.1	EST_HUMAN	nw30d10.s1 NCI_CCAP_CCB0 Hamo septions oDNA olono IMAGE:1241871 3'
6852	i				.5E-01 P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	ı		9	1.5E-01	.5E-01 AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
	i .				A A DA 45 45 4	NAMILL FOR	ob7302.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element
7158	1		9.0		.0E-01 A4811343.1	בים שמשוא	Elita (ground commission)
7366				1		Į.	Homo sapiens HARY (HARY) gene, exon (1 and continue cus
7550	ı	34099	1.63	1		EST_HUMAN	wr62c08.x1 NC_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2491310 3
7764	l	34314	88.0		.5E-01 AF299073.1	LΝ	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764		34315			.6E-01 AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7775				_	.5E-01 AW 500811.1	EST_HUMAN	UFRF:BN0-akk-d-05-0-UI:/1 NIH_MGC_50 Homo sapiens CDNA clone IMAGE:3077409 5'
7776	20832	l		-	.5E-01 AW500611.1	EST_HUMAN	U+HF-BN0-akk-d-05-0-U.: 1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077409 5
7919	ı	34477	0.79	1	.5E-01 U46560.1	INT	Saccharomyces cerevisiae weak multicopy/suppressor of los1-1 (SOL3) gene, complete cds
8248	1			-	.5E-01 P21303	SWISSPROT	MEROZOITE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)
	ł				EE 04 4 40 Z021 Z 4	NAMIN TOO	oo85g12.s1 NCI_CGAP_Kid5 Homo sapiers cDNA clone IMAGE:1573030 3' similar to gb:M26082 INTERI FLIXIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN):
2	ı	07000			March 11.1	10 m	COSESSESSES AND ANOTO THE DATE AND PARTIES OF TAXABLE SALES AND AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE SALES AND THE
8507	21588		1.06	-	.5E-01 BE884799.1	ESI HOMAN	801310322F1 NIN_MICC_11 FOUR SEPTEMBLE CLIVE CHILD INVOCE_201400 F
8594			14.14	_	.5E-01 C16800.1	EST HUMAN	C16800 Cionech human aora polyA+ mixiva (20072) Homo sapiens culva cione octaviosa o
8628	l '				1.5E-01 1.27835.1	닐	Pangasianodon gigas growth hormone (GH) mRNA, complote odo
8793	1	35411	217	,	.5E-01 D84478.1	NT NT	Homo sapiens mRNA for ASK1, complete ods
8814	21893		0.79	•	.5E-01 P43446	SWISSPROT	WNT-10A PROTEIN PRECURSOR
8038	3 22117	35860	3.12	1.5E-01	4501972 NT	본	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (AD I B1), mKNA

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	Top Hit Descriptor	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:298866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;	GV0000404 Human Psoriasis Differential Display Homo saplens cDNA	AV754819 TP Homo seplens cDNA done TPAAHB12 5'	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5	Adpenser transmontano vitallogenin mRNA, partial ods	Human type II 3-beta hydroxysterold dehydiogenase/ 5-delta - 4-delta isomerase gene, complete cds	Aplysia californica carboxypeptidase D mRNA, complete cds	Aplysia californica carboxypeptidase D mRNA, complete cds	P. lentusculus mRNA for Integrin beta subunit	Mesocricetus auratus mRNA for collagen type XVII, complete cds	WK53h12.X1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' cimilar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);	WK53h12.X1 NCI_CGAP_P/22 Homo septens cDNA done IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);	Danio rerio transcription factor Pas8b (Pas8) mRNA, complete cds.	Clayceps purpurea ps1 gene	Claviceps purpurea ps1 gene	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA	CM2-BT0688-210300-122-f11 BT0688 Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C080	IL5-CN0024-030300-025-D04 CN0024 Homo saplens cDNA	qe72e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to db:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);	602128753F1 NIH MGC 56 Homo saplens cDNA clone IMAGE:4285549 5'	Rattus norvegicus chemokine CX3C mRNA, complete cds	Mus musculus mRNA for death inducer-ob/iterator-1 (Dio-1)	yp87e04.r1 Soares fetal liver spicen 1NFLS Homo capiens cDNA clone IMAGE:194430 5'	Bacillus halodurans genomic DNA, section 8/14	Lymphocystis disease virus 1, complete genome	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'	Campylobacter jejuni NCTC11168 completis genome; segment 1/8
100	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	TN	NT.	NT	NT	N	EST_HUMAN	EST HUMAN	N	ΤN	님	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	FST HIMAN	MAN HIMAN	N L	LN LN	EST HUMAN	NT.	3 NT	EST_HUMAN	N
,	Top Hit Acession No.	1.5E-01 N74226.1	1.5E-01 BF585465.1	1.5E-01 AV754819.1	1.6E-01 AU130007.1	1.6E-01 U00465.1	1.5E-01 M77144.1	1.5E-01 AF007570.1	1.5E-01 AF007570.1	1.5E-01 X98852.1	1.5E-01 AB027759.1	1.5E-01 AI814048.1	1.5E-01 Ai814048.1	1.5E-01 U40932.1	1.6E-01 AJ01.1984.1	1.5E-01 AJ011964.1	1.5E-01 BE088492.1	1.5E-01 BE088492.1	1.6E-01 AL163280.2	1.5E-01 AL163280.2	1.5E-01 AW841915.1	1 8E-04 A1593704 1	4 5E-01 RE700582 1	1.5E-01 AF030358.2	1.5E-01 AJ238332.1	1.5E-01 R83077.1	1.5E-01 AP001514.1	9695413 NT	1.5E-01 AV741272.1	1.5E-01 AL139074.2
	Most Similar (Top) Hit BLAST E	1.5E-01	1.5E-01	1.5E-01	1.6E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.6E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.6E-01	1.5E-01	1.5E-01	4 AE_04	1 55.01	1,55.04	1.5E-01	1_		1.5E-01		
	Expression Signal	2.58	1.34	2.52	0.64	6.7	0.71	7.82	7.82	2.59	0.51	2.38	236	122	1.60	8.	1.67	1.67	4.46	4.48	1.38	1 94	28 08	1.64	123	6.64	1.52	1.41	2.59	7.68
	ORF SEQ ID NO:	35932	36033			34609	36856	36761	36762			37161	37182								38042							32002		31857
	SEQ ID NO:	22381	22469		<u> </u>	21055		23163	ì	L	L	<u> </u>		L		_		l_	24139	24139	<u>1</u>	24044		L	1_	<u>L</u>	L	L	1	
	Probe SEQ ID NO:	8305	8394	9401	9605	9652	10022	10125	10125	10407	10495	10516	10316	10598	10761	10761	10935	10935	11063	11063	11331	4.00	1960	12629	12833	12696	12749	12778	12807	12932

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Single Exon Probes Expressed in Tracerita	Most Similar Top Hit Acession Catabase BLASTE No. Source	1.6E-01 AJ276242.1 NT	1.6E-01 8831294 NT	1.4E-01 AF008663.1 NT	1.4E-01 D78638.1 NT	1.4E-01 T91864.1 EST_HUMAN	1.4E-01 6679980 NT	1.4E-01 AE001710.1 NT	1.4E-01 AW 136741.1 EST_HUMAN	1.4E-01 AA720815.1 EST_HUMAN	1,4E-01 P30706 SWISSPROT	1.4E-01]AI933496.1 [EST_HUMAN	1.4E-01 A1699094.1   EST_HUMAN	1.4E-01 A1699094.1 EST HUMAN	1.4E-01 AE001710.1 NT	260601.s1 Sogres_fetal_liver_spleen_INPI.S_S1 Homo eaplane cDNA clone IMAGE:453673 3' similar to	1.4E-01 AA776287 1 EST HUMAN repetitive element;		1.4E-01 5453861 NT	1.4E-01 AJ005180.1 NT	1.4E-01 T90677.1 EST_HUMAN	1.4E-01 AB004558,1 NT	1.4E-01 AB004556.1 NT	1.4E-01 BE326891.1   EST_HUMAN	1.4E-01 AU117147.1   EST_HUMAN	1.4E-01 AU117147.1 EST_HUMAN	1 EST_HUMAN	1.4E-01 BE266536.1 EST_HUMAN	1.4E-01 BF378533.1 EST_HUMAN	1.4E-01 AL118568.1   EST_HUMAN	1.78 1.4E-01 AW016373.1 EST_HUMAN ULH-BID-eat-c-09-0-UI.81 NCI_CGAP_Suit Homo saplens cDNA clone IMAGE:2710289.3'	wi04f12.x1 NCI_CGAP_CIL1 Homo sapieris cDNA clone IMAGE;2389295 3' similar to SW:ICE4_HUMAN P49692 CASPASE-4 PRECURSOR;
	Most Similar (Top) Hit BLAST E Value	1.85点	4.6円之	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01		1.4E-01		1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1 4F-01
	Expression Signal	6.61	2.28	1.23	3.24	2.99	1.48	1.84	1.27	14.84	1.02	3,34	9.45	9.45	4.28		0.7		0.79	290	621	4.33	4.33	3.17	4.45	4.45	3.7	1.61	2.48	0.71	1.78	57.0
	ORF SEQ ID NO:	31932						28032			28793	29077	30421	30422	30475				30820		31598	31621	31622	32981	33161	33162	_		33286			
	Exan SEQ ID NO:	25769	26138	13526	14108		14936	14939	15097	15183	15669	16987	L	L	17495		17869	1	17833	18436	18622	18644	18644	19595	19771	19771	19859	19873	19895	20359	20617	20888
	Probe SEQ ID NO:	13183	13227	310	933	1288	1787	1790	1854	2042	2544	2853	4289	4289	4362		4531		4798	5322	6421	5442	5444	8427	6811	6611	9701	6715	6738	7278	7545	7818

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2d94a04.r1 Soares\_fetal\_heart\_NbHH19W/Homo sapiens cDNA clone IMAGE:357102 6' similar to contains Macromitrium levatum small ribosomal probin 4 (rps4) gene, chloroplast gene encoding chloroplast protain, th92b12.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo expiens cDNA done IMAGE:2126111 3' similar to TR:002710 002710 QAG POLYPROTEIN ; Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinese lal (IAL), and увойти. r2 Stratagene placenta (#937225) Homo sapiens cDNA done IMAGE:68973 5' similar to contains Bacillus subtilis complete genome (section 14 of 21); from 2600461 to 2812870 naggea03.51 NCI\_CGAP\_GCB1 Homo saplens cDNA clone IMAGE:1320364.3'
W70c05.1 Soares breast 2NbHBst Homo saplens cDNA clone IMAGE:154086.5'
xd73e10.x1 Soares\_NFL\_T\_GBC\_S1 Homo saplens cDNA clone IMAGE:2803274.3'
ye47g10.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:20030.6' yd47d03.r1 Soares fekal liver spleen 1NFLS Homo sapiens cDNA clane IMAGE:111365 Oryctolegus cuniculus fructose 1,6, bisphosphate aldolase (AIdB) gene, complete ods q190b12.x1 Soares\_NHHMPu\_S1 Homo septens cDNA done IMAGE:1879583 3 df88b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5' y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5' y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5' d/Z9h08.y1 Morton Fetal Cochlea Homo sepiens cDNA clone IMAGE:2485084 6' d/Z9h08.y1 Morton Fetal Cochlea Homo sepiens cDNA clone IMAGE:2485084 5' MR2-ST0218-211299-013-608 ST0218 Homo sepiens cDNA MR3-ST0218-211299-013-608 ST0218 Homo sepiens cDNA 601894760F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4124199 5 601895465F1 NIH\_MGC\_19 Homo septens oDNA dono IMAGE:4124824 6 EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end Fop Hit Descriptor Cperfringens ORF for putative membrane transport protein AV659047 GLC Homo sapiens cDNA clone GLCFSH08 3' zinc finger protein (DNZ1) genes, complete cds M.vannielii genes rpoH, rpoB and rpoA M.vannielii genes rpoH, rpoB and rpoA element KER repetitive element Single Exon Probes Expressed in Placenta Homo sapiens PHEX gene Homo sapiens PHEX gene Alu repetitive element partial cds EST\_HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN EST HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN **EST HUMAN** EST\_HUMAN EST HUMAN EST\_HUMAN EST\_HUMAN Top Hit Database Source 눋 눋 눋 Top Hit Acession 1.4E-01 Z99117.1 1.4E-01 AA811480.1 1.4E-01 AW104982.1 1.4E-01 AF121361.1 1.4E-01 BF375285.1 1.4E-01 BF375285.1 BF310258.1 AV659047.1 1.4E-01 AF023813.1 1.4E-01 AW021908. 1.4E-01 AW023836. 1.4E-01 AI436093.1 ģ AI305192.1 R53400.1 1.4E-01 W93411.1 1.4E-01 T84293.1 U85645.1 R62746.1 1.4E-01 T96102.1 R62746.1 1.4E-01 X73283.1 153770.1 X73293. 1.4E-01 Y1019B.1 1.4E-01 / 1.4E-01 / 1.4E-01 / 1.4E-01 1.4E-01 1.4E-01 1.4E-01 1.4E-01 1.4E-01 1,4E-01 (Top) Hit BLAST E Value 2 2 2 3 1.84 0.76 0.78 2.57 0.89 0.83 0.54 0.54 0.0 19.0 5.0 5.0 1.07 1.07 8.62 1.65 9.0 1,32 0.81 Expression Signal 37783 36932 37109 38071 37110 34167 34345 35810 35951 36098 36180 36181 36194 36195 34607 36821 37481 34490 ORF SEQ ÖΝΩ 22083 22272 22612 22623 22623 21092 22183 22612 22532 23047 20691 20855 21750 SEQ ID ģ 10293 10463 10483 10948 11081 11354 8849 10192 10293 10825 10009 SEQ ID 9114 9322 9322 9388 9475 9558 8996 7621 7832 8670 9194 9547 9547

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Probe NO: 1475 1905 2014 2014 2014 2015 3639 3816 3816 3816 3816 4162 4162	Even NO: 14628 15048 15154 15154 15158 16688 1608 1608 17064 17064 17064 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068 17068	ORF SEQ. ID NO: 28169 28269 28269 28979 28980 289866 288866	Expression Signal 0.97 1.02 2.73 2.73 3.31 1.38 2.78 0.85 0.85 0.88 0.88 0.88 0.88	Mosts (1948)	SITE TOP Hit Acession ST E No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No. Bute No.	NT NT NT NT NT NT NT NT NT NT NT NT NT N	Top Hit Describtor  Top Hit Describtor  Source  Source  Source  Source  Source  NT Horno saplens adapter protein CMS mRNA, complete cds  NT Bodysis cincrea strain T4 cDNA library under conditions of nitrogan deprivation  NT Bodysis cincrea strain T4 cDNA library under conditions of nitrogan deprivation  REA-STO173-191099-032-412 S10173 Horno saplens cDNA  NT Reassits auretus keratin type I mRNA, complete genome  NT Archaeoglobus fulgidus section 81 of 172 of the complete genome  NT Archaeoglobus fulgidus section 81 of 172 of the complete genome  NT Archaeoglobus fulgidus section 81 of 172 of the complete genome  NT Cerassits auretus keratin type I mRNA, complete cds  NT Archaeoglobus fulgidus section 81 of 172 of the complete genome  NT Cerassits auretus keratin type I mRNA, complete cds  NT Cerassits auretus keratin type action not arms is a complete cds. and L-type section not arms is a complete cds, and L-type section not harms is a complete cds, and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a complete cds. and L-type section not harms is a not L-type section not harms is a not L-type section not not not not not not not not not n
4257	Ш		0.82		1.3E-01 AF020713.1	LN I	Bacteriophage SPBc2 complete genome
4274					.3E-01 AW364341.1	EST HUMAN	QV3-D 10018-081289-030-803 D 10018 Home septens clowd
4281	L				3E-01 AF026805.1	NT FST HUMAN	Schistosoma mansoni iruciose prepriospinate artorase mixiva, compreta cus xx23f10.x1 Soares .NR_T GBC S1 Homb septens cDNA clone IMAGE:2813995 31
4302	17446	30431	1.19		3E-01 AW 2/3/41.1	NT	Homo saplens chromosome 21 segment HS210080
4601	1	30717			.3E-01 M21672.1	TN.	Bowne branched chain alpha-keto acid dihydrolipoyi transacylase mRNA, complete cds
4656	1		ļ		.3E-01 BE272339.1	EST_HUMAN	801126098F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE;2890063 5
4748		L	0.73		.3E-01 BF078854.1	EST_HUMAN	602154308F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4295544 5'
5314		1			.3E-01 AP000005.1	NT	Pyrococcus harikoshii OT3 genomic DNA, 1994001-1166000 nt. pocition (6/7)
5440					.3E-01 AW 466988.1	EST HUMAN	ha07b06x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive etement ;
5478	1				.3E-01 AW804417.1	EST_HUMAN	QVo-UM0083-100400-189-e06 UM0093 Homo sapiens cDNA
5618	LI		0.92		.3E-01 AF107793.1	M	Emericella ridulans DNA-dependent RNA polymerase il RPB140 (RPB2) gene, partial cds

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- edoc		•	_	-	_		
	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5702	18895		19.0	1.3E-01		П	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
6842	18032	32338	0.72	1.3E-01	.3E-01 BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Hamo saplans cDNA clone IMAGE:4101119 5'
6107	19287	32621	0.58	1.3E-01	.3E-01 BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bm67 Homo eqpiens cDNA clone IMAGE:4177233 5'
6107	19287	32822	0.58	1.3E-01	.3E-01 BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo supiens cDNA done IMAGE:4177233 5'
6612	19772	33183	18.92	1.3E-01	.3E-01 AB031326.1		Schizosaccharomyces pombe gene for Alp41, complete cds
8699	19856	33246	2.28	1.35-01	3E-01 X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6927	20242			1.3E-01	.3E-01 W 26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed(sublibrary Homo sapiens cDNA
6974	20202	33628	2'0	1.3E-01		EST_HUMAN	601465987F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868079 6'
6974	20202	33629	2.0	1.3E-01	.3E-01 BE782928.1		601465957F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3869079 5
7155	20289		0.74	1.3E-01	1.1		602044345F1 NCI_CGAP_Bm67 Homo stiplens cDNA clone IMAGE:4181866 5'
7412	20490		1.97	1.3E-01	.3E-01 H48664.1	EST_HUMAN	yr33d02.r1 Soares fetal liver spleen 1NFLS, Homo saplens cDNA clone IMAGE:207075 5'
8146	21228		0.79	1.3E-01	.3E-01 BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8160	21242	34762	1.68	1.3E-01	11423284 NT		Homo sapiona PRO0611 protein (PRO0611), mRNA
8192	21274	34797	1.32	1.3E-01	.3E-01 BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo saplens cDNA clone IMAGE:4299074 3'
8460	21650	35080		1.3E-01	11421556 NT		Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	.3E-01 Z74102.1		S.cerevisiae chromosome IV resding frame ORF YDL054c
8580	21661		4.96	1.3E-01	8923919 NT		Homo sapiens care histone macroH2A2.2 (MACROH2A2), mRNA
8725	21805	35342		1.3E-01	.3E-01 BF690522.1	EST_HUMAN	602187016T1 NIH_MGC_49 Homo saplens cDNA clone IMAGE:4299074 3'
9140	72227	35770		1.3E-01	3E-01 R11172.1	EST HUMAN	y/39g11.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL! PROTEIN ;
						Г	y/38g/11.r1 Soares fetal liver spleen 1NFLS/Homo sapiens cDNA clone IMAGE:129284 5' similar to
9149	22227	35771		1.3E-01	.3E-01 R11172.1	T HUMAN	SP:RIZB KA I PZ8318 60S RIBUSUMAL PRUIEIN
9420	22494	36060		1.35-01	11068003 NT		Pluteila xylostella granulovirus, complete genome
9420	22494	36061		1.3E-01	11068003 NT		Plutalla xylostella granulovirus, completa genome
9672	22634	36204	4.19	1.3E-01	.3E-01 AF023129.1	NT	Oryctolagus cuniculus H+,K+-ATPase alpha 2c subunit mRNA, complete cds
			1				J7837F Human fetal heart, Lambda ZAP Express Homo septens cDNA clone J7837 5' stmilar to B-CELL
8973	23012		0.73	1.3E-01	.3E-01 N86348.1	EST_HUMAN	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10267	23292		1.07	1.3E-01	8383940 NT		Rettus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10335	23370	36980	96.0	1.3E-01	.3E-01 AW861599.1	T_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo saplens cDNA
10603	25864	37244	1.08	1.3E-01	.3E-01 AL163246.2	IN	Homo saplens chromosome 21 segment HS21C046
10743	23776			1.3E-01		EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10797	23830			1.3E-01		EST_HUMAN	2820637.3prlme NIH_MGC_7 Homo saplens cDNA clone IMAGE:2820637 3'
10868	23963		2.31	1.3E-01	1.3E-01 BF330999.1	EST HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo saplens cDNA
11455	24515		1.34	1.3E-01	1.3E-01 BF092708.1	EST_HUMAN	MR4-TN0112-120900-102-e08 TN0112 Homo sapiens cDNA

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	Top Hit Acession Top Hit Descriptor Top Hit Descriptor Source	6671745 NT Mus musculus cofilin 2, muscle (Cft2), mR/VA	EST HUMAN	EST_HUMAN	EST_HUMAN	Ā	64.1 EST HUMAN 601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 6'	EST_HUMAN	EST_HUMAN	TN	LN.	wt.24d09.xt Sogres_Dieckgreefe_colon_NHCD Homo capiens cDNA clone iMAGE:2520977 3' stmilar to 114.1 EST HUMAN TR:060287 050287 KIAA0639 PROTEIN;	t4.1 EST HUMAN ANNEXIN V (HUMAN);		42.1 NT Homo sapiens colon cancer antigen NY-CC-45 mRNA, partial cds	EST_HUMAN	EST_HUMAN	EST_HUMAN	INT	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR SAMISSER INFAT3) (NF-ATC4) (NF-ATC3)	EST HUMAN	LN.	8.1 EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05085
	Top Hit		3E-01 BF677328.1	3E-01 BF677328.1	3E-01 BE279449.1	AF0128	.3E-01 BE619364.1	3E-01 BF683555.1	3E-01 BE618346.1	3E-01 AJ242790.1	3E-01 AB026829.1	3E-01 AW001114.1	2E-01 AI421744.1	2E-01 U66912.1	2E-01 AF039442.1	2E-01 AU149146.1	2E-01 AU149146.1	2E-01 AV735249.1	2E-01 AL445066.1	ZE-01 AA897474.1	2E 04 044034	2E-01 AI285402.1	2E-01 X89211.1	ZE-01 AW 448368.1	.2E-01 BF248490.1	2E-01 Z21405.1	2E-01 AW998556.1	2E-01 U18018.1	2E-01 AI720470.1
	Most Stmilar (Top) Hit BLAST E Value	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.2E-01	1.2E-01	1.25-01	1.25.01	1.25-01		1.2E-9	-			-	-	-	-	1	٦.	「
	Expression Signal	3.2	2.42	2.42	7.96	1.41	1.72	1.52	213	6.39	1.31	1.87	13.87	1.42	3.82	2.32	2.32	3.35	0.04	0.94		2.88	25.75	1.66		0.99	1.84	1.18	1.9
	ORF SEQ ID NO:		38354	38355	Ĺ		38708		32080				26688	L		27636					70026				28514		28893	23098	29162
Ì	Exon SEQ ID NO:	24585	24667	24667	24883	24985	25007	25033	25279	25368	25627	28647	13831	13237	13753	14662	14562	14568	14672	14689	4 404.2	14834	14957	15113	15386	15578	15779	16083	16143
	Probe SEQ ID NO:	11529	11616	11616	11895	12000	12023	12052	12399	12543	12864	12995	386	437	284	1408	1408	1414	1418	1536	4660	100	1808	1970	2253	2450	2658	2905	2987

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PCT/US01/00663

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Single Exon Probes Expressed in Placerita	Top Hit Descriptor	Human creatine kinase-B mRNA, complete cds	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	QV1-BT0259-281089-021-405 BT0259 Homo saplens cDNA	Methanococous jannaschil section 142 of 150 of the complete genome	Bacillus subtilis complete gename (section (15 of 21): from 2795131 to 3013540	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540	601810786R1 NIH_MGC_46 Homo saplens cDNA clone IMAGE:4053668 3'	P.clarkii mRNA; repeat region (ID 2MRT7),	P.clarkii mRNA; repeat region (ID 2MRT7),	Chicken neural cel-adhesion molecule (N-CAM) gene, exon 19	W. suaveclens mitochondrial orf1	Iny63c04.61 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	peorles	zo8402.r1 Soares_parathyroid_tumor_NbHPA Homo capiens cDNA clone IMAGE:321699 5	Homo saplens gene encoding plakophilin (exons 1-13)	M.domestica Borkh. Granny Smith adh mRINA for alcohol dehydrogenase	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI	IL0-CT0031-221099-113-e04 CT0031 Homo saplens cDNA	Mouse galactosylransferase mRNA, complete cds	rx85c01.s1 NCI_CGAP_GCB1 Hamo sapiens cDNA clone IMAGE:1269024 3'	602023112F1 NCI_CGAP_Bm67 Homo seplens cDNA clone IMAGE:4158388 5'	Jp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:183759 5'	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193769 5'	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76,	drbp76 gemma, drbp76 alpha and ILF3)	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA	wc99g03.x1 NCI_CGAP_C63 Hcmo sapleris cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN  Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;	NADH-UBIQUINONE OXIDOREDUCTASIE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)	et71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
e Exon Probe	Top Hit Database Source	NT	IN	EST_HUMAN	NT	TN	IN	NT	NT	EST HUMAN	NT	N	N	١N	EST_HUMAN			EST_HUMAN .	NT	ΙN	EST_HUMAN	SWISSPROT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		NT	EST_HUMAN	EST HUMAN	SWISSPROT	EST HUMAN
Single	Top Hit Acession No.	1.2E-01 M16364.1	X56882.1	1.2E-01 AW370668.1	1.2Ę-01 U67600.1	299118.1	K56882.1	K56882.1	299118.1	1.2E-01 BF128551.1	254255.1	254255.1	1.2E-01 M15861.1	X73416.1	1.2E-01 AA744369.1		1.2E-01 AF223391.1	1.2E-01 W33035.1	298266.1	248234.1	1.2E-01 BE620945.1	P10842	1.ZE-01 AW845Z75.1	1.2E-01 M26925.1	1.2E-01 AA747635.1	1.2E-01 BF347985.1	1.2E-01 H47799.1	1.2E-01 H47799.1		1.2E-01 AJ271741.1	1.2E-01 BE007072.1	1.2E-01 AI913753.1	002369	1.2E-01 AI832691.1
	Most Similar (Top) Hit BLAST E Value	1.2E-01	1.2E-01 X56882.1	1.25-01	1.25-01	1.2E-01 Z99118.1	1.2E-01 X56882.1	1.2E-01 X56882.1	1.2E-01 Z99118.1	1.25-01	1.2E-01 Z54255.1	1.2E-01 Z54255.1	1.25-01	1.2E-01 X73416.1	1.25-01	1	1.2E-01	1.2是-01	1.2E-01 Z98266.1	1.2E-01 Z48234.1	1.25-01	1.2E-01 P10842	1.25-01	1.2E-01	1.2E-01	1.2E-01	1.25-01	1.2E-01		1.2E-01	1.2E-01	1.2E-01	1.2E-01 Q02369	1.2E-01
	Expression Signal	3.44	0.91	2.52	0.74	99.0	1.12	1.12	1.22	0.95	2.1	2.1	0.59	1.94	68.0		0.93	2.5	1.65	1.14	1.9	0.81	2.28	1.52	0.58	1.18	0.64	0.64		0.62	1.13	2.45	0.64	99'0
	ORF SEQ ID NO:	29198	29265	29488			· 29789	29780			30426	30427	30552		31433		١	31601	31700	31885	32858			33022		33338	33731	33732		34320		34751		35119
	Exan SEQ ID NO:	1		l	16503	ŀ	18774	_	16733	17024			17571	18072	18567	l		18626	18683		19500					19940	l	20288		20820	21158	21231		21585
	Probe SEQ ID NO:	3001	3068	3302	3330	3568	3610	3610	3694	3865	4288	4298	4431	4942	5364		5415	5425	5484	5622	6329	6377	6428	6463	6561	6785	7.52	7154		7772	8076	8149	8197	8504

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Single EXUITIONS Expressed in Lacorica	Тор Hit Descriptor	xz49407.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587697 3' similar to gb:M13452 LAMIN A (HUMAN);	Staphylococcus aureus plasmid pSK23 pujative recombinese Sin (sin) gene, partial cds; and transcriptional regulator OacR (qacR) ganes, complete cds	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds	Homo sapiens Xq pseudoautosomal region; segment 2/2	Haemophilus influenzae Kd section 29 of 163 of the complete genome	M.muscallus DNA fregment of Apolipoprotein & gene	S.cerevískae HXT5 gene	AV710857 Cu Homo sapiens cDNA clone CuAAKEU8 5	Yeast MPTS gene for suppressor protein, complete cds	601655578R1 NIH_MGC_65 Homo sepleris oDNA clone IMAGE:3846283 3	601900763F1 NIH_MGC_19 Homo sapients cDNA clone IMAGE:4130103 5	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17	y/80c02.s1 Soares Infant brain 1NIB Home sapiens cDNA clone IMAGE:28880 3	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mKNA, complete cds	AV658033 GLC Homo sapiens cDNA clone GLCFIB123	Homo sapiens Xq pseudoautosomal region; segment 2/2	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-KUN) (CDW136) (CD136 ANTIGEN)	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin	young spatial order carrier antinen NV-CO-45 mRNA partial cds	III O SEPTETO CAROLI CALICA MINERAL TO TO TO THE SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN AND SERVICE CAROLICAN	K. KAYEGICUB NI VOO gelle 101 VOOLGE 1641 VIII ALAA INA CEST 808840 3'	gn20g05XI NCI_CGAP_Lub Hamo sapiens CUNA crone IMA CE: 1090040 5	Xenopus laevis Integrin alpha 3 subunit mRNA, partial cds	CYCLIN T	Vitrio cholerae chromosome II, section 85 of 63 of the complete chromosome	Chryseobacterium meningosepticum GOB;1 carbapenemase gene, complete ods	th18d08.x1 NCI_CGAP_Brn25 Home saplens cDNA clone IMAGE: 216/983 3	nm08g11.s1 NCL CGAP. Co10 Homo sepiens cUNA clone INANGE:100902U 5 SIMILER to gui Audesou Julei HEME OXYGENASE 1 (HUMAN);
EXUIT LIGHES E	Top Hit Database Source	EST_HUMAN (HL	Sta							T_HUMAN		EST_HUMAN 60	T_HUMAN		EST HUMAN yf8		r HUMAN	NT	SWISSPROT (CI			2	Т	EST_HUMAN qu		ISSPROT	NT V		EST_HUMAN fm'	EST_HUMAN HE
arguiro	Top Hit Acession No.	2E-01 AW083652.1	2E-01 AF063772.1			٠.				7.1		.2E-01 BE962324.2	2E-01 BF314481.1	2E-01 AF190493.1	2E-01 R40249.1	.2E-01 M65109.1		2E-01 AJ271736.1	2E-01 Q04912		T	-		-1	.2E-01 L10187.1	.2E-01 096433	28.1	.2E-01 AF090141.1	.1E-01 AI581003.1	.1E-01 AA569008.1
	Most Similar (Top) Hit BLAST E Value	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	-	-	1.2E-01	1.2E-01	1.2E-01	į	1.25-01	1.2E-01	1.25-01	1.2E-01	1.2E-01	1.2至-01	1.2E-01	1.2E-01	-	
	Expression Signal	10.78	3.76	1.09	1.09	1.02	1.44	0.77	1.3	6.0	2.55	3.03	1.73	2.78	1.72	2.47	2.09	4.37	2	,	1.65	18.32	1.4	4.89	3.48	6.44	1.47	1.23	1.56	1.33
	ORF SEQ ID NO:			36266					36338	36835					38329	L			31544					31981			31960		26792	26838
	Exan SEQ ID NO:	21871	21691	1	L.	21879	21988	21888	22767	23245	1_	24383	L	L		_		25355	1	i _		_ :	25574	l	<u>l_</u>	L	L	上	L.	13815
	Probe SEQ ID NO:	8590	8811	8849	8649	8800	8887	8920	9771	10209	11125	11320	11414	11533	11593	11798	12161	12522	12614		12732	12734	12863	12968	12892	12997	13031	13221	578	630

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					3.B		
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
1079	14245	27302	1.61	1.1E-01	.1E-01 BF697308.1	T_HUMAN	602129847F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4286771 5
1109	14274		1.65	Ì	1.1E-01 AL161560.2		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1185	16031		3.67	1.1E-01	1.1E-01 AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1278	L	27505	1.88	ľ	1.1E-01 D64004.1	TN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
1549	14701	L	2.75		1.1E-01 AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5
2255	L		1.73		1.1E-01 AJ006701.1	NT	Homo sapiens mRNA for putative serine/thi eonine protein kinase, partial
2388	15519		2.02		6755215 NT	NT	Mus musculus pre T-cell antigen receptor cipha (Ptcra), mRNA
2603	L		1,08	1.1E-01	6978676		Rattus norvegicus Procalagen II alpha 1 (Col2a1), mRNA
2633	١.		127		9.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2917	16095	29107	08:0		1.1E-01 S82418.1		intarleukin-12 p35 subunit (mice, Genomic, 700 nt, segment 4 of 6)
3098	L		180		1.1E-01 F03265.1	EST HUMAN	HSC1RF022 normalized infant brain cDNA, Homo sapiens cDNA clone c-1rf02 3
3422	L		1.56	1.1E-01	6753231 NT	NT	Mus musculus calcium channel, voltage-dépendent, Ttype, alpha 1G cubunit (Cacna1g), mRNA
3508	ı	29685			1.1E-01 BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sepienis cDNA clone IWAGE:3627066 51
3540	L				1.1E-01 X62135.1	IN	C.reinhardtil nuclear gene on Inkage group XIX
	L						yq62g08.s1 Soares fetal liver spleen 1NFLS Homo capiens cDNA clone IMAGE:200414 3' similar to contains
3580	16745	29763	0.74		1.1E-01 R96946.1	EST_HUMAN	Alu repetitive element;
3873	16836	29846	0.7	L	1.1E-01 Y07695.1	NT	A immersus gene for transposase
3791			96'0		1.1E-01 P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3800	J_	29965	1.28		1.1E-01 X52708.1	N	G.gailus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4228	L				1.1E-01 AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4226	L				1.1E-01 AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Home sapiens cDNA
						Ŀ	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein geno, partial odo;
				_			Notch4, PBX2, RAGE, lysophatidic acid acid transferase-alpha, palmitoy-protein thioesterase 2 (PPT2),
4233	17380		0.83		1.1E-01 AF030001.1	N	CKED-Kr, and chascan A ( 11NA) years, company
4367	17510		11.45		1.1E-01 AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mKNA, complete cos
4	17544	30528	0.76	L	1.1E-01 AW802058.1	EST_HUMAN	ILS-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
	<u>L</u>	<u> </u>			17	Ļ	Tapa-1=integral membrane protain TAPA-1 [mica, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1, sf 21
4782					U4480/		
4953	3 18083	31059	1.23		1.1E-01 Y07695.1	Ā	A immersus gene for transposeese
							Mus muscutus major histocompatibility locits class III reglon:butyrophilin-like protein gene, partial cds;
						!	Notch4, PBX2, RAGE, lysophatidic acid acyl dansierase-alpha, pairmoy-protect uncestated a (PF12),
5134	17380		0.75		1.1E-01 AF030001.1	Į.	CREE-KF, and whaten A (10A) genes, Carples
5787	18079		2.59		1.1E-01 AA747216.1	EST HUMAN	nx76a03.s1 NC_CGAP_Ew1 Homo saplens cDNA done IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
	1						

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					6		
Probe SEQ ID NO:	Exan SEQ ID NQ:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5857	18047	32353	1.32	1.15-01	.1E-01 AF020927.1	TN	მ Homo saplens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32383	78.0	1.1E-01	.1E-01 AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	L		1.1E-01	.1E-01 BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sepiens cDNA clone IMAGE:4186818 5
5927	19113		96.0	1.1E-01	1.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo saptens cDNA clone IMAGE:4186818 5*
5958	L	L	1.79	1.1E-01	.1E-01 X68851.1	TN	S. pombe ste8 gene encoding protein kinase
5992		32498	5.15		.1E-01 M86533.1	NT	Providencia rettgeri penicillin G amidase gene
9150	19326		1.68	1.1E-01	.1E-01 AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347		1.37	1.1E-01	1.1E-01 BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Hoino sapiens cDNA
6191	<u> </u>		7.73	1.1E-01	.1E-01 AW853699.1	EST_HUMAN	RC3-CT0254-280899-011-a01 CT0254 Homo sapiens cDNA
6554				1.1E-01	1.1E-01 AL163282.2	ΙN	Homo sapiens chromosome 21 segment H321C082
6562		l	1.52	1.1E-01	1.1E-01 AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo septens cDNA clone RL43
6602	ŀ	33150		1.1E-01	1.1E-01 AI216307.1	EST_HUMAN	qg78d06.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 31
8742			3.68	1.1E-01	1.1E-01 069635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843				1.1E-01	1.1E-01 AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
9834 4	1_	33684		1.1E-01	11432372 NT	IN	Homo saplens phosphatidylinositol glycan, class B (PIGB), mRNA
7183				1.1E-01	1.1E-01 AE002155.1	TN	Ureaplasma urealyticum section 56 of 59 of the complete genome
7183				1.1E-01	1.1E-01 AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337			1.01	1.1E-01	1.1E-01 BF382758.1	EST_HUMAN	601816624F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4050853.5
7456	l	34007			1.1E-01 AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, i166001-1485000 nt. position (6/7)
7708	L			1.1E-01	1.1E-01 BF684828.1	<b>EST_HUMAN</b>	602140976F1 NIH_MGC_46 Homo sepiens cDNA done IMAGE:4302019 51
7706	20771	L	7.61	1.1E-01	1.1E-01 BF684628.1	EST_HUMAN	B0Z140876F1 NIH_MGC_46 Homo septens cDNA clone IMAGE:4302019 51
7833	20888	34391	2.16		1.1E-01 P41087	SWISSPROT	TRAB PROTEIN
7872	20926		0.64		1.1E-01 Z14098.1	LN	B.subtilis gene encoding hypothetical polykatide synthase
7,87.	2002	34433	308		1.1E-01 AA788784.1	EST HUMAN	af31b06.s1 Soares_parathyrold_tumor_NbHPA Homo sepiens cDNA clone 1240403 3' similar to gb:J03483   CHROMOGRANIN A PRECURSOR (HUMAN);
8155	1				1.1E-01 U67492.1	N	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	24484				1.1E-01 AA483574.1	EST HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sepiens cDNA clone IMAGE:943362
8403	1				1.1E-01 AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo saplens cDNA clone IMAGE:943362
8449	L	L			1.1E-01 X91233.1	TN	H.sapiens IL15 gene
8489					1.1E-01 AW817918.1	<b>EST_HUMAN</b>	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens oDNA
8546		35165	2.31		1.1E-01 AL134349.1	EST_HUMAN	DKFZp547P194_r1 347 (symonym: hfbr1) Homo sapiens cDNA clone DKFZp547P194 5'
	<u>:</u>						Pediococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC
8018	22097	35637	5.67		1.1E-01 U02482.1	LN	and papD genes, complete cds

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wf48c01.x1 Soares\_NFL\_T\_GBC\_S1 Horno saplens cDNA clone IMAGE:2358316 3' similar to contains Alu we08d01x1 NCI\_CGAP\_KId11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 601436972F1 NIH MGC 72 Homo saplens cDNA clone IMAGE:3922048 67
CM3-HT0142-271099-026-31 HT0142 Homo saplens cDNA
MR2-GN0027-040900-005-308 GN0027 Homo saplens cDNA
Arabidopsis shallana DNA chrcmosome 4, contig fragment No. 43
y908-000-01 Socrese placenta Nb2HP Homo saplens cDNA clone IMAGE:147084 3\*
Ceratitis capitate yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
Dictyostellum discoldeum kinesin Unc104f/GF1a homolog (Unc104) mRNA, complete cds
HSC1RF022 normalized Infant brain cDNA Homo saplens cDNA clone c-1rf02 3\*
Carassius auretus ectivih beta A precureor mRNA, complete cds
y436f12r1 Soares placenta Nb2HP Homo saplens cDNA clone iMAGE:131759 5\* similar to contains Alu yd19h03.s1 Soares fetal liver spleen 1NRLS Homo sapiens cDNA clone IMAGE:1087253' similar to gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN); 60168065/RZ NIH\_MGC\_83 Homo sepieris cDNA clone IMAGE:3950604 3' 601806350F1 NIH\_MGC\_54 Homo sepieris cDNA clone IMAGE:4134085 5' DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II ULH-BI3-alc-4-07-0-UI.s1 NCI\_CGAP\_Sub5 Homo saplens cDNA clone IMAGE:2736420 3' 601906489F1 NIH\_MGC\_54 Homo saplens cDNA clone IMAGE:4134071 5' QV2-NT0048-160800-316-605 NT0048 Homo saplens cDNA zp83b12.r1 Stratagene muscle 937z09 Hoino sapiens oDNA clone IMAGE:627743 5 zp83b12.r1 Stratagene muscle 937z09 Hoino sapiens oDNA clone IMAGE:627743 5 Z.mobills tot and lig genes encoding tRNA guanine transglycosylase and DNA tigace forterestart nitH\_MGC\_21 Home saptens cDNA done IMAGE:3959686 5' SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) mobilis tot and lig genes encoding tRNA guanine transglycosylase and DNA ligase rabidopsis thaliana DNA chromosome 4, contig fragment No. 23 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 Top Hit Descriptor RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA Hamo sapiens C16orf3 large protein mRNA, complete cds repetitive element;contains TAR1 repetitive element; P.furiosus partial dph5 gene and argF gene . Single Exon Probes Expressed in Placenta MER7 repetitive element repetitive element EST HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN EST\_HUMAN SWISSPROT EST\_HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN EST HUMAN Top Hit Database Source Top Hit Acession 1.0E-01 BF239818.1 1.0E-01 BF365703.1 1.1E-01 BF239753.1 1.0E-01 O62855 1.1E-01 AL161511.2 1.1E-01 BE787023.1 1.0E-01 AW451365.1 1.1E-01 AA192153.1 1.1E-01 AA192153.1 1.1E-01 Y12727.1 1.1E-01 BE893260.1 1.1E-01 BE142305.1 1.1E-01 BF085149.1 1.1E-01 AL161543.2 BE902974.1 1.0E-01 AI985499.1 1.0E-01 AL161504.2 1.1E-01 AI807474.1 1.1E-01 AF050081.1 AF169032. ģ 1.1E-01 R80590.1 1.1E-01 U60529.1 1.1E-01 AF245277. 1.1E-01 R23708.1 1.1E-01 Z11910.1 T72675.1 R23708.1 1.1E-01 Z11910.1 1.1E-01 1.1E-01 1.1E-01 1.1E-01 (Top) Hit BLAST E Most Similar Value 2.76 0.89 0.89 0.77 1.29 1.38 1.33 3.78 3.18 5 1.78 1.88 0.5 2.25 2.26 0.71 3.11 <u>1</u> Expression Signal 27523 27650 28808 29976 30228 38212 38213 38245 38319 35**737** 35863 35864 35864 38007 31947 36001 37631 29288 ORF SEQ ÖΝΩ 24368 24642 24639 24956 25289 25910 25738 14577 15883 16973 SEQ ID 22320 22320 22411 23152 22441 16274 Ö 2558 3813 4064 1510 11586 433 10544 11300 11483 12649 1228 1301 9113 9243 9243 935 10114 10914 1044 Probe SEQ (D NO: 9696

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4627	17665	30651	1.44	1.0E-01	0E-01 AE002265.2		Chlamydophila pneumonlae AR39, section 91 of 94 of the complete genome
4877	L		92'0	1.0E-01	0E-01 AI792349.1	T HUMAN	an32c04.y5 Gasslar Wilms tumor Homo capiens cDNA clone IMAGE:1700358 5
4834	1	30955	2.17	1.0E-01	0E-01 U50450.1		Drosophila melanogaster tyrosine knase p45 isoform (fer) mRNA, complete cds
6039	1	31143	2.17	1.0E-01	_	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5261	1		0.61	1.0E-01	1.1		601286969F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3813592 5
5438	Ι.			1.0E-01	0E-01 W88490.1	EST_HUMAN	Zh62h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:4166953'
6834	L	[-	79'0	1.0E-01	0E-01 X54015.1	NT	X.campestris genes for sensor and regulator protein
6001	L.		1.08	-		NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6148	19325	32670	13.08	-	0E-01 AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
	1						zv41g10,s1 Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:768268 3' similar to contains
6465	19632			-	1	Т	L1.t3 L1 repeative element
6479	1984B		0.72	1.0E-01	0E-01 AA406039.1	EST_HUMAN	au67c12.c1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:/430b2 3
	L						yn34h06.r1 Soares placenta Nb2HP Homb capions cDNA done IMAGE:131675 5' stmilar to contains Alu
7164	1 20297		1.87	<del>-</del>	.0E-01 R23821.1	EST_HUMAN	repetitive element,
7914	L		2.39	-	.0E-01 Y12488.1	NT	M.muscalus whn gene
							ak32g01.s1 Soares_tests_NHT Homo saplens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-
8118	21200	34721		1	.0E-01 AA861091.1	EST_HUMAN	DEPENDENT PROTEIN KINASE, GAMMA-CATALTTIC SUBUNIT (HOWAN),
8141	21223	34741	2.17	1	.0E-01 AF260225.1	NT	Homo sapians TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8141		L		-	.0E-01 AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
	L						x09bo1x1 NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S
8689	3 21769		96.0	•	.0E-01 AW189797.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.t3 TAR1 repetitive element;
9387	7 22462	36028	1.12		.0E-01 AF102855.2	LN.	Rattus norvegicus synaptic SAPAP-Interacting protein Synamon mRNA, complete cos
9898	L		0.87	_	.0E-01 R44993.1	EST_HUMAN	yg33h04.s1 Soares infant brain 1NIB Horno sapiens cDNA clone IMAGE:34549 3
9707			1.9	1	.0E-01 M76729.1	NT	Human pro-alpha-1 (V) collagen mPNA, complete cds
9750	L		3.15	_	.0E-01 AE001501.1	IN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9764	L			-	.0E-01 W01955.1	EST_HUMAN	zc66c10.s1 Soares_fetal_heart_NbHH19lV Homo saplens cDNA clone IMAGE:327282 3
10026	1_	36661		٦	.0E-01 BF240154.1	EST_HUMAN	601905861F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 6
10139	L	L		-	.0E-01 AB046799.1	NAT	Homo saplens mRNA for KIAA1579 protein, partial cds
10139	L.	L		_	.0E-01 AB046799.1	F	Homo eapiens mRNA for KIAA1579 protein, partial cds
10347					.0E-01 AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
	L						yb239906.s1 Stratagene fetal spleen (#937.205) Homo sapiens cDNA done IMAGE:72562 3' similar to
10351				_	.0E-01 T51952.1	EST HUMAN	contains Alu repetitive element
10537	7 23572				.0E-01 BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Home saplens cDNA clone IMAGE:3838096 5
1080	1	١			.0E-01 AU159127.1	EST HUMAN	EST HUMAN AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
200							

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37891	2.17	1.0E-01	1.0E-01 BF242946.1	П	601877703F1 NIH_MGC_55 Homo saplens cDNA done IMAGE:4106089 5
11286	24352		2.17	1.0E-01	1.0E-01 BF242948.1	EST_HUMAN	601877703F1 NIH_MGC_55 Home septents cDNA clone IMAGE:4106089 5
11685	1		3.64	1.0E-01	1.0E-01 BE780543.1		601582558F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3938734 5
11814	24803		1.75	1.0E-01	1.0E-01 AP000400.1	Ä	Escherichia coli O167:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain:RIMD 0509952
12364			1.73	1.0E-01		EST_HUMAN	601065554F1 NIH_MGC_10 Homo capleins cDNA clone IMAGE:3451933 6'
12609	L.		1.73	1.0E-01	7662165 NT		Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12939			3.11	1.0E-01	1.0E-01 U52691.1		Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12973			1.8	1.0E-01	1.0E-01 BE537719.1	EST_HUMAN	801085554F1 NIH_MGC_10 Homo septens cDNA done IMAGE:3451833 5
13045			25.82	1.0E-01	1.0E-01 U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	L		6.58	1.0E-01	1.0E-01 AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	L		1.45	1.0E-01		NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
							Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-RII) mRNA,
2839	15953	29060	0.96			П	complete cds
2847	L	29070	0.94	9.9E-02	١	╗	601070219F1 NIH MGC_12 Homo sepiens cuna cione image::0400000 0
2847	l		0.94	9.9E-02		EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapleris cDNA clone IMAGE:3456365 5
3340	ı	29528	1.31	9.9E-02	9.9E-02 AF099810.1	본	Homo sepiens neurexin III-alpha gana, partial cds
7110	1		8.96		9.9E-02 D83710.1	LN	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cos
3	1		8		0 OF-02 AW403088 1	FST HUMAN	xz43c09.XI NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' simitar to contains Alu repetitive element.contains element MIR MIR repetitive element ;
SECO	1						xd43c09 x1 NCI CGAP Ov23 Homo capiens cDNA clone IMAGE:2596528 3' similar to contains Alu
8008	21181	34700	0.69		9.9E-02 AW103088.1	EST_HUMAN	repositive element contains element MIR MIR repositive element;
8457	┖	L			5111		Mus musculus phospholipid transfer protein (Pitp), mRNA
12132	L			L	9.9E-02 D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
169	L		2.18		9.8E-02 X56338.1	L	O.sativa RAmy3C gene for alphe-amylase
3214	L				9.8E-02 AF184274.1	NT	Daucus carota teucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allete, complete cds
4339	1_		9.83		9.8E-02 AF257329.1	LN	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4330		30484			9.8E-02 AF257329.1	F	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7851	20719	1	0.98		9.8E-02 X54133.1	LN	Human HPTP delta mRNA for protein tyrosine phosphatase delta
R R			1.18	l	9.8E-02 M61943.1	LN	Human laminin B1 chain gene, exon 28
11747	23833	37559	1.73		9.8E-02 BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_65 Hamo sapiens CDNA cione IMAGE:3854287 5
12332					8393751	5	Rattus nonegious microtubule associated protein tau (Mapt), mRNA
1381	14536	3 27611	1.92		9.7E-02 AB005808.1	된	Alce arborescens mRNA for NAUP-mailc enzyme, comprements

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ORF SEQ Expression (Top) Hit Acession ID NO: Signal BLASTE No. Source	1.01 9.7E-02 4503710 NT	28601 2.58 9.7E-02 BE168660.1 EST_HUMAN	4.05 9.7E-02 Q99786 SWISSPROT	31639 0.59 9.7E-02/AF099189.1 NT	31640 0.59 9.7E-02 AF099189.1 NT	32657 1.39 9.7E-02 AW954476.1 EST_HUMAN	34000 3.06 9.7E-02 Z99119.1 NT	34774 1.54 9.7E-02 N22798.1 EST_HUMAN	34775 1.54 9.7E-02 N22798.1 EST_HUMAN	36873 1.49 9.7E-02 A1953984.1 EST_HUMAN	1.72 9.7E-02 U58337.1 NT	28330 1.33 9.6E-02 A1080721.1 EST_HUMAN	28331 1.33 8.6E-02/AI080721.1 EST_HUMAN	30582 6.67 9.6E-02 Z32686.2 NT	31209 0.95 9.6E-02 AW966230.1 EST_HUMAN	2.76 9.6E-02 BE910039.1   EST_HUMAN	0.79 9.6E-02 6678763 NT	0.65 9.6E-02,AU137084.1 EST_HUMAN	36386 1.49 9.6E-02 AV687898.1 EST_HUMAN	1.34 9.6E-02 BE894895.1	36876 1.04 9.6E-02/AJ243211.1 NT	36877 1.04 9.6E-02 AJ243211.1 NT	36970 0.62 9.8E-02 BF677270.1 EST HUMAN	36998 1.56 9.6E-02 AB013985.1  NT	36999 1.56 9.6E-02 AB013985.1  NT	37113 3.43 9.6E-02[P08174 SWISSPROT	37694 6.27 9.6E-02 Z79702.1 NT	38704 2.8 9.6E-02 AA625755.1 EST_HUMAN	1.7 9.6E-02 H14599.1   EST_HUMAN   ym19h03.61 Soares infant brain 1NIB Horito septens cultar crone invasefocus 3
		28601		31639	31640	32857	34000	34774	34775	35873		28330	28331	30582	31209				36386						36939	37113	37694	38704	
Exen SEQ ID NO:	14769	L	L	1	ł		1	L	<u> </u>		L		15213	17604	18244	19408	7 21068	L	1 22808			5 23280	L		l_	_		9 25003	5 25638
Probe SEQ ID NO:	1617	2335	4091	5461	746	8138	7450	8171	8171	9050	11472	2073	2073	4464	5117	6231	89	8571	974	10076	1024	10245	1032	10354	10354	10465	10981	12019	13015

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					Þ		Only o Lych Copes Expressed in Traceing
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31949	14.1	9.6E-02	9.6E-02 AJ295624.1	NT	Galbus gallus ALPHA 10 nACHR gene for cipha 10 subunit of rocotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.16	9.5E-02	9.5E-02 AW892395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	9.5E-02 P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETJOLASE RELATED PROTEIN)
7455	20532	34006	4.64	9.5E-02		LN	Trimeresurus flavoviridis DNA for phospholipase A2 Inhibitor, complete cds
7741	20802		77.7	9.5E-02	38.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7876	١	32280	18.0	9.5E-02 P51854		SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8084	21146	34666	2.85	9.5E-02	9.5E-02 BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapieris cDNA clone IMAGE:3857243 6
8064	21146		2.85	9.5E-02	9.5E-02 BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapieris cDNA clone IMAGE:3857243 5
10918	24001	37634	60.4	9.5E-02		EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapieris cDNA clone IMAGE:3857243 5
10918	24001		4.00	9.6E-02	9.6E-02 BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo saplers cDNA clone IMAGE:3857243 5
12104	25084		1.82	9.5E-02	7657416[NT	ΙNΤ	Mus musculus odd Ozlen-m homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	9.5E-02 AF272732.1	LN	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	9.4E-02 BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3985			4.64	9.4E-02	9.4E-02 Z33059.1	NT	M.capricolum DNA for CONTIG MC073
6447	19614			9.4E-02	9.4E-02 AF097363.1	LN	Triticum sestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7769	20827	34318	89.0	9.4E-02	9.4E-02 L78833.1	LN	Human BRCA1, Rho7 and vati genes, complete cds, and tot35 gene, partial cds
8799	1		2.5		9.4E-02 Z46883.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS; rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
11174		34318			9.4E-02 L78833.1	ΤN	Human BRCA1, Rho7 and valt genes, complete cds, and tx135 gene, partial cds
12214	<u></u>		7.72	9.4E-02	9.4E-02 U31815.1	LN	Rattus norvegicus calcium channel alpha-†C subunit (ROB2) mRNA, partial cds
13198	25780	31936	4.84	•	9.4E-02 U27699.1	NT	Human pephBGT-1 betaine-GABA transporter mRNA, complete cds
3054	16230		2.37	20-3E-02		NT	Homo sapiens BA/1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	8.3E-02	6912525 NT	۲	Homo saplens nascpharyngeal epithellum specific protein 1 (NESG1), mKNA
3329	16502	29521	217	9.3E-02	9.3E-02 BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4288269 5
4268	١	30400	3.17	9.3E-02	9.3E-02 BE391943.1	EST_HUMAN	601285082F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3607653 5
4268	17413	l	3.17	9.35-02	9.3E-02 BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3607653 5
4857	1		1.82		9.3E-02 AV732224.1	EST_HUMAN	AV732224 HTF Homo saplens cDNA clone HTFAUA06 5
2779	18971		0.67		9.3E-02 AP001507.1	N	Bacillus halodurans genomic DNA, section 1/14
8442	21623	35052	0.56		9.3E-02 AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9324	22400		0.6		9.3E-02 AL113179.1	攴	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8911					9.3E-02 BE962631.2	EST_HUMAN	601655988R1 NIH MGC 66 Homo sapiens CUNA cione IMAGE:3833981 3
10394	23429				9.3E-02 Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	ll	37036	3.6		9.3E-02 Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

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Top Hit Descriptor	A.thaliana RH1, TC1, G14587-5, G14587-3, and PRL1 genes	Rana catesbelana dihydropyridine receptor <sub>i</sub> mRNA, complete cds	Bactertophage Mu, complete genome	zp38h12.s1 Strategene muscle 837209 Homo sepiens cDNA done IMAGE:811783 3' sImilar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA :	Rattus norvegious cell cycle protein p55CDC gene, complete cds	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11	Bombyx mori fibroin heavy chain Fib-H (fib;H) gene, complete cds	FOLATE RECEPTOR ALPHA PRECURȘOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED	ANTIGEN MOV18) (KB CELLS FBP)	hv39g10.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMACE:3176842 3' similar to contains Alu	repetitive element;	11.5-UM0067-240300-050-h08 UM0087 Homo sepiens cDNA	HIV.1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds	Dictyostelium discoldeum spore coat structural protein SP65 (cotE) gene, complete cds	corticosterold-binding globulin [Saimtri scriureus≂squirrel monkeys, liver, mRNA, 1474 ntj	corticosteroid-binding globulin [Salmiri schireus≕squirrel monkeys, liver, mRNA, 1474 ntj	Plasmodium falciparum P-type ATPase 3 gene	za68a12.r1 Soares_fetal_lung_NbHL19Wi Homo sapiens cDNA clone IMAGE:297694 5' similar to Dio.es9414 es9474 email G nodein - human	Therefore A INC. COAP Cotte Home septems cDNA clone IMAGE:3320645 3' similar to contains Alu	repetitive element;	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rorf1), rOrf2 (rorf2), EscR (escR), EscS (escS),	EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN	(escN), SepQ (sepQ), Tir (tir), OrfU (crfU), >	602129030F2 NIH_MGC_58 Homo saplens cDNA clone IMAGE:4285951 5'	602129030F2 NIH_MGC_66 Homo capie ns cDNA clone IMAGE:4285951 5	PMo-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3:	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mKNA
Top Hit Database Source	LN	TN	NT	EST_HUMAN	FZ	LN	NT		SWISSPROT		EST_HUMAN	EST HUMAN	NT	NT	⊥N	ΤN	TN	IN.	1444	EST TOWNIN	EST_HUMAN			5	EST_HUMAN	EST_HUMAN	EST HUMAN	Ā	EST_HUMAN	EST_HUMAN	NT
Top Hit Acessian No.		9.1E-02 AF037625.1	9833494 NT	9.1E-02 AA179901.1	9.1E-02 AF052695.1	9.1E-02 AJ291390.1	9.1E-02 AF226688.1		P15328		9.0E-02 BE220482.1	9.0E-02 AW801364.1	9.0E-02 AF138522.1	9.0E-02 AF138522.1	9.0E-02 AF279135.1	9.0E-02 S68757.1	9.0E-02 S68757.1	9.0E-02 X65740.2		9.0E-02 W 35037.1	9.0E-02 BF062651.1		•	8.0E-02 AF022236.1	8.9E-02 BF701593.1	8.9E-02 BF701593.1	8.9E-02 BE153572.1	8.9E-02 AF286055.1	8.9E-02 AW452122.1	AW452	11433478 NT
Most Similar (Top) Hit BLAST E Value	9.1E-02 Y11187.1	9.1E-02/	9.1E-02	9.1E-02	9.1E-02/	9.1E-02	9.1E-02		9.0E-02 P15328		9.0E-02	9.0E-02	9.0E-02	9.0E-02	9.0E-02	9.0E-02	9.0E-02	9.0E-02		8.0E-02	9.0E-02			9.0E-02	8.9E-02	8.9E-02	8.9E-02	8.9E-02	8.9E-02		8.9E-02
Expression Signal	8.0	2.13	7.04	1.42	1.32	13.49	127		5.89		7.33	1.18	4.99	4.99	1.11	9.0	9.0	2.03		7,	0.83			1.82							3.34
ORF SEQ ID NO:	37341		l_						26930		27899			29089			30542			32634				_	27706	L	L		32474		
Exan SEQ ID NO:	23736	1_	_	L _	١.		L		13944	1	14816	15582		15978	L	L	١.	I_	1	19298	20012	_		25546	1	L.	L	ı	<u>_</u>		19172
Probe SEQ ID NO:	10703	11441	12151	12393	12473	12996	13230		763		1664	2454	2864	2864	3417	4414	4414	4790		6118	6880			12819	1469	1469	2460	4316	5972	5972	5987

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Single Exola Flores Expressed in a good a	Top Hit Descriptor	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE ]	H. sapiens flow-sorted chromosome 6 Hindill fragment, SCGPAZOF8	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (NOS)	602129111F2 NIH_MGC_68 Homo sapiens cDNA clore IMAGE:4285827 5	602129111F2 NIH MGC 56 Homo sapiens cuiva cidra inwace: 4203027 3	EST180187 Liver, hepatocellular cardinoma Homo sepiens culva o end	qu55c05.x1 NC_CGAP_Lym6 Homo septens oDNA clone IMAGE:1908080 3 Smite to contents which the MER10 repetitive element;	quescolar NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1900000 3 Similar to contains intervious	MEKTO repeatuve dement;	ES   44404 Fetal Brain   nomo saprats coris	MYOSIN-2 ISOFORM	602129682F1 NIH MGC 56 Home Saprents Color Gold Invacing Color	Mus musculus nippocampus abuntani gaja uanaanya rivina.	Human 4-hydroxypnenyipyruvara-dloxygenitise gene, contradio cue	Ceratitis capitata mariner transposon transposase gene, comprise	Hellcobacter pylori, strain J99 section 76 or 132 of the complete genome	PROBABLE DNA LIGASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXYRIBONOCLEOTIDE STINTINASE (POLYDEOXY	EST11696 Uterus Homo sapiens CDNA 3 jeno	TRANSCRIPTION INITIALION PACTOR THIS ISSNEY SUBJECT. (172. 17. 17. 17. 17. 17. 17. 17. 17. 17. 17	Homo saplens paired box gene 6 (antildia, keratitis) (PAX6), Isolom b, mixina	Sheep mRNA for angiotensinogen, complete cds	zn89a05.s1 Stratagene colon (#83/2/204) Homo saplens conversional and an arrangement of the colon saplens colon (#83/2/204)	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3339046 3	601191770F1 NIH MGC_7 Homo saplens CDINA CIONE IMAGE 33330046 3	DKFZp434D1313_r1 434 (synonym: htes3) Home capiens cDNA cione DNr 2p434D1313 3	S. cerewistae chromosome XIV reading frame ORF YNL285w	Homo septiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN)	garies, compliate cos, and present
EXOIL FIODES	Top Hit Database Source	SWISSPROT	NT	SWISSPROT	EST_HUMAN		EST_HUMAN	EST_HUMAN		EST HUMAN	EST HUMAN	SWISSPROT	EST HUMAN	Ę	Ę	뒫	N	SWISSPROT	EST HUMAN	SWISSPROT	TN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ᄓ		- N
Single	Top Hit Acession No.			29475	8.9E-02 BF701665.1	8.9E-02 BF701665.1	8.9E-02 AA309319.1	8.9E-02 AI285627.1		8.9E-02 AI285627.1	8.9E-02 AA339356.1	19524	8.9E-02 BF696918.1	6680220 NT	129895.1	J40483.1	8.9E-02 AE001514.1	227474	8.8E-02 AA299128.1	000268	4580423 NT	D17520.1	8.8E-02 AA151872.1	8.8E-02 BE264455.1	8.8E-02 BE264455.1	8.8E-02 AL040129.1	8.8E-02 271561.1		8.7E-02 U82695.2
	Most Similar (Top) Hit BLAST E Value	8.9E-02 P47259	8.9E-02 Z79021.1	8.9E-02 P29475	8.9E-02	8.9E-02	8.9E-02	8.9E-02		8.9E-02	8.9E-02	8.9E-02 P19524	8.9E-02	8.9E-02	8.9E-02 U29895.1	8.9E-02 U40483.1	8.9E-02	8.8E-02 Q27474	8.8E-02	8.8E-02 000268	8.8E-02	8.8E-02 D17520.1	8.8E-02	8.8E-02	8.8E-02				
	Expression Signal	1.6	17	1.10	0.76	0.76	585	980		0.84	0.63	1.8	3.82	2.75	7	1.18	1.54	. 0.96	1.07	6.23	0.75	0.71	2.07	2.79					4.17
	ORF SEQ ID NO:	33886		34839				l		36440	36565	L						27832	١				35807		l				3 29953
	SEQ ID	20423	20702	1	L	21405	21876	1	1	22859	22973	L	L.	L	L	L	1_	L	Ι.,	17207	1	1	1	L	L	24507		l	16946
Ì	Probe SEQ ID NO:	7.43	212	0768	8323	833	8797	0840		9819	9934	12213	12368	12537	12584	12827	12880	1404	4012	24.4	4418	7718	04188	11380	11380	11841	17243		3785

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Single Exon Probes Expressed in Placenta	ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLASTE Na Source		36568 1.24 8.6E-02 AF111170.3 INT	1.4 8.6E-02 AW662153.1   EST_HUMAN	23391 37001 1.07 8.6E-02 AF026504.1 NT Rettus norvegicus SPA-1 like protein p1294 mRNA, complete cds	24257 37892 1.82 8.6E-02 AF206551.1 NT Lacerta media cytochrome c oxidase suburiit 1 gene, partial cds; mitochondrial gane for mitochondrial product	1.82 8.6E-02 AF206551.1 NT	38259 3.02 8.6E-02 BF305608.1 EST_HUMAN	38260 3.02 8.6E-02 BF305606.1 EST_HUMAN	37534 7.67 8.6E-02 AE001073.1  NT	N IN	NAMI IL TOTAL A RECORDING OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF SOCIAL SECTION OF S		8.5E-02 AA985491.1 EST HUMAN	SWISSPROT	AF233885.1 NT	34779 NT	36680 3.27 8.5E-02 BE833054.1  EST_HUMAN	36681 3.27 8.5E-02 BE833054.1 EST_HUMAN	37212 0.64 8.5E-02 X76731.1 NT	37340 0.82 8.5E-02 11418108NT	8.03 8.5E-02 AF155510.1 NT	38173 3.82 8.5E-02 AB001562.1 NT	25888 2.76 8.5E-02 AJ005586.1 INT	25700 2.44 8.5E-02 AA362834.1 EST_HUMAN	16070 28961 4.05 8.4E-02 W69330.1 EST_HUMAN	18627 31603 9.84 8.4E-02 BE267153.1 EST_HUMAN	19981 33388 1.46 8.4E-02 AK024458.1 NT	21300 34821 6.95 8.4E-02 BE095074.1   EST_HUMAN	22122 35664 1.15 8.4E-02[AF218890.1 NT Homo septems awardin precursor (A.I.N.) jgene, axan z
}	SEQ ID NO:		1	1		l		Ļ	<u> </u>	L	 -1	П	1					L	乚	<u> </u>				_	_	ł		l	ı	
l	Probe SEQ ID NO:	8324	8538	9975	10356	11188	11188	11627	11527	11724	11875	2/2/2	7870	5786	5828	6135	8805	10041	10041	10572	10702	11424	11446	12873	13070	2732	5427	6828	8218	8043

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Γ		~			T	T	T	T	T	T		5	T					٦	$\sqcap$		T		T	Ţ	T	T		T		T			_
	Top Hit Descriptor	as88g10.x1 Barstead colon HPLRB7 Homo sepiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 O88312 GOB.4.;	AV730682 HTF Homo sepiens cDNA clone HTFBMG04 5'	W83h12.r1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:145895 5'	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR	th82g06.x1 Soares_NhHMPu_S1 Homo capiens cONA clone IMAGE::2125210 3	th82g08.x1 Soares_NhHMPu_S1 Homo septens cDNA clone tMAGE:2126210 3	C.thummi A2b region open reading frame, complete cds	wc79f11.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2461581 3'	Homo sapiens protocadherin 43 gene, excir 1	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Orp2) mRNA, complete cds	og88908.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1 reportitive element*	Topour Contour, 100 Kide Home seriens CONA clone IMAGE-1692779 3'	Indept of Himen Pennearin telets Home seniors cDNA 3' similar to TR-015332 015332 GAMMA	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE:	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91	Dictyostellum discoldeum DocA (docA) mRNA, complete cds	601644770F1 NIH_MGC_56 Homo saplents cDNA clone IMAGE:3928983 5'	Gallus gallus mRNA for for OBCAM protein gamma isoform	Canis familiaris glutamate transporter (EAA/T4) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C006	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10	Homo sapiens chromosome 21 segment HS21C006	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR	Mus musculus zinc transporter (ZnT-3) gene, complete cds	601439676F1 NIH_MGC_72 Homo sapieris cDNA clone IMAGE:3924523 5	Bos taurus connective tissue growth feater, precursor (CTGF) gans, complete cds	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PWCA3) gene, 5' flanking region	RC2-PT0004-031299-011-d05 PT0004 Homo saplens cDNA	Beet necrotic vallow vain virus RNA-2
1	Top Hit Database Source	EST_HUMAN	EST_HUMAN	<b>EST_HUMAN</b>	SWISSPROT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	TN	TN	MAMILL FOR	TO LONGIN	NEWOL I CO	EST HUMAN	N	NT	EST_HUMAN	TN	NT	TN	NT	NT	SWISSPROT	SWISSPROT	SWISSPROT	NT	EST_HUMAN	NT	EST_HUMAN	NT	EST_HUMAN	INT
.0	Top Hit Acession No.	8.4E-02 AI735184.1	8.4E-02 AV730682.1	8.4E-02 R79408.1	P76334	8.3E-02 AI438797.1	8.3E-02 AI436797.1	8.3E-02 M54964.1	8.3E-02 AI942338.1	8.3E-02 AF052683.1	8.3E-02 AF195787.1	A A COGGO C 4	6.3E-02 AA003263.1	8.3E-02 AA96/6/3.1.	8.3E-02 AW 583503.1	8.3E-02 AL161595.2	8.3E-02 AF020409.1	8.3E-02 BE958458.1	8.2E-02 Y08170.2	8.2E-02 AF167077.2	8.2E-02 AL163206.2	8.2E-02 AL161498.2	8.2E-02 AL163208.2	P48960	P48960	P48960	8.2E-02 U76009.1	8.2E-02 BE897030.1	8.2E-02 AF309555.1	8.2E-02 AV743341.1	8.2E-02 U29397.1	8.2E-02 AW875126.1	8 2E 02 Y04197 1
	Most Similar (Top) Hit BLAST E Value	8.4E-02	8.4E-02	8.4E-02	8.3E-02 P75334	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.35-02	8.3E-02	100	0.35-02	8.35-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02 P48960	8.2E-02 P48960	8.2E-02 P48960	8.2E-02	8.2E-02	8.2E-02	8.2E-02	8.2E-02		l
	Expression Signal	1.84	0.48	1.67	77.7	0.75	0.75	0.68	0.74	2.87	3.08	***	97.	1.31	1.09	2.02	0.72	1.81	9.13	2.03	1.97	1.35	66.0	85.9	89.9	6.58	3.43	1.46	3.16	85.0.	0.69	. 3.24	
	ORF SEQ ID NO:	37211		32114	29853		29874		32917		34771				36377					6922			30268	30523		30525		31629	33741			35593	L
	Exon SEQ ID NO:	23606	23665	26264	16845	l		17558	19558	19662	21251	l		215/6	22803	L	L	L	L	L	16317	17063		ŀ	ı	17542	l	١_		20882	21984		١
	Probe SEQ ID NO:	10571	10831	12351	3682	3709	3709	4417	6389	6496	8169	į	8202	8 8	82.28	9751	10549	12448	1410	1525	3141	3904	4114	4389	4399	4399	5182	5450	7165	7910	8905	8971	9700

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Herpesvirus saimiri transformation-associeted protein (STP), and dihydrofolate reductase (DHFR) gene, s Pssudomonas putida malonate decarboxytise gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcG, mdcC, mdcC, mdcH, mdcL and mdcM genes), complete cds Mus musculus epidermal growth factor reciptor (Egfr) gene, oxons 5 through 28, and complete ods, Home septens hypothetical protein FLJ10090 (FLJ10090), mRNA
Home septens expressibilitar glycoprotein FLJ10090 (FLJ10090), mRNA
Home septens expressibilitar glycoprotein lacritin precursor, gene, complete cds
xv45b11.xr Sceres, NFL\_T\_GBC\_S1 Homio septens cDNA done IMAGE:2735040 3
UI-H-813-akc-g-01-0-UI.s1 NCI\_CGAP\_Sib5 Home septens cDNA done IMAGE:2735040 3 Synechocystis sp. PCC6803 complete genome, 1727, 2137259-2287259
Synechocystis sp. PCC6803 complete genome, 1727, 2137259-2287259
601855348F1 NIH\_MGC\_57 Homo septients cDNA clone IMAGE:4078619 5'
Dictyosellum discoideum cyclio nucleotide phosphodiesterase gene, complete cds Homo capiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA Human gene for ditydrolipoamide succinyltransferase, complete cds (exon 1-16) Human gene for ditydrolipoamide succinyltransferase, complete cds (exon 1-15) PM3-BT0347-17020q-001-b08 BT0347 Homo sapiens cDNA wd86708.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clane IMAGE:2338503 3 601115055F1 NIH\_MGC\_16 Homo saplaris cDNA clons IMACE:3355598 6' Chlamydophila pneumonlae AR39, section |73 of 94 of the complete genome EST386723 MAGE resequences, MAGC Homo saplens cDNA Top Hit Descriptor EST378191 MAGE resequences, MAGI Homo sapiens cDNA QV4-CT0361-021299-049-b01 CT0361 Homo saplens cDNA Xyella fastidiosa, section 152 of 229 of the complete genome A1484F Heart Homo septiens cDNA clone A1484 Homo sapiens chromosome 21 segment HS21CO79 Thermoplasma acidophilum complete genome; segment 5/6 Molluscum contagiosum virus subtype 1, complete genome Homo sapiens ABCA1 (ABCA1) gene, complete cds Homo sapiens chromosome 21 segment HS21C002 complete cds, and small nuclear RNAs (uRNAs) M.musculus gene for geletinase B Single Exon Probes Expressed in Placenta afternatively spliced EST HUMAN EST HUMAN EST\_HUMAN HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN HUMAN EST HUMAN HUMAN HUMAN Top Hit Database Source 토토 Ħ 눋 4503034 NT 11426974 NT Top Hit Acesslon 8.1E-02 AW 269778.1 8.1E-02 AW 450487.1 8.1E-02 AW 450487.1 8.1E-02 AL 163202.2 8.0E-02 AW 964653.1 8.2E-02 BE254318.1 8.2E-02 AE002246.2 8.2E-02 AW862195.1 8.0E-02 D26535.1 8.0E-02 BE067219.1 8.0E-02 D90915.1 8.0E-02 D80915.1 8.0E-02 BF246744.1 8.0E-02 AW966118.1 8.1E-02 T11532.1 8.1E-02 AL163279.2 8.0E-02 M28071.1 8.0E-02 AF276948.1 8.1E-02 1145 8.1E-02 AY005150.1 BE254318.1 8.2E-02 AFZ76368.1 8.1E-02 AB017138.1 8.1E-02 AE004006.1 夕 8.0E-02 U60315.1 8.0E-02 D26535.1 8.1E-02/ 8.1E-02/ 8.1E-02/ (Top) Hit BLAST E Velue Aost Similar 7.99 0.65 11.83 0.83 0.83 1.55 3.59 1.03 0.83 0.99 0.56 0.56 0.70 2.27 3.83 1.43 2.58 0.47 6.87 Expression Signal 31142 27338 ORF SEQ ID NO: 27758 35151 35152 26246 27191 36599 32024 32371 33043 37511 19198 21616 23891 24780 16141 23719 23004 25318 25458 26876 SEQ ID 14677 19674 ÿ 1733 5038 6012 8535 10858 110858 11790 1952 2447 2965 9965 12454 6873 6509 8535 10116 959 4035 Probe SEQ ID 12688 12809 10685 88 1524 ë

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	Top Hit Descriptor	Hamo sapiens ABCA1 (ABCA1) gene, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	H.sapiens AGT gene, intron 4	H. saplens AGT gene, intron 4	Homo sapiens chromosome 21 segment HS21C009	Homo saplens SCG10 like-protein, helicase-like protein NHL, M88, and AUF-moosylation ractor related protein 1 (ARFRP1) genes, complete ods	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mixNA	Drosophila orena hunchback region	Homo sapiens cAMP responsive element trinding proteintike 2 ( Chable 1 ) III was	600943191F1 NIH_MGC_15 Homo seplens cUNA cigne IMAGE.2809310 3	аг98с08.x1 Barstead colon HPLRB7 Home sepiens cDNA clone IMAGE:21 /3646 3 smiler to go.zzos7e 605 RIBOSOMAL PROTEIN L36 (HUMAN);	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA	Arabidopsis thaliana RXW 24L mRNA, partial cds	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA	Saccharomyces cerevisiae suppressor of MIL2 Smi4p (SM14) gene, complete cos	ou63505.s1 NCI_CGAP_Br2 Homo sepieris cDNA clone IMAGE:1632465 3' similar to WP:U3/AZ.z CE08611 ;	ou63505.91 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE::1632465 3 Similer to W F.C-57 Az.z. CE08611;	wg66h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Home sapiens cDNA clane IMAGE:2370097 3'	oo59d02.y5 NC!_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1570467 6' similar to contains L1.t3 L1	repetitive element;	oo59d02,y5 NCI_CGAP_Lu5 Homo sepiens dDNA clone IMAGE:15/046/ 5 similiar to contains L i.i.5 L i repositive element :	DAYS ENDARS 440700 DDS-609 FN0058 Homo saplens cDNA	TWO THE WILL AND A SELECTION CONTINUE AT INDIVIDUAL CONTINUE OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PROPERTY SELECTION OF THE PR	0084505071 NIN MGC 10 Thaile espains color close in the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the c	Homo sepiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and bighoan (BGN) genes, complete cds; and plasma membrane calcium ATP ase Isoform 3 (PMCA3) gene, partial cds	
3.6.	Top Hit Database	NT	NT		IN⊤		Į.				EST HUMAN	EST_HUMAN			П	T_HUMAN	, LN	EST_HUMAN	EST HUMAN	Т	Г	EST_HUMAN	NAME TO T	T	T	EST_HUMAN	<u> </u>	
2.6	Top Hit Acession No.	8.0E-02 AF275948.1	8.0E-02 AL114993.1	3.0E-02 X74208.1	3.0E-02 X74208.1	3.0E-02 AL163209.2		4507608 NT	8.0E-02 AJ005376.1 NT	4503034	7.9E-02 BE250008.1	7.9E-02 AI582029.1	5681044 NT	5681044 NT	7.9E-02 AB008019.1	7.9E-02 BF368016.1	7.9E-02 U27832.1	7.9E-02 Al081644.1	7 OF-02 AIDR1644 1	7.9E-02 A 761639.1		7.8E-02 AI793275.1	, 22000	7.8E-02 AI/932/0.1	7.8E-02 BE836331.1	7.8E-02 BE250048.1	7 RE-02   182695 2	002000.2
	Most Similar (Top) Hit BLAST E Value	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7 OF-02	7.9E-02		7.8E-02		7.8E-02	7.8E-02	7.8E-02	7 85-02	1.00.1
	Expression Signal	1.61	2.41	1.38	1.38	0.49	2.64	1.00	3.54	1.85	3.37	12.63	4.47	4.47	1.16	1.14	3.1	5.6	n a	127		1.49				2.97		-
	ORF SEQ ID NO:	32513	1		ŀ		37747				28504	L					34824					27457	-		31035			33204
	SEQ ID	19196	ı	1		1	ı			l_		1	1_	1_	١.	1		1		25884		14386	1	ı	18045	17003		20087
	Probe SEQ ID NO:	7330	8319	8580	9589	10361	11032	12127	12486	13134	2243	5,5	3953	3953	4932	6836	8221	10234	į	13008	3	1237		1237	4915	5198		7223

Page 132 of 550 Table 4 Single Exon Probes Expressed in Placenta

Top Hit Descriptor	Homo saplens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and bigiycan (BGN) genes, complete ods; and plasma membrarie calcium ATPase teoform 3 (PMCA3) gene, partial cds	601440439F1 NIH_MGC_72 Homo saplens cDNA done IMAGE:3823448 3	S.cerevisiae CAT8 gene	Homo saplens FYVE domain-containing dual specificity protein phosphatase FYVE-USF1b mrdNA, complete cds	Hamo sapiens FVVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cots.	nc68b06.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814	Human interleukin-11 receptor alpha chaln gene, complete ods	Homo saplens envoplakin (EVPL) gene, exans 15 through 18	Homo sapians WRN (WRN) gene, complete cds	Homo sapiens partial AF-4 gane, exons 2 to 7 and Alu repeat elements	zu63d11.r1 Soares ovary turnor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' stimitar to TR:G1173g05 G1173g05 SPLICEOSOME ASSOCIATED PROTEIN: ;	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C	tagobog.x1 NCI_CGAP_HSC2 Home sapiens cDNA clone IMAGE:2050359 3' similar to gb:226876 60S	RIBUSOUNAL PROTEIN LOG (nominal),	B80b08.X1 NCL CGAP TASCZ HOMB SEPIERS CLINA CIGITS IMAGE. 2000035 5 SITTING TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPTEMBER TO SEPT	Homo saplens KIAA0628 gene product (KIAA0628), mKNA	601316426F1 NIH MGC 8 Homo sepiens cDNA clone INIAGE:3634905 3	EST112214 Cerebellum II Homo sepiens cDNA 5 end similar to similar to protoceurarin 43	Homo sapiens ASCL3 gene, CEGP1 gene, C11ar114 gene, C11ar115 gene, C11ar110 generaria C11o117	gene 	MIZOUZAL OSSOIG VIIII MITTO TOTAL OPPOSITOR VIII MANCE SERBATOR R	601236402F1 NIH MGC 44 Homo sapiens cunk cione introcatorio	Homo saplens SCL gene locus	Campylobacter jejuni NCTC11168 complete genome, segment orb	RC1-H10545-020800-017-dub H10545 H0mb sapiens culva	601654915R1 NIH MGC 5/ Homo sapiens cunk cione image: 3038010 3	L. esculentum mKNA for triose phospinate transfocator
Top Hit Datzbase Source		EST_HUMAN	NT	LN	L <sub>2</sub>	EST_HUMAN	NT	Z	IN	Ν	NT	EST HUMAN	SWISSPROT		EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST HUMAN		LN	ES HOMAN	EST_HUMAN	N		EST HUMAN	EST HUMAN	N.
Top Hit Acession No.	8E-02 U82696.2	.8E-02 BE897947.1	.8E-02 X78344.1	8E-02 AF233437.1	BE-02 AF233437 1	.8E-02 AA469354.1	.8E-02 Z99124.1	.8E-02 U3Z3Z3.1	.8E-02 U72847.1	.7E-02 AF181897.1	.7E-02 AJ238093.1	7F-02 AA402949.1	7E-02 P38080		.7E-02 Ai318662.1	.7E-02 AI318662.1	11422757 NT	.8E-02 BE514432.1	.6E-02 AA296447.1		.6E-02 AJ400877.1	.6E-02 AI061275.1	.6E-02 BE378328.1	.6E-02 AJ131016.1	.6E-02 AL139078.2	.6E-02 BE708002.1	7.6E-02 BE959638.2	7.6E-02 X92658.1
Most Similar (Top) Hit BLAST E Value	7.8E-02	7.85-02	7.8E-02	7.8E-02	7 RE-02	7.8E-02	7.8E-02	7.8E-02	7.8E-02	7.7E-02	7.7E-02	7.7F-02	7.7E-02		7.7E-02	7	7.7E-02	7.6E-02	7			7	1		'			
Expression Signal		0.93	0.69	80	C	0.0	0,58	2.19	1.36	122	2.01				0.84	0.84	3.98	3.1				0.69	1.14	1.11	0.99	0.5	1.04	76.0
ORF SEQ ID NO:	33505		35702	1	_							34800		]	36981	36982		Ĺ	29873		28825		L			37064	-	37469
Exan SEQ ID NO:	20087	ı	22160	L	1	22703	1	1		18038	1_	l	23078		23371	23371	L	L	1		- 1		19853	1	1	I _	L	1
Probe SEQ ID NO:	5227	8985	9081	0253	336	9230	10008	10001	12910	1431	3677	5008	4000		10336	10338	11262	3474	3484		3648	6222	6486	9570	10101	10424	10557	10815

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					מונה	E AUIT L'IOUS	Single Extri Flobes Expressed III Flowering
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10815	23848	37470	76.0	7.6E-02	7.6E-02 X92658.1	П	Lesculentum mRNA for triose phosphate translocator
11974			1.93	7.6E-02	6E-02 AW896645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Hormo sapiens CLNA
807	13987	27039	1.66	7.5E-02	5902093 NT	NT	Homo saplens solute carrier family 6 (neurotransmitter transporter, glycine), membor 9 (SLC6A9), mRNA
807		27040	1.66	7.5E-02	TN 8802083	LN	Homo saplens colute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLOGA9), mRNA
1971	L		66.0	7.5E-02	5E-02 AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630				7.5E-02	П	NT	Homo sapiens IL-18 gene for interleukin-18, Intron 1 and exon 2
5974			1.45	7.5E-02	.5E-02 AI848714.1	EST_HUMAN	wq24h09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:247225/3
8533			. 84	7.6E-02	7.6E-02 AI864367.1	EST_HUMAN	wi52b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8705	1	35318		7.5E-02		EST HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5
10238	1			7.5E-02	5E-02 BF221730.1	EST_HUMAN	7c91c05.x1 NCI_CGAP_Prz8 Homo capieno cDNA clane IMAGE:3578504 3' similar to contains element MER27 repetitive element ;
10711	L	37350		7.5E-02	5E-02 BF206809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapieris cDNA clone IMAGE:4100449 5
10816	L		0.82	7.5E-02	5E-02 X79460.1	TN	C. filmi DSM 20113 16S rDNA
480	L	L	1.41	7.4E-02	4E-02 AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0064 Hcmo caplens cDNA
1489	١_	L	1.21	7.4E-02	4E-02 AF030027.1	NT	Equine herpeswirus 4 strain NS80567, complete genome
2648	15771		96'0	7	6755069 NT	F	Mus musculus paired-like homeodomain transcription Tactor 1 (PIXT), mrvvA
3683	16846	29854	1.21	7.4E-02	4E-02 A1807885.1	EST_HUMAN	W443h01.x1 Sogres_NFL_T_GBC_S1 Hanio sapiens curve cione invalue: 2336363 3
4826	17959	30948		7.	L.78810.1	N	Homo saplens ADP/ATP carrier protein (AN I-2) gene, complete cas
4914	18044	31034	2.65	7.4E-02		Ę	Rattus norvegicus Activin receptor like Idnase 1 (Acvir), mixivA
5058	l			7.	6678492	۲	Mus musculus ubiquintin c-terminal hydroliase related polypeptide (Uchrip), mknyk
6824	19784		1.69	7	١	EST HUMAN	yg14g06.r1 Soares intent brain 1NIB Homo sapiens curva cione liwase. 32338 3
6717	19875	33268	0.68	7		닐	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cus
7636	20705	34184	0.64	7	.4E-02 AA605132.1	EST_HUMAN	no71d02.s1 NCI_CGAP_AA1 Homo sapiens cunva ciche iwace: 11 12208 3
8085	L.	34683	1.11	7.4E-02	.4E-02 BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo septens cDNA clone IMAGE:3885264 5
6698	1			7.	4E-02 U56089.1	NT	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cas
7980	22442	36002	1.08	2	4E-02 AW629605.1	EST HUMAN	hi67411.y1 NCI_CGAP_GU1 Homo septens cDNA clone tMAGE/ZB6/861 5 striller to SW: SCAZ_HOWAIN 015127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;
	1				4E_02 AW629605 1	EST HUMAN	hind7d11.71 NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE;2967881 5' similer to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;
6836	1	l			.4E-02 AI672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgreafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2846819 3*
0530	24082	l			4E-02 AI672939.1	EST HUMAN	we74d02.x1 Soares_Dieckgræefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3
200	J	Ì		١			

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Siligie EAULTIONES Expressed III riavelika	Top Hit Descriptor	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds	UI-H-BW1-amg-g-06-0-UI.s1 NCI_CGAP_Sub7 Hamo sapiens cDNA clone IMAGE:3069898 3	z/64e01 r1 Scares retina N2b4HR Homo sepiens cDNA clone IMAGE:381720 5	ao11d07,s1 Barstead acrta HPLRB3 Homo/srpiens cDNA dono IMAGE:1726285 3' strnilar to gb:M86492 GLIA MATURATION FACTOR BETA (HUI/AN);	Homo sapiens histone deacety/ase 5 (NY-ÇO-9), mRNA	CM4-HT0243-081199-037-411 HT0243 Homo saplens cDNA	601453813F1 NIH_MGC_66 Homo saplent cDNA clone IMAGE:3857738 5'	Aspergillus nidulens prnD, prnX, prnA genes	601658738R1 NIH_MGC_69 Homo caplens cDNA clone IMAGE:3886209 31	601658738R1 NIH_MGC_69 Homo saplens cDNA clane IMAGE:3886209 3'	Thermotoga maritima section 101 of 136 of the complete genome	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C102	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds	#224902.st Soares_fetal_liver_spheen_1NFILS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to	STACKED COSTINICADE CODONIL 4 (LOWCAN),	PROLINE-RICH PROTEIN MP-3	PROLINE-RICH PROTEIN MP-3	601896047F1 NIH_MGC_19 Homo saptenti cDNA clone IMAGE:4125515 5'	Homo saplens KIAA0424 protein (KIAA0424), mRNA	Mus musculus cdh5 gene, excn 1, partlai	Homo capiens mRNA for KIAA0518 protein, partial cds	z/24a02.at Soares_feta∐iver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to do:L02428 26S PROTEASE SUBUNIT 4 (HUMAN);	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete	делоте	Methanobactertum thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete	genome	Homo sapiens chromosome 21 segment H\$21C101	Homo saplens chromosome 21 segment HS21C101	Human immunodeficiency virus type 1 isola/a 26 reverse transcriptase (pol) gene, internal fragment, partial ods	THE DWO of a DEDUCTION OF NOT COMP. Suits Home seniors of DNA clone IMAGE: 2732049 3'
EXUIT FTUDGS	Top Hit Database Source	H TN		EST_HUMAN	EST HUMAN G		EST_HUMAN C	EST_HUMAN 8	NT N	EST_HUMAN   6	T_HUMAN		EST_HUMAN C		NT IN		T			EST_HUMAN 6		N. IN	H LN	EST HUMAN	T	NT IN	2	NT PN	TN.	I LN	NT TN	EST WINANI
Siligi	Top Hit Acession No.	.4E-02 U62293.1	.4E-02 BF512678.1	.4E-02 AA059167.1	.4E-02 A1125083.1	25893	7.4E-02 AW379431.1	7.4E-02 BF035099.1	7.4E-02 AJ223459.2	7.3E-02 BE964961.2	7.3E-02 BE984961.2	7.3E-02 AE001789.1	7.3E-02 AW900281.1	7.3E-02 AL163302.2	7.3E-02 U12283.1		7.3E-02 AA//99/1.1	P05143	P06143	7.3E-02 BF316067.1	7662107 NT	7.3E-02 Y10887.2	7.3E-02 AB011090.1	7 3E-00 AA779977 1		7.2E-02 AE000882.1		7.2E-02 AE000882:1	7.2E-02 AL163301.2	7.2E-02 AL183301.2	7.2E-02 U14794.1	7 OF 00 AMODOSOO 4
	Most Similar (Top) Hit BLAST E Value	7.4E-02	7.4E-02	7.4E-02	7.4E-02	7.4E-02	7.4E-02	7.4E-02	7.4E-02	7.3E-02	7.3E-02	7.3E-02	7.3E-02	7.3E-02	7.3E-02		7.35-02	7.3E-02 P05143	7.3E-02 P05143	7.3E-02	7.3E-02	7.3E-02	7.3E-02	7 3F-02					L			
	Expression Signal	-	0.49	1.46	1.42	1.22	3.74	2.61	1.44	1.15	1.15	2.66	3.26	15.79	1.02		1.48	2.37	2.37	0.58	1.38	0.5	1.17	1 78		0.6		9.0	2.6		3.34	
	ORF SEQ ID NO:	36653	36780	37975				31895	31968	26708		26917				Ĺ			34181			35214		221.08		26382	ł	26383		27740		20464
	Exen SEQ ID NO:	23057	23184		<u>L</u>	ı		L	25585		13676		L	16050	L	1	ŀ		20702	乚	L		22485	L	L	13362		13352	L	i		L
i	Probe SEQ ID NO:	10019	10148	11266	11914	12409	12692	12870	12882	481	484	702	1510	1893	5112		6582	7633	7633	7981	8361	8538	9411	44,63	764	2		12	1505	1505	2614	7000

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Top Hit Descriptor	602077757F1 NIH_MGC_62 Homo saplens cDNA clone IMAGE:4251950 5'	Methanococcus jannaschii section 73 of 150 of the complete genome	CALMODULIN	601883905F1 NIH_MGC_57 Homo saplen's cDNA clone IMAGE:4096224 51	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085710 5	Streptococcus pneumoniae putetive response regulator (zmpR), putetive histidine kinase (zmpS), and putetive	Allo Health treate (Lather) generally complete companies	Strongylocentrolus purpuraus miocnonurian, complete generie	PROLINE-RICH PROTEIN MP-3	PROLINE-RICH PROTEIN MP-3	Lactococcus lactis cspE gene	Human gene for sex hormone-binding globtilin (SHBG)	AV712452 DCA Hamo papiens aDNA clans DCAAUG01 5	Homo sapiens plasma membrane calclum ATPase Isoform 1 (ATP2B1) gene, alternative splice products,	pertial cds	601763623F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5	hq24f11,x1 NCI_CGAP_Adr1 Hamo sapieris cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN: ;	os62c07.s1 NCI CGAP GCB1 Homo sapiens cDNA clane IMAGE:1316844 3'		Homo saptiens zinc finger protein 92 (ZFP9/2), expressed-Xq28STS protein (XQ280RF), and biglycan (BGN)	genes, complete cus, and passing mentages conditioned in account of more) gene, produced and advantages of the MCC 53 Home sections colone IMAGE:3685951 5	ACHORAGOET NIET MAC 10 Home seriens cONA clone IMAGE 2451559 5	1978 HOS STATES feltal lives release 1NELS ST Home seatients CDNA clone IMAGE:451641 3'	420100.51 Outso, Data Ind. Special fine of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the Commission of the C	Katus navegicus anizir ususaripusi isaati (Mist) yenta aa	af81a04.rf Soares_NhHMPu_S1 Homo septens cDNA done IMAGE:1048398 o	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3	Ino05h08.s1 NCI_CGAP_Phet Hamo sepiens cDNA clone IMAGE:1099839 3	Homo sepiens ataxia telangiectasia (ATM) gene, complete ede	CM4-NN1009-200300-116-c11 NN1009 Homo saplens cDNA	Z57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5	Human Immunodeficiency virus type 1 (D9) proviral etructural capsid protein (gag) gene, partial ods
Top Hit Database Source	EST_HUMAN	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	<u> </u>		INT	SWISSPROT	SWISSPROT	NT	FZ.	EST HUMAN		TN	EST_HUMAN	EST HUMAN	EST HUMAN		!	NOT TOU	LOI TOWN	NOW TO L	EST_HUMAIN	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	'n	EST_HUMAN	EST_HUMAN	N
Top Hit Acession No.	7.2E-02 BF572307.1	7.2E-02 U67531.1	P11120	7.2E-02 BF217598.1	7.2E-02 BF216086.1	, 007,000	7.2E-02 AF221126.1	5834897 NT	P05143	P05143	7.2E-02 V17217.1	7.2E-02 X16349.1	7.2E-02 AV712452.1		7.2E-02 L14581.1	7.2E-02 BF125399.1	7.2E-02 AW873187.1	7 2F-02 AA768204 1	2000		7.2E-02 U82695.2	7.25-02/05/05/03.1	7.2E-02 0 2020 14.1	7.2E-02 AA/00697.1	7.2E-02 AF049874.1	7.2E-02 AA773696.1	7.2E-02 AJ230796.1	7.2E-02 AA584465.1	7.2E-02 U82828.1	7.2E-02 AW900982.1	7.2E-02 AA401779.1	7.1E-02 [L02290.1
Most Similar (Top) Hit BLAST E Vælue	7.2€-02	7.2E-02	7.2E-02 P11120	7.2€-02	7.2E-02	0000	7.2E-02	7.2E-02	7.2E-02 P05143	7.2E-02 P05143	7.2E-02	7.2E-02	7.2E-02		7.2E-02	7.2E-02	7.2E-02	7.2F.02	1.51.72		7.2E-02	1.25-02	7.25-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02		7.2E-02	7.2E-02	7.2E-02	
Expression Signal	3.07	2.73	8.76	1:11	1.32		0.7	1.53	0.8	9.0	79'0	0.51	2.19		4.88	0.96	234	8	9	-	2.15	0.57	3.47	0.55	4.14	2.12	3.83	2.05	4.23	7:37	1.63	2.06
ORF SEQ ID NO:	30583	$I_{-}$	31577	L	33863		33878		34987				36430		36596							3/331				32104						3 28197
Exan SEQ ID NO:	17605	18604	1	١	ì	<u> </u>	_]	20438	21463	L	L	<u> </u>	L		23000	L	ļ	L.	$\perp$		_		4	ı	24224	25230	ı	ı	l	1	ŀ	
Probe SEQ ID NO:	4465	5402	<u>8</u>	6244	7318		7336	7359	8382	8382	9264	9775	8		9981	10118	10208	4020E	CAFOL		10560	10692	10/16	10837	11153	12315	12350	12411	12474	12488	13048	1953

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Г		Т	Т	T	Т	Т	Т	T	Т		Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	$\neg \tau$			T		Т	П		Т	T	T	7
	Top Hit Descriptor	601872281F1 NIH_MGC_63 Homo sapianis cDNA clone IMAGE:4092981 5'	qd92a10.x1 Soares_testis_NHT Homo capienc cDNA clone IMAGE:1736922.3	Homo sapiens chromosome 21 segment H321C046	601143974F1 NIH_MGC_15 Homo sapiens CDNA Clone IMAGE:3031234 5	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR	Martellia Mtout-1 gene	266f04.s1 Stratagene colon (#337204) Homo sapiens cunna ciona intra cunada sa sa sa sa sa sa sa sa sa sa sa sa sa	UI-H-BIT-acy-0-07-0-UI.S1 NCI CGAP Subs Home saparas curva cigne invadezr 10020 3	ai65a12.s1 Soares_testis_NH1 Home sapiens cUNA cone 137 0076.5 similia to 90.N05002.5003. RIBOSOMAL PROTEIN L32 (HUMAN);	QV4-BT0407-280100-090-e10 BT0407 Homo saplens cDNA	GM6-UM0001-060300-270-e12 UM0001 Homo capiens cDNA	Canis familiaris inducible nitric oxide synthese mRNA, complete ads	601816291F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4050071 5	Lumbriaus rubellus mRNA for cyclophillin B	AV889285 GKC Homo sepiens cDNA clone GKCCAE08 5	Gallus gallus mRNA for partial aczonin, XL spilced variant (acz gene)	African swine fever virus, complete genome	Rat Ig germline epsilon H-chain gene C-region, 3' end	Human myosin binding protein H (MyBP-H) gene, complete cds	ah59e05.s1 Soeres_NFL_T_GBC_S1 Homo sapiens CDNA clone IMACE::132/184 3' similar to go:L1463/ TIGHT JUNCTION PROTEIN 2O-1 (HUM/AN);	Homo saplens hypothetical protein FLJ201/16 (FLJ20116), mRNA	Homo saplens chromosome 21 segment HS210010	Homo sepiens chromosome 21 segment HS21C010	Homo capienc regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)	268 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR AN IIGEN Z1U7)	H. saplens flow-sorted chromosome 6 HindIII fragment, SC6pA24F7	M.hycrhinis 115 kDa protein (p115) gene, complete cds	Canine distamper virus strain A75/17, complete genome	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete das	601340661F1 NIH_MGC_53 Hamo sepiens attiva digne image_second of
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	SWISSPROT	NT	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN ·	NT	EST_HUMAN	NT	EST_HUMAN	NT	NT	된	NT.	EST HUMAN	IN	N	Z	눌	SWISSPROT	SWISSPROT	NT.	FN	TN	TN	EST_HUMAN
agiiio	Top Hit Acession No.	7.1E-02 BF208802.1			7.1E-02 BE304764.1			7.0E-02 AA056343.1	7.0E-02 AW138152.1	7.0E-02 AA815438.1		7.0E-02 AW792962.1	7.0E-02 AF077821.1	7.0E-02 BF381987.1	109143.2	7.0E-02 AV689285.1	/19187.1	9628113 NT	(02901.1	J27268.1	7.0E-02 AA724295.1	11421638 NT	8.9E-02 AL 163210.2	6.9E-02 AL163210.2	4507988 NT	1	Q08364	6.9E-02 Z79163.1	6.9E-02 M34956.1	8.9E-02 AF164967.1	6.8E-02 U12022.1	6.9E-02 BE567435.1
	Most Similar (Top) Hit BLAST E	7.1E-02	7.1E-02 A1125264.1	7.1E-02	7.1E-02 E	7.0E-02 007092	7.0E-02 X96877.1	7.0E-02	7.0E-02	7.0E-02	7.0E-02 E	7.0E-02	7.0E-02	7.0E-02	7.0E-02 Y09143.2	7.0E-02	7.0E-02 Y19187.1	7.0E-02	7.0E-02 K02901.1	7.0E-02 U27268.1	7.0E-02	7.0E-02			6.9E-02	١	6.9E-02 Q08364					
	Expression	8.8	1.08	0.63	6,48	4.1	1.28	1.18	2.02	0.65	1.19	1.14	1.19	79.7	0.82	6.0	0.68	1.24					7.08	7.08	1.58	1.34					1.14	1.01
	ORF SEO ID NO:	28623	34687	37521		26758		28044	29288	30167	30301		30468			34107		1		L	<u> </u>	31958		26745		30051				-		35386
	Exan SEQ ID NO:	15497	L			l.	1_	14950	l	17161	L	I.	1	L	L	L		1	1	L		Ш	1		14518	1	1	ı		1	1	21829
	Probe SEQ ID NO:	2366	8094	10868	12193	54	1529	1801	3095	4004	4155	4268	4330	5045	828	7560	183	929	9797	10158	11854	13022	527	627	1384	3883	3803	5302	5316	7783	8242	8750

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Top Hit Descriptor	801340661F1 NIH MGC_53 Homo sapieris cDNA clane IMAGE:3683030 5	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds	DPH21.=candidate (umor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and	placental dissues, mRNA, 2233 nf)	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) (human, 9 week fetal and	placental tissues, mRNA, 2233 nf)	X laevis XFD2 mRNA for fork head protein	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG	Homo saplens membrane-bound aminopeptidase P (XNPEP2) gene, comprete cas	ee30f02.rd Gessker Wilms tumd Homo sapiens cDNA clone IMACE::897339 5 similiar to go:mzz392. MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);	and the second of the second of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s	MITOCHONDRIAL MATRIX PROTEIN PI PRECURSOR (HUMAN);	Homo saplens putative hepatic transcription factor (WBSCR14) gene, complete cds	MR0-HT0069-071099-001-c05 HT0069 Homo sepiens cDNA	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA	Homo sapiens chromosame 21 segment HS21C068	Dishostellum discoldeum mycsin heavy chain kinase A (MHCK A) mRNA, complete cds	Pyrococus abuses complete genome: segment 5/6	: grococcas appear of the common continent file	Pyrococcus apysar compress generally objects and property of the series of the Color known Charles and Similar to LINE-1	10-700 care from the NUT Home seriene CDNA clone 1320705 3'	ESTORAGE MACE manuse MACA Home seniors CDNA	S 1 30/ 840 MINGE LESSEQUEINES, MACHINE SERVICE CHESSEQUEINES	Mus musculus latent I Gr. peta pinding protecting in this American	Rattus norvegicus Growin Tactor Independente I (Still), Ilinvika Tactor Independente III (Still), Ilinvika Osmalfala Completa Cds	Oncorbynchus mydss 1AP1 protein (Ontrig) AP1) mixin X Olimyi AP1 (Ontrig) AP1	qg78e04.x1 Scares_NFL_T_GBC_S1 Homo sapiens CUNA cione IMAGE: 104 1400 3	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)	Oprinus carplo Rap1b mRNA, complete cds	Opprinus carplo Rap1b mRNA, complete cds	zd20g11.s1 Soares_fetal_heart_NbHH19lW Homo sapiens cDNA clone IMAGE:3412523' sImiliar to contains	Au repetitive element contains element L1 repetitive element;	H. sapiens UNA for claMP phosphodiesrerase (exons +-24)
Top Hit Database Source	EST HUMAN	Γ		N N		TN LN	X	ISSPROT	H	A NAMIN IN	Т	EST HUMAN N	Г	T HUMAN	SSPROT	Г	Т		1 L		T	Т	Т	HOMAN				EST_HUMAN	SWISSPROT	- LN	- L		L HUMAN	Ł
Top Hit Acession No.	8 9F-02 BF587435.1								6.9E-02 AF195953.1	A A A DO TRO 4	0.05-02 704-901 09.1	6.8E-02 AA496759.1			P20782	8 BE-02 P 20/82	41 400 700 7	6.8E-02/AL103200.2	0.10800.1	6.8E-02 AJ24628/.1	6.8E-02 AJ248287.1	6.8E-02 103214.1	8.8E-02 AA758014.1	6.8E-02 AW975839.1	9910585 NT	6978885 NT	6.7E-02 AF115638.1	6.7E-02 AI220285.1	6.7E-02 P17278	6.7E-02 U53783.1	6.7E-02 U53783.1		6.7E-02 W57759.1	8.7E-02 X62695.1
Most Similar (Top) Hit BLAST E·	8 95-02	6 05-021122987 1	70.70	6.9E-02 381752.1		6.9E-02 S81752.1	6.9E-02 X74315.1	6.9E-02 P44621	6.9E-02	000	0.05-02	6.8E-02	8.8E-02	6.8E-02	CPTUCE CO. TR. A	6 RF-02	20.00	6.8E-02	6.8E-02	8.8E-02	6.8E-02	6.8E-02												Ц
Expression Signal	5	280	200	1.46		1.48	10.94	1.58	3,37	,	- T	4.	3.85	490	28.0	0000	68.0	8.22	9.0	6.03	6.03	1.47	1.64	1.34	2.3	1.24	2.71	2.17					99.0	0.74
ORF SEQ ID NO:	25207	25040	00848	38092	١	38083					281//	20478									35100					31660	L	28186						34635
Exon SEQ ID NO:	2000	7 000	DEC 77	24435		24435	25251	25357	25513	1	15075	45075	ľ	L	١	1	_1			21564		26155		25599	25632	26091	L			L	L		21019	LI
Probe SEQ ID NO:	0250	3 8	0723	11274	121	11374	12348	12524	12770		1932	7007	7080	1830		6758	/040 D40/	7432	7861	8483	8483	12141	12276	12908	12972	13203	1558	1942	3811	4065	4065	3	7969	8034

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ .ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8834	21117	34636	0.74	6.7E-02	6.7E-02 X82695.1	TN	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713		67.0	6.7E-02	6.7E-02 AW082688.1	EST_HUMAN	xb61c11.x1 Soares_NFL_T_GBC_S1 Horro sapiens cDNA clone IMAGE:2380788 3'
880		36417	0.59	6.7E-02	6.7E-02 AW137369.1	EST_HUMAN	UI-H-BI1-ecr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3*
886	١.		0.59	6.7E-02	6.7E-02 AW137359.1	EST_HUMAN	UI-H-BI1-ecr-g-01-0-UI:s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716433 3'
1379	14534	27608	0.98	6.6E-02	6.6E-02 AI735509.1	EST HUMAN	et12e09.x1 Barstead acrta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' sImilar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.;
2252	1		3.73	6.6E-02		NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcipts
3552	L		12.38	6.6E-02	6.6E-02 R64306.1	EST_HUMAN	y18b10.s1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3567	L		3.11	6.6E-02	7108357 NT	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3567	16732		3.11	6.6E-02	TN 528917	TN	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.6E-02	6.6E-02 AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5093	L		12.07	6.6E-02 Q61703		SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN HZ PRECURSOR (ITI HEAVY CHAIN HZ)
5003	1_			6.6E-02	6.6E-02 Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN HZ PRECURSOR (ITI HEAVY CHAIN HZ)
						1447	274807.71 Soares_testis_NHT Home sapiens cONA clone IMAGE;728052 6' similar to gb:104270 TUMOR NECESSIS EACTOR DESCRIPTOR 2 BEINATED PROTEIN PRECISES EACTOR DESCRIPTOR 2 BEINATED PROTEIN PRECISES EACTOR DESCRIPTOR 2 BEINATED PROTEIN PRECISES EACTOR DESCRIPTOR 2 BEINATED PROTEIN PRECISES EACTOR DESCRIPTOR 2 BEINATED PROTEIN PRECISES EACTOR PROTEIN PRECISES EACTOR PROTEIN PRECISES EACTOR PROTEIN PRECISE EACTOR PROTEIN PRECISE EACTOR PROTEIN PRECISE EACTOR PROTEIN PRECISE EACTOR PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTE
5130	18255	31220	9.64	6.6E-02	6.6E-02 AA3B3244.1	ESI HOMAN	NECKOSIS PACION NECESTION & NELVILLE PROCESSION (CONTRACT)
2400		24,004	78 0		8 8E 00 4 4 3 2 3 4 4 4	NAME TO THE	z#74g07.rf Soares (estis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gd:104270 1 UMUK NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	上		88	6.6E-02		NT	P. vulgaris mRNA for chalcone synthase
6740	1			8 8F-02	6 6F-02 P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6748	1				6.6E-02 P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6937	1			Ĺ		SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6937	L	L	0.68	6.6E-02	6.6E-02 P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
8133	L.			6.6E-02	6.6E-02 AF052572.1	TN	Home sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8869	1	35287	0.77	8.6E-02	8.6E-02 AF006055.1	NT	Dictyostellum discoideum darlin (darA) gene, complete cds
8979	1		0.53	6.6E-02	6.6E-02 060673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC ȘUBUNIT (HREV3)
9121	l	35741		6.6E-02	9629198 NT	TN	Human respiratory syncyttal virus, completis genome
9121			1.28	6.6E-02	9629198 NT	TN	Human respiratory syncytial virus, complete genome
10157	L				6.6E-02 AI4587521	<b>EST_HUMAN</b>	\$97g08.x1 NCI_CGAP_Lu24 Homo sapleris cDNA clone IMAGE:21494983'
10292		7 36930	1.5		6.6E-02 Y07848.1	LN	Homo saplens EWS, gar22, rrp22 and barr,22 genes
10327	23362	2	0.85	6.6E-02	11430559 NT	NT	Horno sapiens vinculin (VCL), mRNA
10710	23743		0.49		6.6E-02 BF694659.1	EST_HUMAN	602080608F2 NIH_MGC_81 Homo sapieris cDNA clone IMAGE:4245336 5
11205	24274		4.95		6.6E-02 BF374248.1	EST HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12781	<u> </u>		4.64	6.6E-02	9937991	M	Mus musculus DIPB gene (Dipb), mRNA
13124	ı	3	1.28		8.6E-02 AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

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	Top Hit Descriptor	601671046F1 NIH_MGC_20 Homo sapieris cDNA clone IMAGE:3954178 5'	Hamo sapiens E2F-like protein (LOC61270), mRNA	Xenopus laevis alpha(E)-catenin mRNA, cómplete cds	Aquifex aeolicus section 96 of 109 of the complete genome	246h12.¢1 Soares ovary tumor NbHOT Homo sepiens cDNA clone IMAGE:756743 3' similar to gb:M26038 HLA CLASS II HISTOCOMPATIBILITY AVTIGEN, DR-5 BETA CHAIN (HUMAN);	602118887F1 NIH_MGC_56 Homo sapieris cDNA clone IMAGE:4276029 5'	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial ods	601868817R1 NIH_MGC_67 Homo sapleris cDNA done IMAGE:3865637 3'	601656817R1 NIH_MGC_67 Homo sapieris cDNA clone IMAGE:3865637 3'	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5	#32g06.e1 Soares_NhHMPu_S1 Homo expiens cDNA done IMAGE:665144 3'	Rebbit microsomal epoxide hydrolase	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds	A.cartarae precursor of peridhin-chlorophylla-protein (PCP) gene	Thermotoga maritima section 89 of 136 of the complete genome	Thermotoga maritima section 89 of 136 of the complete genome	qe07b01.x1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element ;	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds	Heterodera glycines beta-1, 4-endoglucanaise-1 precursor (HG-eng-1) gene, complete cds	we73g12.x1 Scares_Disckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'	601880425R2 NIH_MGC_83 Homo capiens cDNA clone IMAGE:3950503 3'	Mus musculus chaperonin subunit 6a (zetė) (Cct6a), mRNA	k1419.ceq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5	AF150195 Human mRNA from cd34* stem cells Homo sepiens cDNA done CBDAIA10	RC1-OT0083-150600-014-506 OT0083 Homo saplens cDNA	Homo caplens mRNA for KIAA0554 protein, partial cds	Homo sapiens DNA topoisomerase II bela (TOP2B) gene, exons 18, 17, and 18	Homo saplens DNA topolsomerase II beta (TOP2B) gene, exons 16, 17, and 18	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (r-ILA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete ods
	Top Hit Database Source	EST_HUMAN	LN	N	N	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	TN	TN	NT	EST HUMAN	N	LN LN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	١	TN	FN	L <sub>X</sub>
	Top Hit Acession No.	6.5E-02 BF027639.1	7706088 NT	J47624.1	6.5E-02 AE000764.1	6.5E-02 AA443991.1	8.5E-02 BF685340.1	J22681.1	6.5E-02 BE963200.2	6.5E-02 BE983200.2	6.5E-02 BF106300.1	6.5E-02 AA195648.1	8.5E-02 MZ1496.1	8.5E-02 AF102993.1	6.4E-02 X94549.1	6.4E-02 AE001777.1	6.4E-02 AE001777.1	6.4E-02 Al191958.1	6.4E-02 AF052733.1	8.4E-02 AF062733.1	6.4E-02 AI672896.1	6.4E-02 BE974448.1	6753323 NT	6.4E-02 AA093305.1	6.4E-02 AF150195.1	6.4E-02 BE834083.1	6.4E-02 AB011126.1	6.4E-02 AF087150.1	6.4E-02 AF087150.1	6.4E-02 U91328.1
	Most Similar (Top) Hit BLAST E Value	6.5E-02	6.5E-02	6.5E-02 U47624.1	6.5E-02	6.5E-02	6.5E-02	6.5E-02 U22681.1	6.5E-02	6.5E-02	6.5E-02	6.5E-02	8.5E-02	8.5E-02	6.4E-02	6.4E-02	8.4E-02	6.4E-02	6.4E-02	8.4E-02	6.4E-02	8.4E-02	6.4E-02	6.4E-02	6.4E-02	6.4E-02	8.4E-02	6.4E-02	6.4E-02	6.4E-02
	Expression Signal	1,57	1.3	3.38	2.04	2.07	0.73	1.02	0.57	0.57	0.81	4.45	3.78	3.67	1.49	66.0	66.0	1.11	2.64	2.64	123	4.11	2.47	4.17	96'0	0.04	1.87	0.45	0.45	1,88
	ORF SEQ ID NO:	28805			28016			31486		l	37323				26789		1		L	L	L			35478			36545			38697
	Econ SEQ ID NO:	13785	14183	14576	14922		ı	18539	23185	1	1	ı	25129		ŀ	14919	14918	1	L	19413	18696	20270	21612			22828	l.,	1	1	1
	Probe SEQ ID NO:	988	101	1422	173	5878	6673	7113	10147	10147	10683	10875	12163	12533	589	1770	1770	5566	6239	6239	6532	6957	8631	8865	9327	9785	9918	10468	10468	12008

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	Top Hit Descriptor	Homo saplens SWI/SNF related, matrix essociated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	H. sapiens mRNA for B-HLH DNA binding protein	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3	G01651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3	L3-HT0618-110500-138-C08 HT0618 Hano saplens aDNA	Eptatretus burgeri mRNA for RNA polymerase III largest suburnit, partial cos	S aponicum mRNA for serine-enzyme	1259107.X1 NCI_CGAP_UV35 Home saparis conne invace_125201 3	Homo sapiens chromosome 21 segment HS21000/	Thermotoga maritima section 89 of 136 of the complete genome	EST380924 MAGE resequences, MAGJ Homo capiens cONA	Mesocestades cort mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gin, tRNA-Phe, tRNA-Met,	ATPase subunit 6, and NADH cehydrogenase subunit 2	2p78c04.r1 Stratagene HeLa cell \$3 937215 Homo sapiens CUNA cione liviA GE: 020310 3	2p78c04.r1 Stratagene HeLa cell s3 837216 Homo sapiens CLAVA cione INMACE. 02o3 10 3	EST84266 Colon adenocarcinoma IV Homo sapiens curva o and similar to ussue-specially process	EST84266 Colon adenocarcinoma IV Homo sapiens GUNA 5 and similar to ussue-specific process	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3	RC3-BT0253-011199-013-504 BT0253 Homo sapirans CUNA	W448h05x1 Soares_NFL_T_GBC_S1 Homo septens curva clone timace: 2336673 5 strikta to contains	LT.T. LT. LT repeality draining in the Control of STAFE (SOUND) (STAFE) mRNA	TOTAL SOUTH STATE AND SOUTH STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA	Homo septens surnulated deliverung levin (vo no.g.) 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	Top Hit Database Source	LN TN	N-	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	LN.	EST_HUMAN	NT	LN T	EST_HUMAN		TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN	Z	Ę.	EST_HUMAN	EST_HUMAN	SINT	EST_HUMAN	EST_HUMAN	LN L	NT.	EST HUMAN	
	Top Hit Acession No.	4507070 NT	(99268.1	6.1E-02 BE971853.1	6.1E-02 BE971853.1	6.1E-02 BE179543.1	6.1E-02 AB025333.1	<70969.1	6.1E-02 A1886611.1	6.1E-02 AL163207.2	6.0E-02 AE001777.1	6.0E-02 AW968848.1		6.0E-02 AB031289.1	6.0E-02 AA188730.1	6.0E-02 AA188730.1	6.0E-02 AA372376.1	8.0E-02 AA372376.1	6.0E-02 BE964443.2	6.0E-02 AW370211.1		6.0E-02 AI807537.1	5174698 N	5174698 NT	6.0E-02 BF382349.1	6.0E-02 Al204275.1	11466495	6.0E-02 AI623167.1	8.0E-02 AI623167.1	6.0E-02 AJ245365.1	6.0E-02 AJ245365.1	B DF-02 AA309797 1	
	Most Similar (Top) Hit BLAST E Value	6.1E-02	6.1E-02 X99268.1	8.1E-02	6.1E-02	8.1E-02	8.1E-02/	6.1E-02 X70969.1	6.1E-02	6.1E-02	6.0E-02	6.0E-02		6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02		6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	8.0E-02	6.0E-02	8.0E-02	6.0E-02	6.0E-02		
	Expression Signal	1.57	3,65	9.0	9.0	3.9	1.68	30.03	1.58	6.43	1.58	1.17		4.	1.53	1.53	2.07	2.07	0.76	1.01		+	2.86	2.86	237	1.78	0.48					-	
	ORF SEQ ID NO:		35068	35474	35475	37681	38818				27513	28969			26382			_			L	ı	31467	31468	33880	١		36092			L		
	Exen SEQ IO: NO:	19414	21530	21940	21940	24048	25114	26083	25957	25645	14447	L		15946	L	1	_	16476	1	١	1		18553	18553	Ι.	1	L	1		L	22631	1	2 2 4
	Probe SEQ ID NO:	6240	8458	889	886	10867	12134	12218	12836	12993	1281	2740		2832	3002	3002	3301	3301	3725	5514		6345	7127	7127	7338	7857	8817	9472	9472	9098	9608	3	19109

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Top Hit Database Source Source Source EST_HUMAN EST_HUMAN NT NT NT NT NT NT EST_HUMAN NT EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	sio		Signal Signal 0.72 0.72 0.77 0.77 0.97 1.35 0.97 1.35 0.97 1.58 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 1.35 0.97 0.97 1.35 0.97 0.97 0.97 0.97 0.97 0.97 0.97 0.97
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	1 163283 2	5.8E-02	0.61
Z	M99150.1	5.8E-02	2.78
z	M99150.1	5.8E-02	278
- !	Arosozo4.1	5.8E-02	2.1
EST HUN	AI247505.1	5.8E-02	4.84
MIL TOO	4 1047 505 4	1 2	
EST HUM	A1247505.1	5.8E-02	4.64
			2
EST HUM	AW051927.1	5.8E-02	6.79
EST HUM	AW051927.1	5.8E-02	6.79
NT	AE001775.1	5.8E-02	1.68
SWISSPR	Q61768	5.8E-02	78.0
N	D90110.1	5.8E-02	9
TN		6.9E-02	1.37
EST_HUM		5.9E-02	1.35
LN C	79870	5.9E-02	7.30
EST_HUM	BF242748.1	5.9E-02	76.0
NT	8055249	5.9E-02	2
LN.	AF166111.1	5.9E-02	0.77
<u>L</u> N	AF190269.1	5.9E-02	2.77
EST_HUM	AW934719.1	5.9E-02	5.88
EST HUM	AI809273.1	6.0E-02	5.12
EST_HUM	AA128386.1	6.0E-02	1.42
			+
EST_HUM	AA309797.1	8.0E-02	0.72
	Top Hit Acession Na	(Top) Hit BLAST E Value	
그 발생성 나라 하는 이 선생님 나는 나는 나는 나는 나는 그를 보는 것이 되었다.	Top H Databa Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc Sourc	gi gi gi gi gi gi gi gi gi gi gi gi gi g	Top Hit Acession No. No. No. S. AA128386.1 2 AA128386.1 2 AA128386.1 2 AA128386.1 2 AA128386.1 2 AA128386.1 2 AF166111.1 2 AF165111.1 2 AF16611.1 2 AF16611.1 2 AF16611.1 2 AF16611.1 2 AA1240733.1 2 AA061927.1 2 AN061927.1

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Top Hit Descriptor	Hamo sepiens ABCA1 (ABCA1) gene, complete cds	SOLUTION TELL NIM MACC. 65 Homo saniens cDNA clone IMAGE:3861985 5'	00 144 150 174 111 140 05 10 10 10 10 10 10 10 10 10 10 10 10 10	U144/83/F1 Nin Misc. 35 nuilla sapianis curin misc.	Xenopus lacvis mRNA for fourth component of complement, compleme cus	Xenopus laevis mRNA for fourth component or complement, complete cus	Rettus norvegicus mRNA for potassium channel, alpha subunit (kvs.2 gene)	Mus musculus ect2 oncogene (Ect2), mKNA	cn18b09.y1 Normal Human Trabecular Borie Cells Homo sepiens cDNA clone NHTBC_cn18b09 random	on18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random	Homo saplens chromosome 21 segment HS21C103	Pig DINA for SPAI-2, complete cds	Homo sapiens Xq pseudoautosomal region; segment 1/12	Homo sapiens fragile 16D oxico reductase (FOR) gene, excris 8, 9, and partial cds	Pan troglodytes apolipoprotein-E gene, complete cds	vi64d10.61 Soares breast ZNbH-Bst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1	repetitive element;	Hydrocotyle rotundifolia ribosomel protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product	6014945/8F2 NIH MGC_/O HOMO BARBAIN CIVIS IN CLINICAL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CON	Lycopersicon esculentum LE-ACS6 mRNA for 1-eminocyclopropane-1-carboxylate synthase, complete cds	ZS45c01.81 NCI_CGAP_GCB1 Homo Sapiens culvA dane iliva ce vc+ iv c	xjozcio.xi NCI_CGAP_UZ Hemo sapienti cUNA cicnie limace:.zozozozo 3 sililiari un incocosto de como KIAA0806 PROTEIN.;	od47112.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1371119 3 similar to contains Atu repetitive element:contains element L1 repetitive element;	OVO. BN0147-290400-214-07 BN0147 Homo sapiens cDNA	And And A Species thesits NHT Homo servicers oDNA clone IMAGE:1734308 3'	quovage 1.11 local et al. 200 local et al. 1.10 local et al. 200 local et al. 200 local et al. 200 local et al	60106/108F1 NIT MGC 10 Home caniens cDNA clone IMAGE:3453279 5	00 100 100 100 100 100 100 100 100 100	n48dd/si NCI_CGAP_Ann nomo septejis cann cane importation come.
Top Hit Database Source	L	T	Т	HOMAN		INT	NT		EST_HUMAN	EST_HUMAN		NT	F		LN LN		EST_HUMAN		EST HUMAN		EST_HUMAN	EST HUMAN	EST HIMAN	MANN TOU	TOTAL TOTAL	ES HOMAIN	EST HUMAN	EST_HOMAN	EST HUMAN
Top Hit Acession No.	7E 02 A E27504R 1	21 2010.	5.7E-02 BE871911.1	3.7E-02 BE871911.1	7E-02 D78003.1	3.7E-02 D78003.1	5.7E-02 AJ296090.1	6681280 NT	5.7E-02 AI752685.1	5.7E-02 A1752685.1	6.7E-02 AL163303.2	5,7E-02 D50320.1	5.7E-02 AJZ71735.1	5.7E-02 AF217490.1	5 7E-02 AF281280.1		5.7E-02 R48513.1	5.6E-02 AF094455.1	5.6E-02 BE904308.1	5.6E-02 AB013100.1	5.6E-02 AA290599.1	5.6E-02 AW172708.1	E 6E 02 0 0 888187 1	Troop loc.	6.6E-02 BEUU8UUT.1	5.6E-02 AI183683.1	5.6E-02 BE542663.1	5.6E-02 BE542663.1	5.8E-02 AA482864.1
Most Similar (Top) Hit BLAST E Value	75.02/	0.75-02	6.7E-02	5.7E-02	5.7E-02	6.7E-02	6.7E-02	5.7E-02	5.7E-02	5.7E-02	6.7E-02	5.7E-02	5.7E-02	5.7E-02	5.7E-02	20.710	5.7E-02	5.6E-02	5.6E-02			l			1				
Expression Signal	28.0	6.0	0.68	0.68	0.72	0.72	1.45	0.82	3.14	3.14	188	19.03	217	308	521	140	1.18	1.1	1.95									2.52	1.18
ORF SEQ ID NO:					١.	1	١	L									31929	27789		30878	L	33954	_			34572	1 35823		36651
Exon SEQ ID NO:	18,00	19185	20699	20699	20776	20775	21430	23093			24740	1	L	L	1	69107	25759	14709	15493	17898	L	1	1	ı		21060			1 1
Probe SEQ ID NO:		6000	7630	7630	7710	7710	8340	10055	11464	11484	1	12586	19760	12853	2003	13012	13171	1556	2362	4763	4818	200	8870	789	7301	8010	9005	9005	10017

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Expression (Top) Hit Top Hit Acession Signal Value Signal	2.42 6.6E-02 AF260225.1 NT Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	7.33 6.6E-02 X97869.1 NT	3.33 5.5E-02 6755501 NT	0.98 5.5E-02 L41561.1 NT	3.49 5.5E-02 Q01174 SWISSPROT	4.32 6.5E-02 Q01174 SWISSPROT	1.65 5.5E-02 6755902 NT	0.87 5.5E-02 AF170911.1 NT	0.87 5.5E-02]AF170911.1 [NT	0.76 5.5E-02 10947034 NT	0.76 5.5E-02 10947034 NT		Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhiaD), transcriptional activator (dhaR), 1,3-propanediol	6.31 5.5E-02 U09771.1 NT	0.85 5.4E-02 AJ277458.1 INT Oryza setiva rbbi3-1 gene for putative Bowman Birk trypsin Inhibitor	8.19 5.4E-02[BE073468.1 [EST_HUMAN   RC5-BT0559-140200-012-C03 BT0559 Home sapiens cDNA	0.61 5.4E-02 U85806.1 NT	1,18 5,4E-02 299116.1 NT Bacillus subtlis complete genome (section 13 of 21); from 2395281 to 2813730	5897 0.51 5.4E-02 AF260225.1 NT Homo septens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	1.86 6.4E-02 U20790.1 NT	1.36 5.4E-02 BF371289.1 EST HUMAN	1.38 5.4E-02 BF371289.1 EST_HUMAN	5.4E-02 U44894.1 NT	1.55 5.3E-02 AW391248.1  EST_HUMAN	1.55 5.3E-02 AW391248.1 EST_HUMAN	7768 20.67 6.3E-02 194769.1 EST HUMAN HIA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);	3.22 5.3E-02 AJ276408.1	0.97	0.97 5.3E-02 M58417.1 NT	4.83 5.3E-02 AJ27640B.1 NT	1290 7.98 5.3E-02 M80463.1 NT Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
<b>——</b>	242	7.33	3.33								97.0				0.85	8.19		1.18					3.72								
ORF SEQ ID NO:	51	38 28948	L		68 32272		34083			95 36476	195 38477	36583		37977	09	176	77 30186	198	35897	37663			130	L	244 27301		l		Ì		
Probe Exan SEQ ID SEQ ID NO: NO:	11863 24851	2720 15838	3286 16460	_	5776 18968			8311 21383					L	11271 24339	3084 16260	3509 18476	4020 17177	L	9271 22347		11453 24519	1		ł	i i		ı	3008	3008 16184		5200 18321

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	SEO ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3	10004	04040	250	E 2E 02	2 2 00 AEAAA57 1	LN.	Helicobacter pylort 26695 section 5 of 134 of the complete genome
3	┙		2007	0.35-02	I		Lelizabador miled 26005 cortion 8 of 134 of the commiste menume
5434			239	5.3E-02	-	Z	Heliconactel Divol. Section 1. 194. 1 in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
6228	19403	32753	1.14	5.3E-02	5.3E-02 M85289.1	NT	Human heparan sulfate proteogycan (HSP/GZ) mKNA, complete cos
7024	!		4.02	5.3E-02	9695413 NT	L	Lymphocystis disease virus 1, complete genome
7241	1	33769	1.37	5.3E-02	5.3E-02 U32832.1	NT	Haemophilus Influenzae Rd section 147 of 163 of the complete genome
7617	)		2.3	5.3E-02	5.3E-02 S78221.1		nuclear protein TIF1 Isoform [mice, mRNA, 4053 nt]
8061	_	34585		5.3E-02 P38742		ISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8600	1		89'0	5.3E-02	5.3E-02 U10098.1	NT	Mus musculus 129/Sv cystatin C (cst3) geire, complete ods
9325	22401	35954	1.73	6.3E-02	6.3E-02 X03127.1	NT	Podospora anserina mitochondrial epsilon-san DNA
10462	23497		19:0	5.3E-02	5.3E-02 Y07907.1	Į.	D.rerto mRNA for xp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10538	L	37180	0.70	6.3E-02			B. rerio pou[c] mRNA for transcription factor
13173	<u> </u>		1.58	5.3E-02	5.1	Į.	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2358	1		64.04	5.2E-02	5031908 NT	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3183	16358	29363	2.39			NT	Homo saplens partial LMO1 gene for LIM clomain only 1 protein, exon 1
3183						NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	L	30218	8.0		5.2E-02 AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diliron protein (Crd1) mRNA, complete cds
4383	17536		3.31	5.2E-02	5.2E-02 U07132.1	NT	Human steroid hormone receptor Ner-I mRNA, complete cds
5287	L		0.68		5.2E-02 AB035201.1	LN IN	Rettus narvegiaus mRNA for thyroglabulin, complete ads
6040	L				5.2E-02 U14731.1	L	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
	1					MARKI III FOR	wj80e04.x1 NCI_CGAP_Lym12 Homo sapjens cDNA clone IMAGE:2409150 3' sImilar to contains MER15.b1 MED45 conditing element:
6233	19408		độ C		5.2E-02 Alganago.1	NOWOLL 103	ONA DOLYMERASE BROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-
7424	20601	33972	123		5.2E-02 P36322	SWISSPROT	BINDING GENE 18 PROTEIN)
8389	Ł.			L	2.40	NT	Homo sapiens chromosome 21 segment HS21C004
9931	L	36560				LN	Turntp mosalc virus genomic RNA for Capsid protein, complete cds
9931	L				5.2E-02 D10927.1	TN	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	5 25483		1.6		6.2E-02 Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE AILPHA CHAIN
2437	15565		0.98		5.1E-02 AL134071.1	EST HUMAN	DKFZp647D073_r1 647 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D073 5
5181	18283	31248	0.89		5.1E-02 BE957423.2	EST_HUMAN	601653565R2 NIH_MGC_55 Home sepients cDNA clone IMAGE:3838361 3
6251	18372		96'0		6.1E-02 AL139077.2	TN	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
5349	18462				5.1E-02 U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	19969	33370	0.79		5.1E-02 AF280369.1	ΤN	HIV-1 patient 96 from Italy processe (pol) gene, complete cos

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Exon         ORF SEQ         Expression         Most Similar (Top) Hit Signal         Most Similar (Top) Hit Signal         Ase-02 (Top) Hit Nature           16823         28851         0.78         4.9E-02 (Top) Hit Signal         4.9E	Top Hit Database Source Source EST_HUMAN EST_HUMAN EST_HUMAN I EST_HUMAN INT NT NT NT NT NT NT NT NT NT NT NT NT N	Top Hit Descriptor  248a12.s1 Stratagene hNT neuron (#937/33) Home saplens cDNA clone IMAGE:632926 3' similar to confains Alu repetitive element,confains element MSR1 repotitive element;  278a03.s1 Soares_testis_NHT Home saplens cDNA clone IMAGE:728428 3'  278a03.s1 Soares_testis_NHT Home saplens cDNA clone IMAGE:728428 3'  278a013.s1 Soares_testis_NHT Home saplens cDNA clone IMAGE:283286 3'  278a013.s1 Soares_testis_NHT Home saplens cDNA clone IMAGE:2832386 3'  2786910.x1 NCI_CGAP_U44 Home saplens cDNA clone IMAGE:2632386 3'  2786910.x1 NCI_CGAP_U4 Home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens cDNA clone IMAGE:2632386 3'  278a013.s1 Soares_testis_NHT home saplens connected to somplete cds  278a013.s1 Soares_testis_NHT home saplens connected to somplete cds
16822         0.85           16844         22851         0.78           16844         22852         0.78           18033         31059         2.64           18033         31070         2.64           18033         31070         2.64           18886         31702         1.62           20374         33831         1.77           22031         33831         1.77           22031         36576         0.67           23635         37450         1.57           23836         37450         1.57           23835         37450         1.57           23835         37450         1.57           238376         3.46           238376         3.46           238376         3.46           238376         3.46           13552         2652           13552         2652           1368         28676           1478         28670           16478         28670           16454         29478           1706           17828         10.68	EST_HUMAN EST_HUMAN EST_HUMAN I EST_HUMAN INT INT INT INT INT INT INT INT INT IN	zg 48a12.s1 Strategene hNT neuron (#637;233) Homo caplens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element;contains definent MSR1 repetitive alement; 278a03.s1 Soares_testis_NHT Homo septems cDNA clone IMAGE:728428 3' arg86310.x1 NGL_CGAP_Ut4 Homo septems cDNA clone IMAGE:2832386 3' ag66310.x1 NGL_CGAP_Ut4 Homo septems cDNA clone IMAGE:2832386 3' ag66310.x1 NGL_CGAP_Ut4 Homo septems cDNA clone IMAGE:2832386 3' arg86310.x1 NGL_CGAP_Ut4 Homo septems condition arg872 sights gene, excort 1  Mus musculus SMZ2 sights gene, excort 1  Homo septems prepro placental TGF-beta gene, complete cds
16844         28851         0.78           16844         28852         0.79           18023         31059         2.64           18053         31070         2.64           18856         31702         1.62           20374         33831         1.79           22021         1.07         1.07           22033         3676         0.97           23636         3745         0.64           23835         3745         0.54           23836         37450         1.57           23835         37450         1.57           23835         37450         1.57           23836         37450         1.57           23836         37450         1.57           2468         38376         3.46           13552         2652         2.61           1369         28610         2.08           16478         28610         2.08           16454         29478         1.76           17928         1.06           18359         0.98	EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	artRead3.srl Soares (testis_NHT Homo explens cDNA clone IMAGE:722428 3:  artRead3.srl Soares (testis_NHT Homo explens cDNA clone IMAGE:722428 3:  artRead3.srl Soares (testis_NHT Homo sapilens cDNA clone IMAGE:2322380 3:  artRead3.srl Soares (testis_NHT Homo sapilens cDNA clone IMAGE:26322380 3:  artRead3.srl NoI_CGAP_UtH Homo sapilens cDNA clone IMAGE:26322380 3:  artRead3.srl Soares (testis con 6  Archaeoglobus fulgidus saction 127 of 172 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome Archaeoglobus fulgidus saction 40 of 85 of the complete genome
16844         29852         0.78           18053         31058         2.64           18056         31702         1.62           18866         31702         1.62           20374         33831         1.78           21894         0.07         1.77           22021         0.61         0.07           22033         36676         0.97           23836         37450         1.57           23835         37450         1.57           23836         37450         1.57           24686         38376         3.46           25624         2652         2.61           13552         26562         2.61           13552         26562         2.61           1458         28610         2.01           16478         28676         1.79           17928         1.75         1.79           17828         1.76         1.79           17828         1.06         1.06	EST_HUMAN EST_HUMAN EST_HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	artRea03.srt Scares_testis_NHT Homo saplens cDNA clone IMAGE:728428 3 ag66g10.xrt NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2832386 3 ag68g10.xrt NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2832386 3 Ret elestase il gens, exon 6 Ret elestase il gens, exon 6 Archaeoglobus fugiqus section 127 of 172 of the complete genome Archaeoglobus fugiqus section 40 of 85 of the complete genome Archaeoglobus fugidus section 40 of 85 of the complete genome Archaeoglobus fugidus section 40 of 85 of the complete genome Archaeoglobus fugidus section 40 of 85 of the complete genome Mus musculus SMZZ alpha gens, exon 1 Mus musculus SMZZ alpha gens, exon 1 Homo sapiens propro placental TGF-beta gene, complete cds
18053         31058         2.64           18063         31070         2.64           18686         31702         1.62           18686         31702         1.62           20374         33831         1.79           21894         1.07         1.79           22031         36676         0.97           23635         37145         0.64           23836         37450         1.57           23835         37450         1.57           24686         38376         3.46           25624         2652         2.61           13552         26582         1.19           13552         26562         2.61           13696         28610         2.01           16478         28610         2.08           16454         29478         1.79           17926         1.06           18359         31328         0.98	EST HUMAN I EST HUMAN INT INT INT INT INT INT INT INT INT IN	ag66g10.x1 NCI_CCAP_Ut4 Homo sapients cUNA clone IMAGE::2632386 3  ag68g10.x1 NCI_CCAP_Ut4 Homo sapients cDNA clone IMAGE::2632386 3  Ret elestase il gens, exon 6  Ret elestase il gens, exon 6  Archaesqiobus fulgidus section 127 of 172 of the complete genome Archaesqiobus fulgidus section 40 of 85 of the complete genome Altabidopsis Veniana DNA chromosome 4, complete genome Archaedoposis Veniana DNA chromosome 4, complete genome Mus musculus SMZZ alpha gens, exon 1  Mus musculus SMZZ alpha gens, exon 1  Homo sapiens propro placental TGF-beta gene, complete cds
18083         31070         2.64           18686         31702         1.62           18686         31703         1.62           20374         33831         1.78           21894         1.07         0.51           22021         36676         0.97           23635         37745         0.64           23836         37450         1.57           23836         37450         1.57           24686         38376         3.45           25624         3.23           13552         26582         1.19           13552         26582         1.19           13696         28726         1.153           16478         28610         2.01           16478         28476         1.79           17926         1.06           18359         31328         0.96	NT NT NT NT NT NT NT NT SEST_HUMAN NT SWISSPROT	Agricultus SMZZ eipha gene, exon 1  Rat elestase il gene, exon 6  Rat elestase il gene, exon 6  Rat destase il gene, exon 6  Rat destase il gene, exon 6  Archaeoglobus fulgidus section 127 of 172 of the complete genome Chiamydia mundarum, section 40 of 85 of the complete genome Archaeoglobus fulgidus section 40 of 85 of the complete genome Archadopasi velaina DNA chromosome 4, contig fragment No. 59  TRANSCRIPTION FACTOR Es  Mus musculus SMZZ alpha gene, exon 1  Mus musculus SMZZ elpha gene, exon 1  Homo sapiens propro placental TGF-beta gene, complete cds
18686         31702         1.62           18686         31703         1.62           20374         33831         1.07           21894         1.07         1.07           22033         36676         0.97           23635         37445         0.64           23835         37450         1.57           23835         37460         1.57           24686         38376         3.46           25624         3.23           13552         26582         1.19           13552         26582         1.19           13696         28726         1.153           1478         28610         2.08           17628         31328         0.86           18559         31328         0.86	NT NT NT NT SET_HUMAN NT SWISSPROT	Rat elestase II gene, exon 6 Ret elestase II gene, exon 6 Archaecglobus fugidus section 127 of 172 of the complete genome Chlamydia muridarum, section 40 of 85 of the complete genome Chlamydia muridarum, section 40 of 85 of the complete genome Arabidopsis theilana DNA chromosome 4, contig fragment No. 59 TRANSCRIPTION FACTOR Es Mus musculus SMZ2 alpha gene, exon 1 Mus musculus SMZ2 alpha gene, exon 1 Homo sapiens propro placental TGF-beta gene, complete cds
18686         31703         1.62           20374         33831         1.78           21894         1.07         1.07           22023         36676         0.61           23835         37445         0.54           23836         37490         1.57           23836         37490         1.57           24686         38376         3.48           25624         3.23           13552         26582         1.19           13562         26782         1.16           16478         28610         2.08           16454         28476         1.79           17628         31328         0.98	NT NT NT EST_HUMAN NT SWISSPROT	Rat elestase if gens, exon o Archaeoglobus fulgidus section 127 of 172 of the complete genome Chlamydia muridarum, section 40 of 85 of the complete genome MRQ-HT0408-170800-003-a08 HT0408 Homo saplens CDINA Arabidopsis theilana DINA chromosome 4, contig fragment No. 59 TRANSCRIPTION FACTOR Es Mus musculus SMZ2 alpha gene, exon 1 Mus musculus SMZ2 alpha gene, exon 1 Homo sapiens propro placental TGF-beta gene, complete cds
20374         33831         1.79           21894         1.07         1.07           22021         0.61         0.61           22033         36676         0.97           23656         37445         0.64           23835         37480         1.57           24686         3876         1.57           24686         38376         3.46           25624         3.23           13552         26582         1.19           13552         26582         2.61           13696         28672         1.18           16478         28672         1.76           17928         1.06           17928         1.06           18359         31328         0.98	NT NT EST_HUMAN NT SWISSPROT	Archaeoglobus fulgidus section 127 of 172 of the compare genome Chlamydia muridarum, section 40 of 85 of the complete genome MRQ-HT0408-170800-003-a08 HT0408 Homo saplens cDNA Arabidopsis theilana DNA chromosome 4, contig fragment No. 59 TRANSCRIPTION FACTOR E3 Mus musculus SMZZ alpha gene, exon 1 Mus musculus SMZZ alpha gene, exon 1 Homo sapiens propro placontal TGF-beta gene, complete cds
21894         1.07           22021         0.61           22033         36676         0.97           23555         37445         0.64           23856         37450         1.57           23826         37460         1.57           24686         38376         3.23           25624         3.23           13552         26582         1.19           13552         26582         2.61           13696         28670         2.61           16478         28670         2.08           17928         1.06           17928         1.06           18359         31328         0.98	NT EST_HUMAN NT SWISSPROT	Chlamydia muridarum, section 40 of 85 of the complete genome MR6A-HT0408-170800-003-a08 HT0408 Homo saplens cDNA Arabidopsis theilana DNA chromosome 4, contig fragment No. 59 TRANSCRIPTION FACTOR E3 Mus musculus SMZZ alpha gene, exon 1 Hurs musculus SMZZ alpha gene, exon 1 Homo saplens prepro placental TGF-beta gene, complete cds
22021         0.61           22033         36676         0.97           23635         37445         0.54           23835         37459         1.57           23836         37460         1.57           24686         38376         3.23           13522         26582         1.19           13552         26582         2.61           13552         26562         2.61           13696         28670         2.08           16478         28670         2.08           17928         1.76           17859         0.88	EST_HUMAN NT SWISSPROT NT	MR0-HT0408-H70800-003-a08 H10408 Homo saptens CLINA Arabidopsis theliana DNA chromosome 4, contig fragment No. 59 TRANSCRIPTION FACTOR E3 Mus musculus SMZ2 alpha gene, exon 1 Hus musculus SMZ2 alpha gene, exon 1 Homo sapiens prepro placental TGF-beta gene, complete cds
22033         36676         0.97           23535         37445         0.64           23835         37450         1.57           23826         37460         1.57           24686         38376         3.46           25624         3.23           13552         26582         1.19           13552         26582         2.11           13566         28676         1.153           16478         28610         2.08           17928         1.76           17859         31328         0.98	9.2 NT SWISSPROT NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. ce TRANSCRIPTION FACTOR Es Mus musculus SM22 alpha gene, exon 1 Mus musculus SM22 alpha gene, exon 1 Homo sapiens prepro placental TGF-beta gene, complete cds
23535         37445         0.64           23835         37459         1.57           23835         37450         1.57           24686         38376         3.46           25624         3.23           13552         26582         1.19           13552         26582         2.01           13696         28726         11.53           16478         28610         2.08           17928         1.76           18359         31328         0.98	SWISSPROT	TRANSCRIPTION FACTOR ES  Mus musculus SM22 alpha gene, exon 1  Mus musculus SM22 alpha gene, exon 1  Homo aapiens prepro placental TGF-beta gene, complete cds
23835         37459         1,57           23836         37460         1,57           24686         38376         3,45           25624         3,23           13552         26582         1,19           13552         26562         2,61           13562         26562         2,61           13696         28726         11,53           16478         28610         2,08           16454         29476         1,79           17926         1,06           18359         31326         0,96	LN	Mus musculus SM22 alpha gene, exon 1 Mus musculus SM22 alpha gene, exon 1 Homo aapiens prepro placental TGF-beta gene, complete cds
228356         37460         1.57           24686         38376         3.46           25624         3.23           13552         26582         1.19           13552         26582         2.01           13552         26582         2.01           13696         28726         11.53           16478         28610         2.08           17926         1.79           17859         31328         0.86		Mus musculus SM22 alpha gene, exon 1 Homo sapiens prepro placental TGF-beta gene, complete cds
24686         38376         3.45           25624         3.23           13552         28582         1.19           13552         26382         2.61           13696         28726         11.53           16478         28610         2.08           17648         29476         1.79           17628         31328         0.86	INI	Homo sapiens prepro placental 1 GF-beta (Jene, complete cos
25624     3.23       13552     28582     1.19       13552     26382     2.61       13696     26726     11.53       16478     28610     2.08       17628     1.79       17859     31328     0.88	NT	
13552         26582         1.19           13552         26582         2.61           13696         26726         1.133           16478         28610         2.08           17646         29478         1.75           17626         1.06           18359         31328         0.88	FN	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
13552         26582         2.61           13696         28726         11.83           1647e         28610         2.08           17928         1.75           18359         31328         0.88	LN.	Human mRNA, Xq teminal portion
13696         28726         11.83           1647e         28610         2.08           18454         2947e         1.75           17928         1.06           18359         31326         0.88	NT	Human mRNA, Xq terminal portion
16476 28610 2.08 18454 29476 1.75 17628 1.06 18359 31328 0.88	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
18454 29476 1,79 17928 1,06 18359 31328 0,88	EST_HUMAN	22/49/02.51 Socres_senescent_fibroblatte_NbHSF Homo squens cunna clone invalve_3220.11.5 sinilien to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
17928 1.06 18359 31328 0.98	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
18359 31328 0.98	NT	S.scrafa gene for skeletal muscle ryanodine receptor
	MT	Streptococcus constellatus D-alanine: D-alanine ligase gene, partial cos
21414 34940 1.41	1 EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Home seplens cDNA
22405	MT	Fugu rubripes rps24 gene
22405 35968 1.01	Ę	Fugu rubripes rps24 gene
24288	Ę	S.carevisiae NUM1 gene, involved in rudical migration control
37929 1.84	N	S.carevistae NUM1 gene, involved in nuclear migration control
25350 1.48		Streptococcus thermophilus becretopnege Strie, compreme genoune
5122 18248 31214 0.74 4.7E-02	6981261 NT	Rettus norvegicus Nestin (Nes), mixina

Page 148 of 550 Table 4 Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	ys97709,r1 Soares melanocyte 2Nb-IM Honto saplens cDNA clone IMAGE:291017 5' similar to conteins Alu repetitive element.	602143554F1 NIH_MGC_46 Homo saplent cDNA clans IMAGE:4304772 6	602143554F1 NIH_MGC_46 Homo saplens cDNA clone IMAGE:4304772 5	Rat statin-related protein (s1) gene, complete CDS	B.taurus mRNA for RF-36-DNA-binding protein	H.sapiens DNA for endogenaus retroviral like element	Gallus gallus Wokci-8 gene, complete cds	B.ta⊔rus mRNA for RF-36-DNA-binding protein	we79c10.x1 Scares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2347314 3	Bos taurus paired box protein (pax-6) gene, partlal cds	Bos taurus paired box protein (pax-6) gene, partial cds	AV648521 GLC Homo sapiens cDNA clone GLCBKD023'	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome	em60d02.s1 Johnston frontal contex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR.P90533	P90533 LIMA ;contains element LTR1 repetitive element ;	AV727059 HTC Homo saplens cDNA clone HTCBWC01 5'	INTEGROS.X1 NCI_COAP_Kid11 Home sapilers CDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN	TAILED OF VIOLE OLD COUNTY TO THE TAIL THE STATE OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TAILED OF THE TA	PMO-H 1035E-251189-003-gus Figure Septens Canna	PM0-HT0338-261 199-003-g05 H10339 Homo sapiens CONA	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cL/NA	Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnm2)	gene, complete cds	Creinhardtii atp2 (atpB) mRNA	C.reinhardtii atp2 (atpB) mRNA	qc60b06.x1 Soares_placenta_8to9weeks_2:NbHP8to9W Homo sapiens cDNA clono IMACE:1713971 3	similar to contains L1.13 L1 repetitive element;	Rattus norvegicus Cathepsin H (Ctsh), mRNA	PMO-HT0339-060400-009-G12 HT0339 Homo saplens cDNA	ol27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737.3
	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	LN.	N L	FN	NT	NT	EST_HUMAN	TN	TN.	EST_HUMAN	EST HUMAN	Z		EST HUMAN	EST HUMAN		ES TOMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT		N	Ā	٤		EST HUMAN	INT	EST HUMAN	EST_HUMAN
`  	Top Hit Acession No.	4.7E-02 W01153.1	4.7E-02 BF686625.1	4.7E-02 BF686625.1	4.7E-02 M82752.1	X15543.1	4.7E-02 X89211.1	4.7E-02 AB026678.1	4.7E-02 X16543.1	4.7E-02 AI873042.1	4.7E-02 U73621.1	4.7E-02 U73621.1	4.7E-02 AV648521.1	4.6E-02 BE153583.1	4.6E-02 AE000445.1		4.6E-02 AI014265.1	4.8E-02 AV727059.1		4.6E-02 AW 236023.1	4.6E-02 BE153583.1	4.6E-02 BE153583.1	4.6E-02 BE153583,1	4.8E-02 BE153583.1	4.6E-02 AF220365.1		4.6E-02 AF076962.1	4.6E-02 X61624.1	4.6E-02 X61624.1		4.6E-02 AI149574.1	TN 0278720	4.6E-02 BE154008.1	4.6E-02 AA913328.1
	Most Similar (Top) Hit BLAST E Vatue	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02 X15543.1	4.7E-02	4.7E-02			4.7E-02	4.7E-02	4.7E-02	4.6E-02	4.6E-02																	4.6E-02		
	Expression Signal	3.34	0.69	0.69	1.7.1	9.44	1.31	2.97	7.75	0.7	1.43	1.43	4.31	0.69	2.89		1.49	5.39		2.34	1.78	99'0	0.69				1.67				1.41	0.63		3.39
	ORF SEQ ID NO:	33823	33581				35777		36068		38535				26984			27620	<u>.</u>								32348		32888	L	33687			
	Exan SEQ ID NO:	20197	ì	20161	L		L	L	22502	L	L	L	1	<u> </u>	L	L	14478	1	_	_		16249	L	16249	ı		19042	Į.	Ł	1	20251	L		1
	Probe SEQ ID NO:	6969	7025	7025	7058	8446	20.00	9178	8428	9836	11852	11862	12446	281	758		1320	1390		2557	2869	3073	3410	3585	4239		5852	6359	88		6938	8007	8856	11689

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	Top Hit Descriptor	Human germiline immunoglobulin lambda light chain gene	RETINOIC ACID RECEPTOR BETA (RAR-BETA)	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds	Marburg virus strain M/S. Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	Kylella fastidiosa, section 110 of 229 of the complete genome	Hamo septens chromosame 21 segment HS21C078	Homo sapiens ASCL3 gene, CEGP1 gene, C11or114 gene, C11or115 gene, C11or116 gene and C11or117	United and the second of second by MCM CABA	Idno squens cindioscine zi segmenti icz i ococ	Methanosarcina frisia carbon monoxda dahydrogenasa larga subunit (odniA) gene, darbon monoxoe dehydrogenase amali cubunit (odhiB) gene, complete ods	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (odhIA) geno; oarbon menoxide	dehydrogenase small subunit (cdhlB) gene, complete cds	Arabidopsis thallana CCAAT-box binding factor HAP3 homdog gene, complete cds	EST28167 Cerebelum II Homo saptens cDNA 5' and similar to similar to neuro-D4 protein	A.europaeum mRNA for legumin-like protein	Galtus gallus mRNA for alpha1 integrin, complete cds	Homo sapiens ret finger protein-like 3 (RFFL3), mRNA	2243f11.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5	Drosophila melanogaster extradenticle (EXD) mRNA, complete cds	HYPOTHETICAL PROTEIN (ORF 2280)	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA	Myxococcus xanthus serine/threcaine kinasa Pkn10 (pkn10) gene, complete cds	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,	pertial cds	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,	partiel cds	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds	nw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA done IMAGE:1239221 3	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete	Ods
	Top Hit Database Source	Į.	SWISSPROT		TN TN	ISSPROT	Ť	±N				, ,		NT	/ IN	r_HUMAN	/ NT			EST_HUMAN	EST_HUMAN			EST_HUMAN			NT			NT	NT	EST HUMAN		LN
	Top Hit Acession No.	.6E-02 X57808.1		30.1	.6E-02 AF005730.1		94.1	1.5E-02 AL 163278.2			4.5E-02 AL163280.2	26487.1			4.5E-02 AF036884.1			4.5E-02 AB000470.1	11418013 NT	4.6E-02 AA191097.1	3.1		P31588	4.4E-02 AW875475.1	4.4E-02 AF159160.1		4.4E-02 AF109907.1		4.4E-02 AF109907.1	4.4E-02 AF095824.1	4.4E-02 AF095824.1	4.4E-02 AA736969.1		4.4E-02 AF080869.1
	Most Similar (Top) Hit BLAST E Value	4.6E-02 >	4.5E-02 P22448	4.5E-02	4.6E-02 /	4.5E-02 P32182	4.5E-02	4.5E-02/		4.55-02/	4.55-02/	4.5E-02   L26487.1		4.5E-02 L26487.1			4.5E-02 X95508.1	4.5E-02	4.8E-02			4.4E-02 L19295.1	4.4E-02 P31588	4.4E-02	4.4E-02									_}
	Expression Signal	3.14	2.24	1.52	1.62	4.83	2.2	5.04		1.63	0.84	0.59		0.59	2.24		0.47		2.61	3.70	4.35						1,33		1.33	0.59	0.69	2.34		2.64
	ORF SEQ ID NO:		26693				L				33184	33574	L	33575	35207				L		L	27273	l	28809			30866		30867			35572	L	38034
$\left[ \right]$	Exon SEQ ID NO:	25708			L	1	15312	L	1	- 1	19796	20154	1	20154	L		L	ı	L	1_	L	<u>L</u>	L	L	$I_{-}$	L.	17885	L.	17885	20350	L	L	_	24389
	Probe SEQ ID NO:	13079	480	1245	1245	1847	2177	3817		888	9839	7018		7018	8587	10155	10305	10421	12442	12891	727	1050	2163	2559	3730		4760		4750	7287	7287	8952		11326

WO 01/57272 PCT/US01/00663

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Probe E SEQ ID SE NO:	SEO ID III	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	4.4E-02 AA496739.1	EST_HUMAN	ве33f04.r1 Gessler Wilms tumar Hamo saplens cDNA clone IMAGE:897631 5'
L	25128		4.55	4.4E-02	4.4E-02 AB040928.1	П	Homo saplens mRNA for KIAA1493 protein, partial cds
_	28192		1.65	4.4E-02		T_HUMAN	601878748F1 NIH_MGC_55 Hamo saplens clone IMAGE:410/418 3
	13982	27034	7.25	4.3E-02	4.3E-02 AF003249.1		Morone saxatilis myosin heavy chain FM3A (FM3A) mKNA, complete cds
	15757	28871	1.55	4.3E-02	4.3E-02 AV704878.1	T_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5
	16682	29693	9.18	4.3E-02	4.3E-02 AL163210.2		Homo saplens chromosome 21 segment HS21C010
	16910		121	4.3E-02	4.3E-02 AF060568.1	П	Homo sapians promyelocytic leukemia zinc finger protein (PLZF) gene, complete cas
L	19785	33172	484	4.3E-02 P30427	P30427	$\neg$	PLECTIN
ı	19785	33173	494	4.3E-02	4.3E-02 P30427	П	PLECTIN
6871	20023	33433	0.8	4.3E-02	4.3E-02 AA652268.1	HUMAN	ns69c12.s1 NCI_CGAP_Pr2 Homo septents cDNA clone IMAGE:1188888
1	21791	35327	0.69	4.3E-02	4.3E-02 AF283359.1	N.	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, atternatively spliced
_	22080	35821	1,32	4.3E-02	4.3E-02 X55322.1		H.sapiens NCAM mRNA for neural cell adhesion molecule
Ţ,	-22080	35622	1.32	4.3E-02	4.3E-02 X55322.1		H.saplens NCAM mRNA for neural oall adhesion malocule
L	25291		12		4.3E-02 AL139077.2		Campylobacter Jejuni NCTC11168 complets genome; segment 4/6
	14023	27081	1.74		4.2E-02 AU123327.1		AU123327 NT2RMZ Homo sepiens cDNA clone NT2RMZ000020 5
L_	14065		2.4		4.2E-02 AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5
<u> </u>	-						wx34g01 x1 NCI_CGAP_Pitt Home sepiens cDNA clone IMAGE:2545584 3' similar to TR:U63291 U63291   U63291   U63291 U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291   U63291
919	14094	27159	1.51	4.2E-02	4.2E-02 AW003645.1	EST_HUMAN	LT RETROPOSON, OARS WINE, CONTRACT I THE PORT OF
1768	14907		1.37		4.2E-02 AL445066.1	L	Thermoplasma acidophilum complete generie, segment 4.0
1819	14968	28080	66.0		4.2E-02 P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3754	16915	28918	1.66		4.2E-02 P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
<u> </u>	17998	30882	0.59		4.2E-02 BF342995.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Hamo seplens cDNA clone IMAGE:4192072 3
L.							Homo sepiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide
200	18028	2000	0.74		4 2F-02 AF280/107.1	뒫	4 (CITSA4) and syliculturer 430 pulpepage (CITSA4) gained company and polypeptide 5 (CYPSA5) gene, partial cds
	07700				÷ ••		Homo sapiens cytochrome P450 polypeptice 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide
							4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
5735	18928	32225	0.74		4.2E-02 AF280107.1	Ŋ	polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61		4.2E-02 BE268285.1	EST_HUMAN	601124596F1 NIH MGC 8 Hano sapiens cDNA cione IMAGE: 2989319 5
7695	20760	34244	4.35		4.2E-02 AF276752.1	¥	Legionella pneumophila catalass-peroxidaso (katA) gene, compiste cos
7117	20781	34267	0.61		4.2E-02 AV730347.1	EST_HUMAN	AV730347 HTF Homo sepiens GUNA clone HTPAVHU4 3
9010	22089	35631			4.2E-02 P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAK (F-ACTIN CROSS LINNING FINCILLIN)
10367	23402	37013	1.48		4.2E-02 Q16650	SWISSPROT	I-BRAIN-1 PROTEIN (1-BOX GRAIN PROTEIN ) (1BA-1) (1ES-30)

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	Top Hit Descriptor	on33b11.s1 NCI_CGAP_Lu5 Homo sepiens cDNA clone IMAGE:1558461 3' similar to gb:M55290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);	PMS-BN0174-250500-009-d10 BN0174 Hcmo saprens cDNA	PMS-BN0174-250500-009-010 BN0174 Home sapiens cons	PRAS solate PARSV36 envelope glycqprotein gene, contracte cus	W48g10X1 NCI_CGAP_Pan1 Hamo septems contentioned as a september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september and the september an	Staphylococcus aureus H3P*10 and H3P*04 genes	Homo sapiens HPS1 gene, invol 3	Chemydia muridarum, section ou or or or the Compilere genome	601177907F1 NIH MGC 17 Home sapiens cultar crate limace. 3355555 5	601177907F1 NIH MGC 17 Home sapiens cours citate invace. Coccos o	QV1-NN0012-180400-164-106 NN0012 Homo sapiens cunh	L monocytogenes type 3 partial lap gene (strain 443)	601107635F1 NIH_MGC_16 Homo saplens cDNA ctore livia ct. 334363 5	601107635F1 NIH_MCC_16 Homo sapiens cDNA cione IMAGE::3343630 3	A thallana mRNA for plasma membrane Intrinsic protein 1a	Ursaplasma urealyticum section 33 of 59 of the complets genome	Homo sapiens KIAA0867 protein (KIAA0867), mRNA	Auto missistic proving retroducing in sertion in the CGMP-phosohodiesterase (rd beta PDE) gene, intron 1, with	Mus museulus program to organization in the environment of the proving insert encompassing the environment of end) and 3 LTR	Fugu rubiipes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1	(PUT1) gene, partial cds; mitosis-specific chromosomo eegregation protein SMC1 homolog (SMC1) gene,	complete cds; and calcium channel alpha-1 subunit>	ADAIA-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIES 1) (ADAMTS-1) (ADAM-TS1)	CITICIE COLI AGEN 34	Total College College College College CONA 5' and	ESTAZIO COION AGENDOBICITOTINI IV TOUTINI SECUENCIA CONTROL	Brassica napus gin gene tor plastid glutamire synutouses, excus	Homo saplens mRNA for KIAA1471 protein, partial cds	Human retinoblastoma susceptibility gene exons 1-27, complete ods	Homo sepiens cytochrome P450 polypopitie 43 (CYP3A43) gene, partial cds; cytochrome P450 polypopite 4 (CYP3A4) and cytochrome P450 polypopitide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CYP3A5) gene, partial cds	
	Top Hit Database Source		П	HUMAN	П	HUMAN		Ę		П	П	T_HUMAN	TN	EST_HUMAN		NT	N L			F			뉟	TORGOSIMO	CWICEDDOT	OW ISSUACE	EST HUMAN	N	F	뒫		N	
2815	Top Hit Acession No.	2E-02 AA976118.1	2E-02 BE815822.1			2E-02 A1983494.1	2E-02 D14711.1	1E-02 AF200629.1	.1E-02 AE002330.2	1E-02 BE297236.1	1E-02 BE297236.1	.1E-02 AW893484.1	.1E-02 X85880.1	.1E-02 BE251894.1	1E-02 BE251894.1		1F-02 AF002132.1	TMCASCART	TOO TOO	.1E-02 L02110.1			4.1E-02 AF026198.1	202007	ra/63/	73408/	4.1E-02 AA372398.1	4.1E-02 AJ271909.1	4.0E-02 AB040904.1	4.0E-02 L11910.1		4.0E-02 AF280107.1	
	Most Similar (Top) Hit BLAST E Value	4.2E-02/	4.2E-02	4.2E-02	4.2E-02	4.2E-02	4.2E-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4.15-02	4.1E-02	4.1E-02	4.1E-02	4.1E-02	4 1F-02	100	4.15-02	4			4.1E-02			`	,	Ĺ					
	Expression Signal	1.62	2.83	2.83	1.52	9.64	1.17	1.85	1.06	19.0	0.61	8.4	0.61	1.06	1.08	0.98	1 38	30.7	A/:L	20.08			284				0.87	9.91				5.31	
	ORF SEQ ID NO:	38002	38320	38321				26743		30168				32263	32254	1	22770		34228	34325	1		34502			35462	35988					31710	
	Ewn SEQ ID NO:	24361	24640	24640	24786	28109	25705	13716	15853	ļ.	L	1	1	1	Т	L	. L	1	20747	76806			20002	_	ł	21924			١.	1	1	18694	ı
	Probe SEQ ID NO:	11295	11587	11687	11795	12729	13076	523	2741	4005	4005	4595	232	57,50	2780	10.00		Q#7)	7682	8222	3		70/2	758/	8402	8845	9355	13112	3348	3	8	5485	

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Unigle Excit riches Expressed in raconna	Top Hit Descriptor	7h52h07.x1 NCI_CGAP_Lu24 Homo seplens cDNA clone IMAGE:3568380 3' similar to TR:O75288 O75296 R29124_1 ;	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35	Homo sapiens DNA for GP Lanchared molecule-like protein, complets ads	Homo sapiens DNA for GP-anchored molecule-like protein, complete cds	Homo sapiens erythrocyte tropomodulin (E-,TMOD) gene, exon /	GLUCOANYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)	602153884F1 NIH_MGC_83 Homo saplents cDNA clone IMAGE:4294724 5	Methanobacterium thermoautotrophicum strain Marburg, Thich turnarate reductase subunit A	Human mRNA for KIAA0082 gene, partial cds	Kluyveromyces lactis gene for Ce++ ATPase	Ovis aries mRNA for acetyl-coA carboxy/ase	UI-H-BW1-anx-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA cione IMAGE:3084134 3	FAS ANTIGEN LIGAND	M.musculus DNA for desmin-binding fragment DesD7	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (5DHC) mRNA	RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA	601649874F1 NIH_MGC_74 Homo septents cDNA clone IMAGE:3933642 6	602/38132F1 NIH_MGC_83 Homo sapiens cDNA clone INAGE:42/4910 5	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3048630 3	601506848F1 NIH_MGC_54 Homo septems cDNA clone IMAGE:41347/9 5	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3	Homo sapiens 959 kb contig between AML1 and CBR1 on onromocome 21q22, segment 1/3	ANTIGEN GOR	Felis catus G-CSF gene to granulocyte colory-sumulating textor, whithere was
CACIL I IONAL	Top Hit Database Source	EST HUMAN R	Stro				NT	SWISSPROT G				NT			ISSPROT	NT		T HUMAN				EST_HUMAN 6		T_HUMAN	H	╗	SWISSPROT	ヿ
elgi iic	Top Hit Acession Na.	4.0E-02 BF110434.1		5.2			4.0E-02 AF288153.1		76.1			4.0E-02 AJ001018.1	4.0E-02 AJ001056.1	3.9E-02 BF516149.1		3.9E-02 AJ403386.1	TN CR89034	3 9F-02 AW392417.1	8924019 NT	8924019 NT	3.9E-02 BE968841.1	3.9E-02 BF675203.1	3.9E-02 BE271437.1	3.9E-02 BF239613.1	3.9E-02 AJZ29041.1	3.9E-02 AJ229041.1		3.9E-02 AB042553.1
	Most Similar (Top) Hit BLAST E Value	4.0E-02	4 OF 001 23838 4	4 0F-02	4.0E-02	4.0E-02	4.0E-02	4.0E-02 P08640	4.0E-02	4.0E-02	4.0E-02	4.0E-02	4.0E-02	3.95-02	3.9E-02 P41047	3.9E-02	3 05.03	3 9F-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02	3.9E-02
	Expression Signal	0.98	60 4	0 71	0.8	9.8	0.61	2.62	0.63	2.48	1.88	1.52	18.34	2.79	2.15	3.22	107	790	0.9	6.0	-	0.65	76'0	1.44	9.0	9.0	1.56	3.54
	ORF SEQ ID NO:	32870	944.30	37	34503	34504				36495			31859		L			21334					L				34582	
	Econ SEQ ID NO:	19513	5	2007	20983	1	l	1	1	L	1	İ.	L		1_	1_	<u>.                                    </u>	10004	1_	1_		1	ı	ł	١	Ι_	u	26059
	Probe SEQ ID: NO:	8743		7007	7943	7843	7980	8914	9844	9869	10180	12073	12333	1144	1375	2016	3	60/7	5279	5279	5849	6977	7203	8023	8260	8250	11695	12184

Page 153 of 550 Table 4 Single Exon Probes Expressed in Placenta

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	Top Hit Descriptor	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV18S1P, TCRBV15S1, TCRBV1SS1P, TCRBV18S1P, TCRBV14S1, TCRBV18S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TC	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 3 gene, ∠inc tinger protein ∠ro, ∠inc finger protein 92, mmxq28orf	Human protein C gene, complete cds	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)	Homo sapiens ATP-binding cessette, sub-tamily A (ABC+), member o (ABCA6), mixton	Human von Willebrand lactor gene, excits 33 uniquin 34	Homo sapiens PRO0514 protein (*RO0514), mrnva	Homo sapiens PELOTA (PELOTA) gane, compiete cos	LAMININ ALPHA-1 CHAIN PRECURECHICAMININ A CHAIN)	wr85e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA cione liviAcE.x494502.5	Homo sapiens mRNA for KIAAU/18 protein, partai cas	EOWESODERMIN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5	Mus musculus potassium large conductance pH-sensitive channel, subtamily M, alpna member 3 (normas), mRNA	Aeropyrum pernix genomic DNA, section 6/7	Хую la fastidiosa, section 121 of 229 of the complete genome	ai55c09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens CLINA Gone 1300912.3	601762117F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:4024973 5	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SECCENT), minute	Odontella sinensis chloroplast, completa gianome	H.vulgare Ss1 gene for sucrose synthese	Homo saplens genomic region containing hypervariable minisatellites chromosome 10/10q26.3J or nomo saplens	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo	saplens	C.glutamicum gap, pgk and tri genes for glyceraldehyde-3-phosphate, phosphoglycerate knave and thosephosphate isomerase	Ciglutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and	
	Top Hit Database Source	۲	LN	NT	SWISSPROT	NT.	LN-	NT	NT	SWISSPROT	EST_HUMAN	NT	SWISSPROT	EST_HUMAN	LN	LN LN	N	EST_HUMAN	EST_HUMAN	NT	NT	NT	ħ		LA	ĽΝ		Z
	Top Hit Acessian No.		2		, ,	3005700	A60875.1	32563	52.2	719137	3.7E-02 AI984806.1	3.7E-02 AB018261.1	278944	3.7E-02 BF312963.1	6680541 NT	3.7E-02 AP000063.1	3.7E-02 AE003975.1	3.7E-02 AA782516.1	3.7E-02 BF124974.1	11418392 NT	11467432 NT	3.6E-02 X73221.1	3 6F-02 AL096806.1		3.6E-02 AL096810.1	3 AE-02 X59403 1		3.6E-02 X59403.1
	Most Similar (Top) Hit BLAST E Value	3.9E-02 U66061.1	3.9E-02	3.8E-02 M11228.1	3.8E-02 P10284	3.8E-02	3.8E-02 M60675.1	3.8E-02	3.8E-02	3.7E-02 P19137	3.7E-02	3.7E-02	3.7E-02 P78944					3.7E-02	3.7E-02	3.7E-02	3.7E-02	L						
	Expression Signal	2.35	64.89	0.8	1.04	1.72	1.51	0.64	1.71	4.05	6.19	76.0	1.13			0.95				3.71	1.23				0.67	2		0.61
	ORF SEQ ID NO:			31792	32736	34018		37446	37603	27248			L	L			34430	l	38837			29909			31400			31774
	Exon SEQ ID NO:	25595	ł _	1_	L	_	21943	23822	L	<u>t</u>	1	L	L	$I_{-}$	<u> </u>	1	1	1_		L	L	L	1		18430	<u> </u>		18740
	Probe SEQ ID NO:	12898	13036	5558	6212	7471	8864	10789	10888	1016	2310	2645	3115	3117	3543	7228	7880	10219	12227	12861	13069	3744	256	3102	5313		3	5543

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Single Exon Probes Expressed in Placelita	ExamMost SimilarTop Hit AcessionTop Hit AcessionTop Hit DescriptorEQ ID ID NO:SignalBLASTE No.Source	П	33408 4.48 3.6E-02 AW945516.1 EST_HUMAN	33407 4.48 3.6E-02 AW945518.1 EST_HUMAN	33761 1.79 3.6E-02 AF025952.1 NT	34009 2.89 3.6E-02 AA714521.1 EST_HUMAN	34360 0.94 3.6E-02 BE143078.1 EST_HUMAN	38218 2.18 3.8E-02 U20608,1 NT	36217 2.16 3.6E-02 U20608.1 NT	38431 0.84 3.6E-02 BF347686.1   EST HUMAN	38183 1.48 3.6E-02 BF131609.1 EST_HUMAN	38184 1.46 3.6E-02 BF131609.1 EST_HUMAN	27158 0.39 3.5E-02 U09506.1 NT	2.43 3.5E-02 AF253417.1 NT	1.4 3.5E-02 BF678085.1   EST_HUMAN	27832 1.4 3.5E-02 BFB78085.1 EST_HUMAN	17472 30457 1.83 3.5E-02 AE001773.1 NT Thermotoga maritima section 85 of 136 of the complete genome	SWISSPROT	32878 1.76 3.6E-02 J01238.1 NT	EST_HUMAN	3.6E-02 BE958970.1   EST_HUMAN	36848 0.94 3.5E-02 X76642.1 NT	36902 0.51 3.5E-02 BE561042.1 EST_HUMAN	38471 1.79 3.6E-02 AW861641.1 EST_HUMAN	38472 1.79 3.5E-02 AW861641.1  EST_HUMAN		r HUMAN	47.29 3.4E.02 AK024424.1 NT	26803 47.29 3.4E-02 AK024424.1 NT	13783 28802 3.28 3.4E-02 AK024424.1 NT Homo sapiens mRNA for FLJ00013 protein, partial cds
		L					l.													747			١.			283	304			
	SEQ ID	L	_	l	L	1	1		<u>L</u>		L	<u>L</u>	L	乚	L		ı		ł				乚	<u> </u>		_		592 1378	592 1378	
	Probe SEQ ID NO:	5617	6848	6846	7234	7458	7811	959	959	9812	11456	11456	918	1033	1595	1595	4329	4436	6351	8165	8824	10224	10270	11785	11785	12876	12956	ြိ	ຼິ	ျိ

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Top Hit Descriptor	Homo sepiens mRNA for FLJ00013 protein, partial cds	xv28d07.x1 Sogres_NFL_T_GBC_S1 Homb explens cDNA clone IMACE:2214253 3 similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE CLYCOPROTEIN C210RF1 PRECURSOR;	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA	yo20e06.r1 Stratagene lung (#937210) Homo sapiens CUNA cione IMAGE:81250 5 similiar to contains MER29 repetitive element	Homo saplens chromosome 21 segment H\$210008	RC3-FN0155-060700-011-d10 FN0155 Hamo saplens cDNA	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA	M.musculus S-antigen gene promoter region	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTORINITICEN MONICLOS)	Ceenorhebditio elegans mRNA for DYS-1 protein, partial	Human Iysyl oxidase-like protein gene, oxon 3	wi99d04.x1 NCI_CGAP_Bm25 Hamo septens cDNA clone IMAGE:2433031 3	nu70f08.s1 NCI_CGAP_Alv1 Homo septiens cDNA clone IMAGE:1216071 similar to contains Aiu repetitive element, contains element MER26 MER25 repetitive element;	annetta et Stratanene muscle 937209 Horio saplens cDNA done IMAGE:628749 3' strailer to	INCOME SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR SECURIOR 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Top Hit Database Source	NT HO	T_HUMAN .		ST HUMAN MI	Г	T_HUMAN	EST_HUMAN   RO	П	SWISSPROT L			EST_HUMAN W	EST HUMAN el	Г		П	7	T_HUMAN	S			П	L HUMAN				I HUMAN	_	EST_HUMAN 7	_
Top Hit Acession	4E-02 AK024424.1		3.4E-02 11346469 NT		12			.4E-02 X59799.1		.1		4E-02 Al869629.1	4E-02 AA684886.1			.4E-02 AA194308.1	3.4E-02 A1092719.1	3.3E-02 AA398735.1	.3E-02 AB035867.1	.3E-02 AF110783.1	.3E-02 AE000700.1	3.3E-02 R09112.1	3.3E-02 H02389.1	AF11078	6755862 NT	3.3E-02 BF245995.1	3.3E-02 BF245995.1			3.3E-02 BF115621.1
Most Similar (Top) Hit BLAST E Vatue	3.4E-02	3.4E-02	3.4E-02	3 45-02	3.4F-02	3.4E-02	3.4E-02	3.4E-02	3.4E-02 Q28457	3.4E-02	3.4E-02	3.4E-02	3.4E-02			3.4E-02	3.4E-02	3.3E-02	3.3E-02	3.3E-02	3.3E-02									
Expression	3.26	2.57	5.43	* *		0.81	3.72	2.77	1.9	1.81	4.68	3.15	1.18			5.28	0.68	6.8	1243	1.23	1.37	2.02	0.86	3.74					0.74	
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Probe SEQ ID NO:	88	1076	1233	3070	2647	3875	4030	4720	5172	5189	6983	8456	9047	3		9118	0868	383	1193	1669	1778	2149	3445	4293	4589	6560	6560	7877	8523	9523

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Top Hit Descriptor	ad08f09.s1 Soares_NbHFB Homo saplens; cDNA clone IMAGE:871673 3' similar to gb:X70844_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D6 (HUMAN)	ad08f09.s1 Soares_NbHFB Homo saplens; cDNA clone IMAGE:877673 3 similar to gp:X70844_cd31 MYOBLAST CELL SURFACE ANTIGEN 24.105 (HUMAN);	602247171F1 NIH MGC 62 Homo sapiens curva cione images 4332487 3	yek9f11.11 Soares fetal liver spicesn 1NFLS Homo sapiens cunn digne invace: 1211019	Mus musculus Eir44 gene, partiai cas, Lilwin i gene, comprete cus, and Etan gene, parca cus	Human interleukin 11 (IL.11) gene, compiese mixivA	Oryconagus cuniculus gene encoding lieal scoulin dependent bilb add authorated a	osophila melanogaster near snock protein do (nspoo) gare, napodo anate, compare de	Drosophila melanogaster near anock protein do (fishbo) gate, risposa enero, contracto dos	Homo saplens telomerase reverse transcriptase (TEKT) gone, exons 7-10 and complete cos	LARGE TEGUMENT PROTEIN	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile actor ir ansporter	601442431F1 NIH MGC 65 Homo sapiens cDNA clone IMAGE:36467.27 3	Homo sapiens chromosome 21 segment HS21CU03	H.saplens RP3 gene (XLRP gene 3)	Saxfrega nidifica maturass (maik) gene, chloroplast gene encoding chloroplast protein, partial ode	IL3-C10219-271099-022-004 C10219 Homo saplens cDNA	8. griseocameum whiG-Siv gene	S.griseocerneum whiG-Stv gene	Ratipolyomavirus left junction in cell line W98.14	ydd3h12.s1 Soares fetal Iiver spleen 1N-IIS Hamo septens CLNVA clone IMAGE i 10061 5 Sillingi to Contains. Alu repetitive element.contains LTR1 repetitive element ;	Saguinus oedipus tissue kallikrein gene, complete cds	Homo sapiens cytochrome P450, subfamily IIB (phenoberbital-Inducible) (CTF2B), misus	Mus musculus kinesin family member 3c (Kif3c), mRNA	Homo sapiens chromosome 3 subtelomeric region	qm17b04.x1 NCI_CGAP_Lu5 Homo sapians cDNA clane IMAGE:18820633	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3	zg54b12.s1 Sogres_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb.L08441 CYTOCHROME C OXIDASE[POLYPEPTIDE III (HUMAN);	Macaca mulatta chemokine receptor CCR3 mKNA, complete cus
Top Hit Database Source	EST_HUMAN M		╗	LHOMAN							ISSPROT		HUMAN	╗	E E		r_HUMAN		NT		EST_HUMAN A					T HUMAN	Г	T_HUMAN	NT
Top Hit Acession No.	3.3E-02 AA488202.1	3.3E-02 AA488202.1	3.3E-02 BF691107.1		***				3.2E-02 AF098275.1	3.2E-02 AF128894.1	3.2E-02 P28956	3.2E-02 AJ002005.1	3.2E-02 BE867353.1	3.2E-02 AL163203.2	3.2E-02 X94768.1	3.2E-02 AF114182.1	3.2E-02 AW850159.1	3.2E-02 X88709.1	3.2E-02 X68709.1	3.2E-02 M32437.1	3.2E-02 T88367.1	3.2E-02 AF173845.1	11424049 NT		AF10971	3.2F-02 AI278971.1	3.2E-02 AI278971.1	3.2E-02 AA719785.1	3.2E-02 U96762.1
Most Similar (Top) Hit BLAST E Value	3.3E-02	3.3E-02	3.3E-02	3.3E-02	3.3E-02	3.3E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02	3.2E-02			3.2E-02	3.2E-02	3.2E-02	3.2E-02		١		3.2E-02
Expression	0.67	0.57	3.28	3.1	1.6	1.85	1.79	6.32	6.32	1.08	1.09	0.87	13.21	0.94	16.42	3,85	0.93	1.49	1.49	2.4	30.91	3.7	0.92	8.04	0.67			4	1.1
ORF SEQ ID NO:	36248						28394	27370	27371			26394				31005	L	L			l	33290	L			l	36066		37207
Exon SEQ ID NO:	22679	22670	24444		ì	25398	13360	14314	14314	14961	15322	13360	16379	_	17477		L		1	i		1	L	1	1	L			23801
Probe SEQ ID NO:	9624	9624	11383	12428	12667	12591	<u>\$</u>	1150	1150	1812	2187	2902	3204	3806	4334	4890	6310	5652	5682	6653	6656	6743	7070	80%		1416	acvo	10282	10568

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Top Hit Descriptor	Homo sepiens dual specificity phosphatase 4 (DUSP4) mRNA	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)	Mus musculus adaptor-related protein complex AP-3, deta subunit (Ap3d), mRNA	Human leukemia Inhibitory factor receptor (LIFR) gene, promoter and partial exon 1	zs81e08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5	602086783F1 NIH_MGC_57 Hamo sapiens cDNA clone IMAGE:4065789 5	AV695098 GKC Homo sapiens cDNA clone GKCAVH09 5	601658879R1 NIH_MGC_69 Homo capiens cDNA clone IMAGE:3680291 3	wm57d09x1 NCI_CGAP_Ut2 Homo septents cDNA clone twa ce. 2440449 3	Enterococcus feecalis surface protein preculsor, gene, complete cos	Pityokteines minutus cytochrome oxdasse I gene, pertial ods; mitochondrial gene for mitochondrial product	ZIGSH03.r1 Scares_tests_NHT Homo sapieris cDNA clone IMAGE:727253 6	Psaudomonas fluorescens family II aminotransferase gene, complete cds	QV2-ST0298-150200-040-e09 ST0296 Homo saplens cDNA	EST74530 Pineal gland II Homo sapiens cDNA 5' end	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternativaly spliced	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo saplens mRNA for KIAA1573 protein∜parttal cds	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens CDNA clone IMAGE:294906 5' similar to contains	element TAR1 repetitive element;	za39a10,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284800 5 similar to contains	element TAR1 repetitive element;	Cyprinus carplo mRNA for inducible futric oxide synthase (INC) general	601512206F1 NIH_MGC_71 Homo capiens cuna cione imade: 3913046 3	60/512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5	Homo sapiens nuclear factor of kappa light holypaptide gene enhancar in b-cais 1 (NFKB1) gene, complete	cds	Homo sapiens nuclear factor of kappa light polypeptide gene enhancar in B-cells 1 (Nr.N.D.1) gene, complete	spo	Human dystrophin gene	602/54364F1 NIH_MGC_83 Home sapient; cDINA clone invAcE: 4250034 3	601171626F1 NIH MGC 15 Homo sapiens cDINA clone IMAGE::35450417 3	L5-H10/04-290500-108-504 H10/04 morphisms curva
Top Hit Database Source		/ISSPROT		LN TN	EST_HUMAN				T_HUMAN	뉟	- - -	EST_HUMAN	Г	T_HUMAN	Г	Т				EST_HUMAN		EST_HUMAN	NT	EST_HUMAN	EST_HUMAN		NT		LN⊤	N	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	4503418 NT		6871564 NT	U78104.1	3.1E-02 AA278478.1	1E-02 BF687742.1	3.1E-02 AV696098.1	3.1E-02 BE965092.2	3.1E-02 AI872302.1	.1E-02 AF034779.1	3.0E-02 AF187125.1	3.0E-02 AA402242.1	3 DE-02 AF247644.1	3.0E-02 AW820223.1	0F-02 AA364003.1	OE-02 AF281074.1	.0E-02 AF281074.1	0E 02 ABOAR703 4	1:00 (0.00)	.0E-02 N89615.1		3.0E-02 N99615.1	3.0E-02 AJ242906.1	3.0E-02 BE889948.1	3.0E-02 BE889948.1		3.0E-02 AF213884.1		3.0E-02 AF213884.1	3.0E-02 M86524.1	3.0E-02 BF679706.1	3.0E-02 BE512670.1	3.0E-02 BF353889.1
Most Similar (Top) Hit BLAST E Value	3.1E-02	3.1E-02 P18845	3.1E-02	3.1E-02 U78104.1	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.0E-02	3.0E-02	3 0F-02	3.0E-02	3 OF-02	3 0E-02	3.0E-02	200.00	3.01-02	3.0E-02		3.0E-02	3.0E-02	3.0E-02	3.0E-02		3.0E-02			3.0E-02			ı
Expression Signal	1.92	1.46	1.28	1.29	28	0.77	0.58	0.48	0.48	2.67	2.41	1.08	2 82	0.93	0 0	8 17	8 17	6	3.41	0.67		0.67	2.87				28.1		1.92	1.22	0.48		0.74
ORF SEQ ID NO:		27569	28184	31449		32259		35764		36864			20008				34254	1		32910		32911		١	1	l	33497		33498				35459
Exon SEQ ID NO:	14445	İ		Г	1		21204	ļ	22415	<u></u>	44805		I.		1.	_L		1	00/81	19553	L	19553	20244	ì	20100	1_	20083	L	20083			1	21921
Probe SEQ ID NO:	1280	1333	1940	5378	5476	5784	8122	9142	9339	10237	1852	2852	277.5	2830	907	4000	200	5	ğ	6384		288	6929	787	7647		7218		7218	7380	8317	8821	8842

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				٠	: 5	5221	
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Sœurce	Top Hit Descriptor
8993	22072		1.93	3.0E-02	3.0E-02 AF275654.1	TN	Ornithorhynchus anathrus coagulation factor X mRNA, complete cds
10677	1	37319	2.03	3.0E-02			Thermotoga maritima section 109 of 136 of the complete genome
10770	1	37426	0.47	3.0E-02	3.0E-02 Z21211.1	T_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	<u> </u>		2.26	3.0E-02	3.0E-02 M81367.1	NT	Human coagulation factor VII (FT) gene exon 1 and factor X (F10) gene, exon 1
11989				3.0E-02	3.0E-02 AA483219.1	EST_HUMAN	ne87f04.s1 NCI_CGAP_Kid1 Home sapiens cDNA clone IMAGE:911263
12536	1	L	1.95	3.0E-02	.0E-02 R32019.1	EST HUMAN	yhe3d04.s1 Soares placenta Nb2HP Homo sapiens cDNA cione IMAGE::134407 3
12943	1		11.62	3.0E-02	.0E-02 AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Hcmo sapiens cDNA
12989	26161		4.97	3.0E-02	3.0E-02 AF048687.1	M	Rettus norvegicus UDP-Galiglucosyceremide bete-1, 4-galactosytransferase mRNA, complete ods
3650		29826		2.9E-02		뒫	Sheep gene for ultra high-sulphur keratin protein
4039		30208		2.9E-02	2.9E-02 H72805.1	EST_HUMAN	yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5
6188	1		1.39	2.9E-02	29E-02 AF060221.1	M	Sus sorofa deoxyribanucleace II mRNA, complete cds
6421	ı				2.9E-02 BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_65 Homo sepient oDNA clone IMAGE:3856598 5
7398	1	l	9.95	``	2.9E-02 BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Home saplens cDNA clone IMAGE:3049830 5
7584	1	l		``	.9E-02 D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
	1					!	Buchnera aptidicola natural-host Schlechtendalla chinensis gluconate-8-phosphate dehydrogenase (gnd)
8187	21269	34793	0.82	2.9E-02	28E-02 AF129279.1	Z	gare, para wa
8487	21200	34704	0.82	2.9E-02	2.9E-02 AF129279.1	Z	Buchneta aphidiona naturarnos, contecnicana universible graduina o proopriedo de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Service de 1900. Serv
9850	1			2.9E-02	2.9E-02 AW875979.1	EST HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
0850	1_			2.9E-02	2.9E-02 AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo saplens cDNA
10078		l			2.8E-02 AW976597.1	EST HUMAN	EST388706 MAGE resequences, MAGN Homo saplens cDNA
10553	l				2.9E-02 AP000064.1	FN	Aeropyrum pernix genomic DNA, section 7/7
11303	L	29826			2.9E-02 X65294.1	TN	Sheep gene for ultra high-sulphur keratin protein
12538	<u></u>				2.9E-02 AU135817.1	<b>EST_HUMAN</b>	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5
579	L		0.76		2.8E-02 AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo caplans cDNA
3453	┸	29639			2.8E-02 AF066063.1	LN LN	Homo saplens retinal fascin (FSCN2) gene, exon 2
3453		\			2.8E-02 AF068083.1	LN TN	Homo sapiens retinal fascin (FSCN2) gene, exon 2
4430			0.76	2.8E-02	2 8393751 NT	1	Rattus norvegicus microtubule-associated protein tau (Mapt), mKNA
5805		31866	11		2.8E-02 BE741083.1	EST_HUMAN	601594078F1 NIH MGC 9 Hamo sapiens CUNA cione IMACE: 3948007 9
8948	<u> </u>	33699	1.08		2.8E-02 T78960.1	EST_HUMAN	yd21b08.r1 Soares fetal liver spieen 1NFLS Home sapiens cunA done IMAGE: 100000 o
8523	L.	35142	1.67		2.8E-02 AJ005820.1	L'N	Craterostigma plantagineum mKNA for nomeodomain leudine zipper protein (III2-1)
9219	L		0.75		2.8E-02 AA280762.1	EST HUMAN	2898c06.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IIMACE:7114c0 o
9409	L		1.41		2 AF187872.1	L	Cavia porcellus inwardly-rectifying potassium channel Nrz.1 (NCNJZ) gene, complete cus

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Single Exoli Propes Education	Top HIt Descriptor	Vaccinia virus ORF1L, strain Wyeth	Rattus norvegicus Nerve grawth factor receptor, fast (Ngtr), mKNA	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	ak2f04.s1 Scares_testis_NHT Homo sapleris cDNA clone IMAGE:1406719 3	Homo sapiens KIAA1070 protein (KIAA1070), mKNA	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (A i P9) gene, mitochonaria gene encoding mitochondrial protein, complete cd®	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (A I P9) gene, mitocnondra gene encoding mitochondrial protein, complete cdė	Homo sapiens chromosome 21 segment HS21C103	zs84c02.r1 NCI CGAP GCB1 Homo sapieris cDNA clone IMAGE:704162 5	III.HE-RND-aki-2-10-0-ULT NIH MGC 50 Homo sapiens cDNA clone IMAGE:3077468 5	SPONTRANTET NCI CGAP Bring Homo sariens cDNA done IMAGE:4160944 6	100000 Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches Inches In	mo sapiens nypognegical prodein FLU 10124 (FLU 10124), ilin ilin ilin ilin ilin ilin ilin ili	yos607.51 Soares Intent brain 1NIB Homo Rapiens CLINA Clure IMAGE. 22043 3 Suring N. Comains Down	repetitive element;	ONZBIOS yo NCI_CGAP_LUO HOMO Saplaire (CDAP_CLOSO)	on26f08.y5 NCI_CGAP_Lu5 Hcmo sapiens cl./NA cione IMMAGE: 135/02/13	601880305KZ NIH MGC 33 HOMO SEPTEMS CON ALL HAVE CORPORATE	601680305R2 NIH MGC 83 Homo sapiens culva done liwa de 33500000 3	Rettue norvegicus rabpniin-34 mrtna, complete cus	H.carterae mKNA Tor Tucoxentrin chigophyl age binging process.	-	PMZ-NN0128-08070U-001-a12 NN0126 moins sapiens conn	PM2-NN0128-080/00-001-612 NN0128 Homo sapiens conva	hf36h08.x1 Soares_NFL_T GBC 31 Homo saprens cDNA done INAGEL: 20-20-20-20-20-20-20-20-20-20-20-20-20-2	2x83c10,x6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:610354 3	7630e09.x1 NCI_CGAP_Lu24 Home sapieris cDNA done IMAGE:3284008 3' simitar to contains L1.t1 L1	repetitive element;	601579393F1 NIH_MGC_9 Homo septens cDINA clone IMAGE:3928004 o	Chlamydomones reinhardtii VSP-3 mRNA, complete cos	602070562F1 NCI_CGAP_Bm64 Homo sapiens cUNA clone IMAGE:4213409 3	602070562F1 NCI_CGAP_Bm84 Home sapiens cDNA clone IMAGE:4213406 5	Chiamydomonas reinnardul class II DIVA prigudyase (Frink) gene, company co
EXOIL FIGURES D	Top Hit Database Source	NT		SWISSPROT AL	EST_HUMAN ak		S) IN	S E		T HI IMAN	T	Т	ביייייייייייייייייייייייייייייייייייייי			╗			1	T HUMAN				_	HOMAN	EST_HUMAN h	EST HUMAN Z		EST_HUMAN R	T HUMAN		П	T_HUMAN	5 ₩
algue	Top Hit Acessian No.	2.6E-02 Z99064.1	6981271 NT		46.1	11432020 NT	2.6E-02 AF114952.1	2 AE_02 AE114952 1	Ī	I	AMERICAN 4	2.6E-02 AW 500547.1	2.6E-02 BF343827.1	11422936 NT		2.6E-02 R43678.1	Ai793130.1	2.5E-02 AI793130.1	2.5E-02 BE974314.1	2.5E-02 BE974314.1	2.5E-02 U12571.1	2.5E-02 X99597.1	2.6E-02 X99697.1	2.6E-02 BE701165.1	2.5E-02 BE701165.1	2.5E-02 AW592114.1	2.5E-02 AI732776.1		2.5E-02 BE670128.1	2.5E-02 BE746888.1	2.5E-02 L29029.1	2.5E-02 BF528722.1	2.5E-02 BF626722.1	2.5E-02 AF129458.1
	Most Similar (Top) Hit BLAST E Value	2.6E-02	2.6E-02	2.6E-02 P21894	2.8E-02	2.6E-02	2.6E-02	2 AE.02	2 BE-02	20102	2.0E-02	2.65-02	2.6E-02	2.6E-02		2.6E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.6E-02	2.5E-02	2.6E-02				2.5E-02				
	Expression Signal	0.83	6.63	0.65	0.73	1.24	0.78	0 70	200	10.0	8.	1.35	1.43	1.32		1.39	1.75	1.75	9.64	5.83	2.53	2.95	2.95	0.92	0.92	4.66	0.72		4.88	3.72	0.8			0.64
	ORF SEQ ID NO:	33620	33520	33999	35316				24064				31553				28762	<u> </u>	27088			29219	L	30302	30303			L			32894	34400		34570
	Exon SEQ ID NO:	20194	20103	20528	1.	L			L			- 1		25392	L	25658	13738	L	14010	ı	15935	16197	16197	18468	18468	1	L	L	19494		L		1	21058
	Probe SEQ ID NO:	8988	7050	7449	8703	9560	9915	. 8		41001	11670	11861	12480	12583		12947	545	546	832	892	2821	3021	3021	4156	4156	4322	5R30		6322	6338	6466	28	7843	8008

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	Top Hit Descriptor	801108291F1 NIH MGC 16 Homo sapiens CDNA clone IMAGE:3344278 5	A CONTRACTOR OF THE SPECIFIC SECRETED DORSALIZING FACTOR)	CHOKUIN PRECORSON (Chokularis Child Chokularis Marie 1981)	WILDER OLD TO THE GOOD THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE 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complete ode	GO1652365R2 NIH_MGC_82 Homo saplent cDNA clone IMAGE:3935513 3	tc72c07.x1 Soares_NhHMPu_S1 Homo sapiens aDINA dana IMAGE.2010130 3	W75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens clove clone INASCE. 211149 5	H-2 CLASS I HISTOCOMPA HIBITITY ANTICEN, N-B ALTHA CHAIN PRECURSOR (H-2K(B))	H-2 CLASS I HIS I OCOMPA I DICIT I AN I I GEN, IND ALL II A CHINA COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION COMPANION 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Homo saplens dJNA done IMACE:2535/0.5 stituital to contains. All repetitive element contains A3R repetitive element;	7x35cr1 st 3cares feld liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:294596 3' similar to	objK02909JRATSR7K Rat (rRNA);contains A3R.b1 A3R repetitive element;	Borrella burgdorferi (section 11 of 70) of the complete genome	zuj91006.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:745364 3' similar to go04424 iSLE I AMYLOID POLYPEPTIDE PRECURSOR (HUMAN);contains Atu repetitive element;contains element XTR	XTR repetitive element;
	Top Hit Database Source	MAN ILL TOD	LONDI LICE	SWISSPROT	EST_HUMAN	Ę	EST_HUMAN	SWISSPROT	SWISSPROT		TN	IN	NT	IN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	۲	EST HUMAN	EST_HUMAN	Ę	¥	EST_HUMAN	LN.	EST HUMAN		EST_HUMAN	N TN		EST_HUMAN
,	Top Hit Acession No.	100,000	-		.5E-02 AW025821.1	71303.1	.5E-02 AI147615.1	10335	110335		5E-02 AF050157.1	2.5E-02 AB007546.1	11420078 NT	11433220 NT	160169.1	2.6E-02 BE973327.1	2.4E-02 AI378582.1	165884.1	901901							2.4E-02 AW813007.1	2.4E-02 M16780.1	2 AE.02 H78376 1	5.00	2.4E-02 N69442.1	2.4E-02 AE001125.1		2.4E-02 AA625660.1
	Most Similar (Top) Hit BLAST E Value	- 60	2.5E-02 B		2.5E-02 A	2.5E-02 X71303.1		2.5E-02 Q10335	2.6E-02 Q10335		2.55-02	2.5E-02	2.6E-02	2.5E-02	2.5E-02 U60169.1	2.8E-02	2.4E-02	2.4E-02 H65884.1	2.4E-02 P01901	2.4E-02 P01901	2.4E-02 J05110.1	2.4E-02	2.4E-02	2.4E-02 X12925.1	2.4E-02	2.4E-02	2.4E-02	20.70	7.4.7				
}	Expression Signal		0.5	0.92	0.57	0.63	0.65	1.71	1.71		2.83	1.87	2.17	1.29	183	88.	4.			1.38	1.69	98.0	1.2	1.11	1.11		0.57	2 67	600	11.69			0.81
	ORF SEQ ID NO:		34768	35645	35785		37468									32032						32871			33929					35344	l		35831
	Exan SEQ ID NO:	1	21249	22104	22242	23306	23843	24125	24125		24182	25046	ı		1_	L	L			L	1		1	1	20464	ı	L		2/12	7.808			22289
	Probe SEQ ID NO:		8167	9025	9164	10271	10810	11048	11048		11120	12065	12410	12821	40740	12760	178	1828	2102	2102	4488	48	7370	7386	7386	8074	8120		8636	8778	2 6	Ď.	9211

Page 162 of 550 Table 4 Single Exon Probes Expressed in Placenta

					Vingi	EXOII FILLI	Single Exon Probes Expressed in Fracelina
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
9893	22933				2.4E-02 AF124160.1	뒫	Arebidopsis theliana motybdopterin synthase sulphurylase (cnx5) gene, complete cds
9893	<u>L</u>	36517					Arebidopsis thaliana molybdoptenn symhase sulphurylase (crixo) gene, cumpled cus
- - - - -	L	36643	2.75		2.4E-02 AV692954.1	EST_HUMAN	AV692954 GKC Home sapiens culvia cione civicus cus o
10186	ŀ	36817	2.82		2.4E-02 AA493894.1	EST_HUMAN	nh07b12s1 NCI_CGAP_ITM Homo sapiens CDNA clone Invace: 945305 similar to contains and reproduce element:
10839	1		0.6			EST HUMAN	801274962F1 NIH MGC_20 Hamo septens aDNA clone IMAGE:3013902.3
11874	ļ	38557	2.45		2.4E-02 AF109905.1	Fu	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11874	1	38558	2.45		2.4E-02 AF109905.1	TN	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12210	1	Į.	3.98			TN	Bacteriopinage bl. 67, complete genomo
12362		32116	4.45	2.4E-02	6753635 NT	뒫	Mus musculus DinB homolog 1 (E. Odi) (Dinb1), mKNA
12478	l				2.4E-02 U78167.1	LZ LZ	Rettus norvegicus cAMP-regulated guanina nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12478	į .	32098	1.38		2.4E-02 U78167.1	TN	Rettus norvegicus cAMP-regula:ed guanine incleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12888	25445		10.87		2.4E-02 AB008569.1	NT	Ceenorhabdius elegans michal id transmilli subuint o michala accominate conjugate desperance de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala accominate de la confusion michala acco
12697	L		1.28		2.4E-02 N42980.1	EST_HUMAN	W08a08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2/0010 0
12883		31858	1.25		2.4E-02 AA179693.1	EST_HUMAN	2013h01.r1 Stratagene fetal retina 937.202 Homo sapiens cipira cipira livia CE.300204 9
192	1_	L	625		2.3E-02 W05340.1	EST_HUMAN	Z884g08.r1 Soares fetal lung North Few Homo sapiens CONA civile intro China Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Co
1836	1		16.26		2.3E-02 U94165.1	LN L	4 Homo saplens mammary tumor-associated protein INTO (INTO) gene, excit 4
2065	1		66.0		2.3E-02 AW 797355.1	EST HUMAN	CM2-UM0038-290400-172-011 UM0030 Remo 38ptens volva
2426	L				2.3E-02 Z74293.1	Ŋ	S.cerevisiae chromosome IV reading frame Cirk Tolkasok
377;	L		7.02		2.3E-02 Z20377.1	EST HUMAN	HSAAACADH P. Human togtal brain Whole ussue notific september of the
3807	7 16867		0.67		2.3E-02 L23429.1	LN.	Canis bela-galactosides-cinding facin (LCALSS) mixtry, sella
4267	7 17412	30398		1	2.3E-02 L24789.1	LN L	Gallus gallus connexin 45.6 (CX45.5) gene, complete cus
4267		2 30399	1.17		2.3E-02 L.24799.1	LN.	Gallus galus connexin 45.0 (CAAS.O) gales, compress con
454	17678	30660	1.08		2.3E-02 AW899107.1	EST HOMAN	CM4-NN0080-Z9040U-10U-0U4 NN0000 From Septems CDNA
4571	1 17709	30689			2.3E-02 BE935225.1	EST HUMAN	CM3-MI 0118-010900-316-gu/ MI 0110 Fiding Sapiens CDNA
4571	17709				2.3E-02 BE935225.1	EST HUMAN	CMA-MID118-010900-310-got MID United Septemble Colors
4572	ı	9 30691			2.3E-02 AW 593693.1	EST HUMAN	XS25408 X1 NC; CGAP, OL nomo sapiens conva cio le livroci. 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1 con 1

Page 163 of 550 Table 4 Single Exon Probes Expressed in Placenta

WO 01/57272

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslan No.	Top Hit Database Source	Top Hit Descriptar
4572	18469	30692	1,2	2.3E-02	2.3E-02 AW593693.1	EST_HUMAN	xs25d08.xf NCI_CGAP_Ut2 Hamo saplens cDNA done IMAGE:27705713'
4717	17852		3.01	2.3E-02			601672279F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:3855386 5
4717	17852	30836	3.01	2.3E-02	2.3E-02 BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Hano sapiens cDNA clone IMAGE:3955385 5
5144	18267	l	6.0	2:3E-02		EST_HUMAN	RC2:CN0051-290100-011-e07 CN0051 Homo sapiens cDNA
5265	18384	31349	0.62	2.3E-02	2.3E-02 AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma sudunit 11 minnA, compieie cus
5285	18384			2.3E-02	2.3E-02 AF257110.1	NT	Rattus norvegious guanine nucleotide binding protein gamma subunit 11 mKNA, compiete cos
				20 20 0	225 02 (188303 1	5	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cos, and propriorry-con- cerboxylase beta chain (occB) homolog gene, partial cds
2481 2365	18080	32804	0.62	2.3E-02	-	EST HUMAN	601822821R1 NIH_MGC_77 Homo septent cDNA clone IMAGE:4042829 3'
878g	1001		4	2.3E-02			Arabidopsis thallana DNA chromosome 4, contig fragment No. 17
710	18545		0.69	2.3E-02		EST_HUMAN	MRG-HT0080-011099-002-c09 HT0080 Haino sapiens cDNA
7810	20680			2.3E-02		N.	Homo sapiens chromosome 21 segment HS21C103
8080	21143		4.62	2.3E-02		LN	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8887	1				-	Ę	Home sapiens PDX1 gene for tipoyl-containing component X exons 1-11
8667	L				2.3E-02 AJ298105.1	TN	Home sepiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	1	L				EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147.3
8894	ı	35510	0.75		2.3E-02 AI685380.1	EST HUMAN	wa76h10.x1 Soaras_NFL_T_GBC_S1 Homo sapiens cDNA clone liwAGE:2302147.3
8338	1		0.84			SWISSPROT	HYPOTHETICAL 55.8 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10063	_	38704			2.3E-02 P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	1_		1.44			L	Escherichia coli K-12 MG1655 section 89 di 400 di the complete genome
10236			1.44		2.3E-02 AE000199.1	NT	Excherichia coli K-12 MG 1655 section 89 di 400 di the complete genome
1102	l	37739	2.38		2.3E-02 P08840	SWISSPROT	GLUCOAMYLASE 31/32 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-GLUCOAN) GLUCOHYDROLASE)
12338		L			2.3E-02 BE278331.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3346567 5
12801	<u>L</u>		1.78		2.3E-02 BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sablens cUNA clone living CE.4101434 5
12801	L		1.78		2.3E-02 BF528462.1	EST_HUMAN	602043628F1 NCI_CGAP_Brn87 Homo sapiens cUNA cione liviA cE. 4 to 1454 5
12819	L	31974	2.47		2.3E-02 U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase procursor gene, complete cos
12975		l	1.88		2.3E-02 U11077.1	LN L	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
	L.				2 DE 02 NEW 10287 1	FA	Columba livia nucleoside diphosphate Knasė (NDPK) gene, ruclear gene encoding mitochondrial protein, complete cds
756	1	70987			Arutozot.		Hammedomein believes OND hinding protein 2 (CHD2) mRNA
1786					4557448 NT	N	HOMO SAPERIS CHICATOLIST CHICATOLIST CONTROL FOR THE CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL C
1800				١	2.2E-02 P07313	SWISSPROT	MYCON LIGHT CHAIN KINAGE, ONE LETAL MICOLE (MECK)
1800	14949	9 28043	2.94		2.2E-02 P07313	SWISSPROT	MYCSIN LIGHT CHAIN RIPAGE, GRELE INT. WOOGLE (WEGG)

Page 164 of 550 Table 4 Single Exon Probes Expressed in Placenta

Top Hit Descriptor	S.pneumonlae popA gene and open reading frames	m24e04.c1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:10847823	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds	PM0-BT0340-170100-004-b03 BT0340 Homo saplens cDNA	S.cerevisiae chromosome IV reading frame ORF YDL245c	S.cerevisiae chromosome XVI reading frame ORF YPL241c	AV699721 GKB Homo saplens cDNA clone GKBAND03 3'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	P. wigata alpha tub 2 mRNA	Mue musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5	Mus musculus partial FBPass 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (ULEC1, ORC1L3, ORC1L4 genes,	(complete cds)	Mus musculus Sjogren syndrome anugen A1 (5881), mKNA	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive	element	AV761502 MDS Hamo sepiens dUNA cione MDSADGUT 3	Dictyostelium discoideum histidine kinese C (dhkC) mRNA, complete cas	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes,	complete cds	Mus musculus macrophage migration inhibitory tactor (MIF) gene, 3 hanking region and partial cas	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5 Hanking region and partial cos	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	Tegula aureotincta major acrosomal protein precursor (TMAP) mRNA, complete cds	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens oDNA	PM2-BT0548-120100-001-f11 BT0546 Horio sapiens cDNA	yx43h07.r1 Soares melanocyte 2NbHM Honio saplens cDNA clone IMAGE:264541 5'	2x63b09.r1 Scares_total_fetus_Nb2HF8_9w Home sapiens cDNA clone IMAGE:798121 5	S.cerevisiae chromosome IV reading frame ORF YDL245c
Top Hit Database Source		EST_HUMAN	TN	EST_HUMAN	NT	L	EST_HUMAN	NT	TN	NT	NT	NT		ΝŢ		Ā	NT		EST HUMAN	EST_HUMAN	LN		INT	NT	NT	SWISSPROT	SWISSPROT	SWISSPROT	¥	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT
Top Hit Acession No.	2.2E-02 Z82001.1	2.2E-02 AA577785.1	2.2E-02 AF083094.1	2.2E-02 AW601317.1				2.2E-02 AL161515.2	2.2E-02 AL161515.2	2.2E-02 X79468.1	2.2E-02 AJ243025.1	2.2E-02 AJ243025,1		2.2E-02 AB026898.1		2.2E-02 AB026898.1	6678140 NT		2.2E-02 AA503553.1	2.1E-02 AV761502.1	2.1E-02 AF029726.1		2.1E-02 U72073.1	2.1E-02 AF204395.1	2.1E-02 AF204395.1	2.1E-02 P02438	2.1E-02 P02438	2.1E-02 P02438	2.1E-02 AF190899.1	2.1E-02 BE072546.1	2.1E-02 BE072548.1	2.1E-02 N29266.1	2.1E-02 AA481271.1	2.1E-02 Z74283.1
Most Similar (Top) Hit BLAST E Value	2.2E-02	2.25-02	2.2€-02	2.2E-02	2.2E-02 Z74293.1	2.2E-02 Z73597.1	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02	2.2E-02		2.2E-02		2.2E-02	2.2E-02				2.1E-02			2.1E-02	2.1E-02	2.1E-02								
Expression Signal	2.17	2.03	4.09	0.98	68.0	1.37	3.43	1.41	1.4.1	0.82	0.48	0.48		2.73		2.73	1.26		6.8	4.48	6.62		6.65	1.31	1.31	0.87	0.97	0.97	0.97	1.16	1.18			
ORF SEQ ID NO:	28329	L		30116	30195				35189			1		36511		36512							27514	27644	L				28264					
Exan SEQ ID NO:	15212	ı		•	L	18299	1		L	1_	L			22928		22928	23444		25421	13627	_	L	14448	14571		L		L	1	1			1	
Probe SEQ ID NO:	2072	3521	3736	3968	4028	6177	7398	8568	8568	808	9856	9826		8888		9888	10409		12625	432	462		1292	1418	1418	1823	1823	1823	\$ E	2000	2000	787	3674	4249

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Top Hit Descriptor	602016306F1 NCI_CGAP_Brin64 Homo sapiens cDNA clone IMAGE:4151161 5'	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Home sapiens cDNA clone IMAGE:2371509 3	A.thaliana mitochondrial genome, part A	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA cione IMAGE:1120918.3	wh54e05.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2384528 3	601671411F1 NIH_MGC_20 Hano sapiens aDNA clone IMAGE:3954410 b	CM4-HT0244-111199-040-h05 HT0244 Harno sapiens cDNA	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens GUNA	Mus musculus sorting nexth 1 (Shx1), mKNV,	em83e07.s1 Stratagene schizo brain S11 Homo sapiens cunna done imAGE:10287323 strillar lo contains Alu repetitivo element;contains element MER11 repetitive element ;	Homo sapiens partial 5-HT4 recoptor gene, exons 2 to 5	Homo saplens partial 5-HT4 receptor gene, oxons 2 to 5	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and	UmuD MucA homolog genes, complete cds; and unknown genes	am83e07,e1 Stratagene schizzo brain 911 Hörnö sapiens cDNA clone iMAGE:1629732 3' similar to contains. Atin remettine element contains element MER11 repetitive element ;	B. III. Eddings contain DNA confirm 12/14		Mus musculus heat shock protein, 74 kDa, A (rispasa), minna	RC4-CN0050-130200-012-n04_1 CN0050 From Sapiens curva	Homo capiens putative psin-fibA pseudogene for neir Keraiur, exturis 2 w /	Human germline UBETL gene similar to trie ijene ior ubiquiur activatiig erizyriie, exciis 1722.	Azospirilum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds	7g51c08.x1 NCI_CGAP_Pr28 Home saplen's cDNA clone IMAGE:3308998 3' similar to contains MEK1.t3	MER repetitive element;	QV4-NNB038-270400-187-h05 NNB038 Homo saprens curva	Mus musculus DinB homolog 1 (E. col) (Umb1), many	ea15510.r1 Soares_NhHMPu_S1 Homo caplens cDNA clone IMAGE:813307 5	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mKNA	Homo capiens genomic region containing hypervariable minisaleilles chronosome 1 (1550-55) ur numo sepiens	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
Top Hit Database Source	EST HUMAN 6	NT	EST_HUMAN W		EST_HUMAN a	EST_HUMAN w	П		T HUMAN		EST HUMAN A	Г		63	ار LN		NUMPL SI			T. HUMAN		Į.	NT		П	T_HUMAN		EST_HUMAN		Ę	
Top Hit Acession	2.1E-02 BF343655.1		-	.1E-02 Y08601.1	2.1E-02 AA665737.1	.1E-02 AI823432.1	.1E-02 BF026405.1	.1E-02 AW379529.1	.1E-02 BF086199.1	9790238 NT	2.1E-02 AA984288.1	Γ			29324.1	;		2.1E-02 AP001519.1	6754255 NT	2.1E-02 AW844320.1	2.1E-02 Y19213.1	2.1E-02 L34170.1	2.1E-02 AF183913.1		2.0E-02 BF002932.1	2.0E-02 AW895565.1	F153635 NT	2.0E-02 AA456538.1	6753635 NT	2.0E-02 AL086805.1	8922391 NT
Most Similar (Top) Hit BLAST E Value	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02/	2.1E-02		2.1E-02 L29324.1	1	Z.1E-0Z/	2.15-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02		2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02
Expression	0.89	2.14	29.	5.95	0.75	0.89	16.0	0.6	0.73	99'0	0.54	2.49	2.49		1.15		0.73	0.49	1.48	1.42	11.16	1.22	3.82		128	14,95	5.03	2,95	3.63	860	
ORF SEQ ID NO:	30549			30953			31402		33490		36322		36454		36820				38474			31862	31938		26257						ł
Exon SEO ID NO:	17887	17705	17714	17864	L	_	1.	L	<u> </u>	İ	77757	ŀ.	22871	L	23226			23880	L	L	1		25712	L	13257	L	L	1	<u></u>	1	1
Probe SEQ ID NO:	4477	4567	457	4831	4852	4940	6316	5756	7212	8716	200	983	983	3	10189		10266	10856	11787	12063	12602	12647	13091		19	8	269	ဗ္ဗ	821	;	1226

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Top Hit Acesskon Dalabase No. Source	8922391 NT Homo sepiens hypothetical protein FLJ10379 (FLJ10379), mRNA	8922453]NT Homo sepiens hypothetical protein FLJ10486 (FLJ10486), mrkNA		ĽZ		EST_HUMAN		05474 NT	¥		EST_HUMAN	F	LN	LN.	NT		N.	D88184.1 NT Equus capallus DNA for 1 tapties not services, consistent of management of tables and tables and tables are serviced to take tables and tables are serviced to take tables and tables are serviced to take tables and tables are serviced to take tables and tables are serviced to take tables are serviced to take tables and tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables are serviced to take tables		7055	EST_HUMAN		EST_HUMAN		ESI HUMAIN	N	N	EST_HUMAN	EST HUMAN	F	EST HUMAN	2.1 FST HUMAN		EST HUMAN
	TN T	3 NT	TN &	'n		EST_HUMAI		TN 4	Ę	Ľ.	EST_HUMA	LN	TN	TN	NT	EST_HUMA	N N	Ę	55 NT	55 NT	EST_HUMA	L N	EST_HUM	10	ESI HUM	Ž	۲.	EST_HUM	EST_HUM	Ä	EST HUM	EST HUM		EST HUM
Top Hit Acessla No.	892238	892245	892246	2 0F-02 At 181532.2		2.0E-02 BF002832.1		73054	2.0E-02 AF095588.1	2.0E-02 M18095.1	2.0E-02 AIZ71995.1	2.0E-02 1.35321.2	2.0E-02 AP000004.1	2.0E-02 AP000004.1	2.0E-02 U70408.1	2.0E-02 AI640342.1	2.0E-02 Z73968.1	2.0E-02 D88184.1	109470	109470	2.0E-02 AA456538.1	2.0E-02 AL 161532.2	2.0E-02 T80037.1		1.9E-02 AA57Z764.1	1.9E-02 AL163303.2	1.9E-02 AL163303.2	1.9E-02 AA713858.1	1.9E-02 AV648689.1	1.9E-02 AB033611.1	1 0F.02 N52250 1	4 OF 02 BE738088 1	100000	1.9E-02 Al301183.1
Most Similar (Top) Hit BLAST E Value	2.0E-02	2.0E-02	2.0E-02	2 OF 402		2.0E-02		2.0E-02	2.0E-02	2.0E-02	2.0E-02	20E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02															
Expression Signal	0.91	187	1.84	200	2.72	1.56		1.13	1.89	1.57	0.74	0.59	0.95	0.95	2.39	1.84	1.85	191	2.04		1.8	2.26	5.63				4.85	9.15			1 12	21.1	6	0.83
ORF SEQ ID NO:	27449					26257				30267		32520				37210	37592		38684	L	31535					L	28359	L	29217	l				9 29971
Exen SEQ ID NO:	14386	15085	15085	200	200	13257	1	16387	١.	<u> </u>	18341	ļ	1	20787	23119	23805	L	1_		<u> 1</u>		15973		i .		16237	L	L	1	1	L		16804	16968
Probe SEQ ID NO:	1228	1625	1022		7827	3148		3213	3299	4113	6248	8518	1123	77.23	10084	10570	10879	11653	11978	11978	12149	12844	13186		711	2097	2897	2970	39.48	3333		999	3783	3808

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. Top Hit Descriptor		Mus musculus carbonic anhydrase IV gene, complete cds	QV2-NN1073-220400-159-h09 NN1073 Homo septens cDNA	Mus muscufus microtubule-associated protein 2 (Mtap2), mMNA	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5	601877026F1 NIH_MGC_65 Home sapiens cDNA clone IMAGE:4105303 5	aj62/09.s1 Sozres_testis_NHT Homo sapleris cDNA clone IMAGE:1384921 3' similar to gb:L11672 ZINC	FINGER PROTEIN 91 (HUMAN);	601463545F1 NIH MGC 67 Homo sapiens CUNA cione IMAGE: 3600363 3	L.stagnalls mRNA for myomodulin neuropepide precursor	Homo sapiens mRNA for KIAA0339 protein, ipartial cds	Homo septens mKNA for KIAAU339 protein, parual dos	Pyrococcus harlkoshii OT3 genamic DNA, 1166001-1486000 nt. positian (9/7)	Zea mays ecidic ribosomai protein P2a-3 (rpp2a-3) mRNA, partial cds	Plasmodium falciparum erythrocyte membraire essociated glant protein antigen 332 (Ag332) gene, partial cds	EAN-1-10-25E-1 NIH MGC 44 Home saplens CDNA clone IMAGE: 3632190 5'	OCCUPATION NOT THE TOP OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE	Integrals XI Oceans In L. 1. 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contains element MER24 repetitive element;	yeasttos.rt Soares fetal liver spleen 1NFLS Homo sapiens cDNA olone IMAGE:124647 5	qm08g07.x1 NCI_CGAP_Lu5 Hamo sapients cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC	FINGER PROTEIN 30 (HUMAN);	hr34s03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:2833740 3' smillar to contains L1.tt L1 repetitive element ;
Top 出	Source	M	EST_HUMAN	N	EST HUMAN	EST_HUMAN		EST HUMAN	EST_HUMAN	NT	L	NT	LN	NT	<u> </u>	TOT LILITARI	EST HOMEN	EST HUMAN		EST HUMAN	N	NT	NT	EST_HUMAN	144	EST HUMAN	OWIGGING	EST HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN
Top Hit Acession	Ö	E-02 U37091.1	1.8E-02 AW905327.1	6678943 NT	3E-02 BF241924.1	3E-02 BF241924.1		E-02 AA897543.1	BE-02 BE778274.1	8E-02 X96933.1	8E-02 AB002337.2	BE-02 AB002337.2	8E-02 AP000006.1	8E-02 U62749.1	AF202180.1		BE394869.1	7F-02 AW 573183.1		7E-02 AW 573183.1	.7E-02 AL163204.2	TE-02 AB004816.1	7657495 NT	.7E-02 AI147615.1		.7E-02 AW827368.1	7E-02 P04929	7E_02   A A E G G R 1 8 1	7E-02 R02506.1		.7E-02 Al305279.1	.7E-02 AW573183.1
<del></del>	BLAST E Value	1.8E-021	1.8E-02	1.8E-02	1.8E-02	1.8E-02		1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1 8F.02	30.10.1	1.7E-02	4 7F-02		1	L	1	1.7E-02	-		-		,			•	
Expression	Signal	0.88	0.46	0.78	0.57	0.57		2.23	1.7	1.29	1.78	1.76	1.55	2.45	1 78	2	1.34	2 12		2.12	2.85	13.13	1.36			4.64	0.83	***	200		0.74	
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	SEO ID NO:	21404	1	1		22742		22882	L	١_	23907	23907			1	- 1	14104	44070	2	14979	15063	L	L	1_			16877	3,1,			17713	1
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Page 169 of 550 Table 4 Single Exon Probes Expressed in Placenta

	Top Hit Descriptor	Messenger RNA for anglerfish (Lophlus americanus) somatostatin II	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840838 3	wg35f09x1 Soares_NSF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3 similar to	contains Alu repetitive element;	oy85h03x1 Soares fetal liver spieen INFLS ST Homo saprens curve duris infract. 1012001 3	Macaca fascicularis protein tyrosine phosphatase (PKL-1) mKNA, complete cos	Homo sepiens nebulin (NEB), mRNA	Hünnan apolipoproteln (a) gene, exon 1	Human apolipoprotein (a) gane, exon 1	Homo sapiens hyperion gene, exchs 1-50	Casnorhabditis elegans cCAF1 protein gene, complete cas	DKFZp434[0314_r1 434 (synonym: htes3) Hamo sapiens CUNA ciana UNFZp43410314 3	Homo sepiens serum constituent protein (MSE66), mRNA	CM4-NN1030-040400-130-106 NN1030 Homo septens cDNA	oe08d04.61 NCI_CGAP_Ov2 Homo saplens cDNA clone IMAGE:1385287 sImilar to contains element MSK1	repetitive element;	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162	Treponema maitophilum flaB2, flaB3 and filiD genes for flagelin subunit proteins and CAP protein homologue	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)	LIVER CARBOXYLESTERASE 22 PRECUISOR (EGASTN) (ESTERASE-22)	Hamo capiens KVLQ11 gene	ne81d06.s1 NCI_CGAP_Ew1 Homo sepiens convenients convenients are convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the convenients of the 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ciutifium tesis tance procesi, compacio cos
#I aol		П	EST HUMAN ov			T_HUMAN					Į.	$\neg$	EST HUMAN D		EST_HUMAN C	8	EST HUMAN re		$\vdash$		SSPROT	П	EST HUMAN IN	7	EST HUMAN	2 1		Т	Т	HUMAN				NT NT
	Top Hit Acession No.	7E-02 V00641.1	,7E-02 A1015076.1		.7E-02 AI769247.1	.7E-02 Al038280.1	.7E-02 AF190930.1	8400716			.1	.7E-02 U21854.1	.7E-02 AL040554.1	2007	.7E-02 AW903482.1		.7E-02 AA846926.1	8E-02 AL021929.1		.6E-02 Q64176	.6E-02 Q64176				.6E-02 AW850852.1			1.6E-02 AF110520.1	1.6E-02 AW875407.1	1.6E-02 AI281385.1	6671715 NT	1.6E-02 AB015281.1	1.6E-02 AB027571.1	1.8E-02 AB027671.1
<del> </del>	(Top) Hit BLAST E Vatue	1.7E-02	1,7E-02		1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1.7E-02		1.7E-02	1.6E-02	1.6E-02	1.6E-02	1.6E-02	1.6E-02	1.6E-02	1.6E-02	1.6E-02	·								
	Expression Signal	1.91	5.98		1.69	1.23	1.26	1.9	1.08	1.08	1.71	0.89	1.28	1.68	2.35		1.48	4.05	1.37	1.81	1.81	0.97	1.75	1.01	5.33					0.59	1.42	2.18		1.14
	ORF SEQ ID NO:	30857			32773	33256		33894	l	34061		34591					31928	ł	27926	L	L		28941		29793				30543	31438	32234	33331	l	33540
1	SEG ID	17969	18064		19427	19867	1	ì	1	20587	1		ı		L		25757	ı		1	1	ŧ	1	15875	16778	L			17556	18570	18934	19935	١.	20124
	SEQ ID	4836	4934		6253	6709	7195	7353	7513	7513	7921	9636	866	12093	12891		13166	F.24	1689	2323	2323	2631	2708	2758	3614			4291	4415	5367	5741	8780	7071	7071

Page 170 of 550 Table 4 Single Exon Probes Expressed in Placenta

					28:13:	LAU!!!!!	Gilgie Extra Copea Expressed in Section
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	98.0	1.6E-02	1.6E-02 AL161508.2	Ę	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	<u> </u>	34919	0.74	1.6E-02	1.6E-02 AJ277662.1	ŊŢ	Homo sapiens partial TUB gene for tubby (niouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	1			1.6E-02			Human apoC-II gene for preproapolipoprotein C-II
10246	L		2.97	1.6E-02	1.6E-02 AF079764.1	N	Drosophila melanogaster enhancer of polycomb (E(PC)) mRNA, complete dus
10633		37278		1.6E-02	1.6E-02 AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_Pr1 Homo eaplens/cDNA clone IMAGE:914260 similar to Sw.: IELO_NAB! P29294 TELOKIN. [1]:
10633	L.			1.8E-02		EST_HUMAN	nf16g03.s1 NCI_CGAP_Pr1 Homo septens cDNA clone IMAGE:514260 similar to SW: 1 ELO_NAB11 P29294 TELOKIN. [1]:
11149	I_		2.9		1.6E-02 Z94828.1	NT	G.gailus microsatellite DNA (LEI0260 (= I 1¢IIIE11))
11488	1	L				IN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	L	L		1.6E-02		NT	Arabidopsis thaliana DNA chromosome 4, contig tragment No. 20
11801	L	L			1.6E-02 Al373558.1	EST_HUMAN	qz98e10.x1 Soares_pregnant_uterus_NbHFIU Homo capions cunw cione inwayer_zu*z444.3
12348	L				1.6E-02 Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348					Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
270	1	L	9.38		8923734	LN	Homo sapiens transcription factor (HSA130894), mRIVA
2209	1_	28469	3.58		1.5E-02 N39521.1	EST_HUMAN	W27b07.s1 Sogres (etgl    wer splagn 1NFLS   Hamo saptens clowed cione invince 243920 3
244	1					NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3128	$l_{-}$	L	1.04		1.5E-02 AJ006216.1	ΙΝ	Hamo sapiens CACNA1F gene, exans 1 to 48
3128	1_		1.04		1.5E-02 AJ006216.1	NT	Hamo sapiens CACNA1F gene, exons 1 to 48
3846			1.14		1.5E-02 BF092942.1	EST HUMAN	MR4-TN0115-080900-201-b12 TN0115 Home sapiens CUNA
4590		30710	0.72	Ŀ	1.5E-02 AF260225.1	L	Home sapiens TESTIN 2 and TESTIN 3 genes, compress cas, avainance years.
8423	1				Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN CIOBILLO4 IN CHROMOSOME.
747.	L		1.69	1.6E-02		NT	Cyanophora paradoxa cyanelle, complete genome
756	1	34108	1.57	1.5E-02	11418713 NT	Ę	Homo sapiens KIAA1009 protein (KIAA1009), mrvA
802	ı				1.5E-02 AL163303.2	INT	Homo saplens chromosome 21 segmen 1527100
8085	1			1.5E-02	11417739 NT		Homo saplans valy-tRNA synthetase 2 (VARSZ), mRNA
ğ	1	L	1.42		1.5E-02 BF345554.1	EST HUMAN	602019135F1 NCI_CGAP_Bring/ Homo sapiens clow a cione invace i Dator o
9868	1				1.5E-02 AF096774.1	ΝΤ	Homo sapiens kinase-related protein Isotorm 1 mKNA, compiete cos
9770	L	36337	1.59		1.5E-02 D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid Gabo
10016	L	L	1.3		1.5E-02 R32667.1	EST_HUMAN	y#54510.r1 Soares placenta Nb2HP Homo capiens cDNA Gone IMAGE: 155351 5
10018	L		1.3	١	1.5E-02 R32687.1	EST_HUMAN	yr54510_r1 Soares placenta Nb2H/ Homo capiens cunva conte invavor
10860	L				1.5E-02 T92198.1	EST_HUMAN	ye17f10.s1 Stratagene lung (#937210) Homo sapiens CUNA clone IMAGE: 118027 3
41058	1				1,5E-02 D28647.1	Ψ	Rice gene for thioredoxin h, complete cds
פטנוי				١			

Page 171 of 550 Table 4 Single Exon Probes Expressed in Placenta

Γ		$\neg \tau$	Τ	Τ	T	Τ	Τ		Τ	Τ	T	T	T	T	T	T	T	T	9			T	Ţ	T	T	T	$\cdot$		1	٦	Jact	7
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the comment of the comment of the comment of	Top Hit Descriptor	Plesmodium feldparum (strain FCR3) varianit-epecific surface protein (var-2, var-3) genes, complete cds's	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA	Chlamydophila pneumoniae AK39, section 36 of 84 of the Configura Garottie	Homo sapiens NESH protein (LOC61225), mRNA	Haemophilus influenzae Kd section 110 of 105 of the confluence general as	Xenopus laews neurogenin related 10 (X-1/4-1/10) ilinuva, cultipless cas	Bifidobacterium longum Na+/H+ antiporter (inhaB), cytosine deeminase, and alpha-galactosidase (agil.)	genes, complete cds, and N-acodyguicosamine xylose repressor processor (regions) and processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor processor 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Hamo sapiens curva	EST374761 MAGE resequences, MAGG Homo sapiens culna	601567403F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3642.250 5	601567403F1 NIH MGC 21 Homo Sapiens CUINA GIOTE IMPACE 30422500 3	H. sapiens La/SS-B pseudogene 3	ni 11004 st NCI_CGAP_BTZ Hono septens duna ciono innoci. I ozesso o similar di come dementi:	inf1604.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive	element;	Mycobacterium tuberculosis H37Rv compiele genome, segment og 192	Candida boldinii methanol oxidase (AOD1) gene, complete cos	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, expris 1-0	601078239F1 NIH MGC 12 Homo sapiens cDNA clone IMAGE:3464241 5	Homo saplens chromosame 21 segment HS210018	Human JFNAR gene for interferon alpha/beta receptor	Arabidopsis thaliana F21J9.2 mRNA, complete cds	Homo sablens sperm essociated antigen 7 (SPAG7), mRNA	Rhaum x cultorum NADH dehydrogenase subunit F (ndhF) gene, partial cds, chloroplast gene for chloroplast	product
EVOIL LIONE	Top Hit Database Source	NT	EST_HUMAN	N	NT	NT	Ę		Ĭ	EST_HUMAN	Ę	Ę	LN	IN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN		EST_HUMAN	NT	NT	LN	EST_HUMAN	NT LN	Į.	Į	NIT		뒫
Sign	Top Hit Acessian No.		1.5E-02 AW750834.1	1.4E-02 AE002230.2	T705980 NT		J67779.1		1.4E-02 AF160969.2	1.4E-02 AW074212.1	1.4E-02 AL161686.2	1.4E-02 AL161586.2	4503628 NT	6996918 NT	1.4E-02 AW962689.1	1.4E-02 AW962688.1	1.4E-02 BE733142.1	1.4E-02 BE733142.1	1.4E-02 X91338.1	4 4E 02 AAERON30 1		1.4E-02 AA559030.1	1.4E-02 AL022073.1	1.4E-02 M81702.1	1.4E-02 AJZ72265.1	1.4E-02 BE544581.1	1 4F-02 At 163218.2	1 4F-02 X80459 1	4 AE 02 AE324985 1	14.4280RBINT		1.4E-02 AF238059.2
	Most Similar (Top) Hit BLAST E Value	1.5E-02 L40609.1	1.5E-02	1.4E-02	1.4E-02	1.4E-02 U32800.1	1.4E-02 U67779.1		1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	4 45 03	-	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02			ì	1	1.45.02	
	Expression Signal	221	238	1.54	3.81	2.12	2.49		1.83	1.23	6.9	6.9	0.75	12.14	9.97	9.97	6.22	6.22	0.74	23.7	7:05	4.52	1.56	1.4						5	J.40	1.51
	ORF SEQ ID NO:	38171			27363				20478		١								L		20000	33084		35722		36227		20250				
	SEQ (D	24503	25970	13626	14307	14441	14483		16458	16663	16739	16738	L		17749	17749		<u>1</u>	<u> </u>	l	/0/61	19707	ı		22431	┸	L	L	L		22625	25704
	Probe SEQ ID NO:	11442	12576	430	1142	1285	1326		3284	3485	3573	3573	3608	3746	4612	4612	4998	4998	5911		8	8545	8333	808	9356	2000		10/00	2077	12840	12959	13075

Page 172 of 550 · Table 4 Single Exon Probes Expressed in Placenta

Single Exol Close Expressed in Lacona	Top Hit Descriptor	601556462F1 NIH_MGC_58 Homo saplens cDNA clone IMAGE:3826335 5'	Hano sapiens chromosame 21 segment HS210001	Netsseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome	602129475F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4286203 5	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5	Mus musculus beta-sarcoglycan gene, complete cds	Rice gene for thloredoxin h, complete cds	Mus musculus chromosome X contigB; X-liriked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92. mmxa28orf	Mus musculus chromosome X contigB; X-liriked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc	finger protein 92, mmxq28orf	Homo sapiens basic transcription factor 2 p44 (bt/2p44) gene, partial cds, neuronal apoptosis inhibitory profeso (nein) and survival motor neuron protein (cmn) genes, complete cds	C contractili the loce 1 5-hischerschafe carbovdase/oxygenese activase mRNA, complete cds	Arabidosis thaliana DNA chromosome 4, contig fragment No. 46	Arabidansis theliana DNA chromosome 4. contin fragment No. 45	Augustups statement of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company o	owoegus.X1 Soares paranydou wind nonry noine sapiers con consinued to contain soares and soares contains Alu repetitive element.	Homo sapiens human endogenous retrovirus W gagC3 37 G gag (gag) gane, complete cds	Mouse kidney androgen-regulated protein (KAP) gene, complete cds	Chlamydia trachomatis secilor 31 of 87 of the complete genome	xv34e03,x1 Soares_NFL_T_GBC_S1 Home septens cDNA clone IMAGE:2815036 3	xv34e03,x1 Soares_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:2815038 3	Bacillus subtilis complete genome (section 14 of 21); from 2599451 to 2512670	Human harpesvirus 6B, complete genome	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds	H.sapiens DIMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes	zf65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element	L1 repetitive element;	HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3'REGION	qd68e12.x1 Soares_testis_NHT Hamo sapiëns cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1 repetitive element ;	Homo saplens chromosome 21 segment HS21C013
EXUIT LINNES L	Top Hit Database Source	EST_HUMAN 60	H H	N N	EST_HUMAN 60	Γ		NT RE	E E		NT TN	H H					EST_HUMAN ©	Г		NT			NT		H	<u> </u>		EST_HUMAN L	SWISSPROT	EST_HUMAN re	П
	Top Hit Acession No.	.3E-02 BE739263.1	.3E-02 AL163201.2					Γ		T	.3E-02 AL049868.2			1.3E-02 M62962.1	I	.3E-02 AL161548.2	1.3E-02 A1031593.1	1.3E-02 AF156961.1	1.3E-02 M83707.1	1.3E-02 AE001304.1	1.3E-02 AW 268563.1	1.3E-02 AW268563.1	1.3E-02 Z99117.1	1N 69022069	1.3E-02 AF162238.1	1 0E-00 X87344 1		1.2E-02 AA059299.1	1.2E-02 P38898	1.2E-02 AI183522.1	
•	Most Stmilar (Top) Hit BLAST E Value	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1 25 00	1011	1.3E-02		1.35-02	1.3E-02	20-10-1	1.3E-0Z	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02	1.3E-02					1.2E-02	1.2E-02
	Expression Signal	1.18	2.13	0.98	2.41	2.41	12	3.02	3	2	1.61		1.2	-05	2	1.3	9,	1 67	8.	0.95	3.35	3.35	1.7	2.56	30.16	6	700	4.38	1.43	2.67	203
	ORF SEQ ID NO:	<u> </u>	28254	28769	29479	28480			5		31479			Ì		31482	34303				l	l						26606			
	SEQ ID	15058	1	Т	ı	1		Ĺ.,	1	3	18563			19499	07001	18528	20812	1		L	L		$1_{-}$	L	L	1	2	13676		1	1
	Probe SEC ID NO:	1913	2010	2512	3285	3285	4078	5275		3	5360		6283	6327		7101	7752	8478	10411	10485	11239	11239	12645	12753	12985	1	RI7	365	485	767	2246

Page 173 of 550 Table 4 Single Exon Probes Expressed in Placenta

Singie exon prodes expressed in praventa	Top Hit Descriptor	x/37e09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:2859432 3'	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE::2659432 3	zm88e03.r1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE: 645020 6	y11b08.s1 Soares placenta Nb2HP Homo saplens cDNA done IMAGE:138903.3	zb66a07x5 Scares_fetal_lung_NbHL19W Homo sapiens dDNA clone IMAGE:308532 3 similar to contains element MER22 repetitive element;	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete ods	Cynops pyrthogaster CpUbiqT mRNA, partial cds	AV731704 HTF Homo saplens cONA clone HTFBHG11 5'	Rana rugoca mRNA for calreticulin, complete cds	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genco, complete cdc, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5	y34h12.s1 Soares placenta NbZHP Homo saptens cDNA clone IMAGE:150695 3'	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 6	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA- GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-5T) (GAL-NAC6S) (GAL-BETA-1,3-	GALNAC-ALPHA-2.3-SIALYLTRANSFERASE) (3T3GALA.2) (SIAT4-B)	y43f06.s1 Soares placenta Nb2HP Homo stiplens cDNA done IMAGE:142019 3	y43f06.s1 Soares placenta Nb2HP Homo sipiens cDNA done IMAGE:1420193	Homo sapiens fringe protein mRNA, partial cds	Homo sapiens fringe protein mRNA, partial cds	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo saptens cDNA clone IMAGE::137743	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds	Hamo saplens Spast gene for spastin protein	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA done GEN-557 (205 5	zm69e11.s1 Stratagene neuroeptihelium (#§37231) Homo sapiens cDNA clone IMAGE:530924 3	H. sapiena LIPA gene, exon 4	H.sapiens LIPA gene, exon 4	לבי אייייי ודי בייייי הואיז הואיז הואיז הואים הואים הואים הואים האיחם ביייים הואים הואים הואים האים ביייים היי
Exon Propes	Top Hit Databese Source	П			EST_HUMAN M	EST_HUMAN e	<u>I</u> E	LN	П	NT R	<u>+                                    </u>		EST_HUMAN X	EST_HUMAN A	EST_HUMAN 6		SWISSPROT	EST_HUMAN V	EST_HUMAN S	NT	NT TN	T_HUMAN		-		EST_HUMAN (	EST_HUMAN 3		Т	EST_HUMAN
Single	Top Hit Acession No.	2E-02 AW172350.1	2E-02 AW172350.1	2E-02 AA075418.1	2E-02 R62805.1	ZE-02 A1668694.1	2E-02 U91328.1	7.			2E-02 AF045555.1	2E-02 AF1754121	ZE-02 H02197.1	2E-02 AV732093.1	2E-02 BF216650.1		2E-02 Q11205	.2E-02 R68831.1	.2E-02 R68831.1	2E-02 AF193612.1	2E-02 AF193612.1	2E-02 T76987.1	2E-02 AB031013.1	2E-02 AJ246003.1	2E-02 P17139	2E-02 C18119.1	.1E-02 AA070364.1	.1E-02 X75491.1	.1E-02 X75491.1	.1E-02 BF345263.1
	Most Similar (Top) Hit BLAST E Value	1.2E-02/	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.26-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02		1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2€-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.1E-02	1.1E-02		
	Expression Signal	1.02	1.43	7.3	205	0.59	2.02	1.97	1,31	1.78	0.72	8.67	1.42	8.54	0.66		2.3	0.50	0.56	1.22	1.22	-	2.54	1.24	1.16	6.24	1.22	1.48	1.48	5.35
	ORF SEQ ID NO:	28762	28762		29545		31139		31286								34792	L		L	34994		36461							
	Exon SEQ ID NO:	15840	l	l	L	l	18483	1			L	L	20520	ı	1		21268	ı	21403	ı	21467		1	ı	L	L	L	1_	1	15236
	Probe SEQ ID NO:	2514	2701	3170	3369	3362	5035	5154	5185	5871	8243	7147	7443	7485	7729		8188	8321	8321	8386	8386	9091	9839	8872	12757	12974	1288	1743	1743	2086

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					TA IN	222	Single Exert Flores Expressed in Flores
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Descriptor
2942	16119		5.31	1.1E-02	1.1E-02 N99523.1	EST_HUMAN	za40e05,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5
3612	1	28782		1.1E-02	1.1E-02 AI653508.1	EST HUMAN	tq95010 x1 NCI_CGAP_Ov23 Homo septem; cDNA clone IMAGE;2218539 3' similar to SW:XPF_HUMAN Q82889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4222				1.1E-02	1.1E-02 AW813708.1	EST_HUMAN	RC3-ST0197-120200-015-911 ST0197 Homo sepiens cDNA
4951	ı	31057		1.1E-02	1.1E-02 AL048383.2	EST_HUMAN	DKFZp588E0924_s1 586 (synonym: hute1) Homo sapiens cDNA done DKFZp588E0924
	1						Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GinR (ginR), glutamine synthetase (ginA), YnaB (yneB), YnaC (ynaC), YnaD (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (ynaC), YnaC (yn
6277	19461	32800	0.89	1.1E-02		L <sub>N</sub>	(yngH), Ynal (ynal), YnaJ (ynau), xylan beta- i 4-xylosi>
7773		34321	2.19	1.1E-02	1.1E-02 BE149811.1	EST_HUMAN	RC1-HT0256-100300-016-h07 H10256 Homo sapiens cDNA
7989	l_	34561	1.25	1.1E-02	9631294 NT	ΝΤ	Melanoplus sanguinipes entomopoxwirus, complete genome
8451		L	0.48	1.1E-02	1.1E-02 P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	L	l		1.1E-02	1.1E-02 P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8841	21820		69.0	1.1E-02	1.1E-02 AW996160.1	EST HUMAN	QV3-BN0045-220300-128-h02 BN0046 Horno capiens cDNA
8022	Į.		0.7	1.1E-02	1.1E-02 C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA done 3NHC4040
9103	1		7.44	1.1E-02	1.1E-02 Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10133	23171	36769	2:02		1.1E-02 AA082578.1	EST_HUMAN	zn24e01.r1 Stratagene neuroopäthelium NT2RAMI 937234 Homo caplens cDNA clone IMAGE:548328 5'
10289	ı				1.1E-02 AA314665.1	EST_HUMAN	EST186494 Colon cardnoma (HCC) cell line II Homo sapiens cDNA 5' end
11224	24293	37634	2.41	1.1E-02	11435505 NT	NT	Homo sapiens T-box 5 (TBX5), mRNA
12105	l	ļ	4.04	1.1E-02	1.1E-02 AA668239.1	EST HUMAN	ab7711.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3 similar to contains Alu repetitive element;
	1	26247		1.0E-02	1.0E-02 AW846120.1	EST_HUMAN	MR3-C70176-111099-003-e10 C10176 Homo saplens cDNA
1552				1.0E-02		EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Haino sapiens cDNA
2838	L		1.71	1.0E-02		EST_HUMAN	oczzho8.s1 NCI_CGAP_GCB1 Homo sapiens cUNA dane ilwAGE:11350495 3
3169	16334		2.88		1.0E-02 BE835556.1	EST HUMAN	RC0-FN0028-250500-021-d02 FN0025 Home squens culva
3336	L	29825	1.24		1.0E-02 BE968999.1	EST_HUMAN	601648967R1 NIH_MGC_74 Homo sapiens culva cione liva cic. 3633009 3
3598	L	2	0.7		1.0E-02 AW845821.1	EST_HUMAN	MR0-CT0060-081099-003-h10 C10060 Homo sapiens GUNA
3986	3 17143	30148	3 0.85		1.0E-02 A1065086.1	EST_HUMAN	HA0921 Human fetal liver CUNA library Homo sapiens CUNA
4007	17159	30185	0.59		1.0E-02 AL 163302.2	NT	Homo saptens chramosome 21 segment HS21C102
4899	18029		9		6753524 NT		Mus musculus carticotropin releasing hormone receptor 2 (Crinz.), marky
4988	18098	31074	4.14		1.0E-02 R96567.1	EST_HUMAN	yc54h01.r1 Soares fetal liver spiech TNPLS Indino sapiens curva clothe living control in social control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the control in the
5116	18243	3 31208	3 0.83		1.0E-02 AL161593.2	¥	Arebidopsis thaliana UNA chromosome 4, contig tragment No. 69
5242	18364	31332			1.0E-02 P06599	SWISSPROT	EXTENSIN PRECURSOR
5632	18729	31745	3 0.81		1.0E-02 H52681.1	EST_HUMAN	y CBhil r1 Soares ovary tumor nono! Haino sapiens acin's ciane invision.

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Probe SEQ ID NO:	SEO ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5865	18055	32382	99'0		1.0E-02 AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6242	19416	32764	1.29		1.0E-02 AF257303.1	Z	Mus musculus synaptotagmin II (Syt2) gene, complete cds
6310	L		2.78		1.0E-02 AW577113.1	EST_HUMAN	WR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6310	1	l			1.0E-02 AW577113.1	EST_HUMAN	WR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6901	20216				I.0E-02 229842.1	ΙN	Z.mays U3snRNA pseudogene
9583		1	6.34		1.0E-02 BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5
9593	ł		6.34		1.0E-02 BF036331.1	EST_HUMAN	801459570F1 NIH_MGC_66 Hand sapiens cDNA clone IMAGE:3863177 5'
							Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for
11542	24598		2.12		1.0E-02 AF157559.1	F	mitochondrial product
							tg56h07.x1 NCI_CGAP_Pr28 Homo sapients cDNA clone IMAGE:2112733 3' stintlar to gb:X15183_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN);contains Alu repetitive element;contains element MER5
11573	24628		1.7		1.0E-02 A1417961.1	EST_HUMAN	repatitive element;
11649	<u> </u>	38420	1.95		1.0E-02 AV780019.1	EST_HUMAN	AV760016 MDS Homo capiens cDNA clone MDSBDC10 5
12278	<u> </u>				1.0E-02 Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12339	l	31762			1.0E-02 AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Home saplens cDNA
12355	26002		4.31	1.0E-02	1.0E-02 S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12764	25974		4.4		1.0E-02 AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12949	26060		2.91	1.0E-02	1.0E-02 X62654.1	NT	H. septens gene for Me491/CD63 antigen
							w422/09.X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
916		27158			9.0E-03 AI796126.1	EST_HUMAN	MER22 MER22 repetitive element;
1293	14449		1.66		9.0E-03 BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens/cDNA clone IMAGE:3873346 5
2469	15598	28721			9.0E-03 AL161559.2	MT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2971	L	L	0.81			EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 31
2971	16147	29166			9.0E-03 AI251744.1	<b>EST_HUMAN</b>	qh80f08x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3758		28921	99.0		9.0E-03 J05184.1	TN	S.acidocaldarius thermopsin gene, complete cds
5931	i				9.0E-03 AI809792.1	EST_HUMAN	wf77f04x1 Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:2361631 31
6788	١_		4.01	L	BE745988.1	EST_HUMAN	801573438F1 NIH_MGC_9 Home sepiens cDNA clone IMAGE:3834752 5'
7623	L	34169	0.61	L	9.0E-03 A1242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_GBC_S1 Home saplens cDNA done IMAGE:1853974 3'
7640		34188	0.91	L	TN 0722298	TN	Hame sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8059	L		0.8		9.0E-03 AL039991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: htcs3) Homo capieno cDNA clone DKFZp434L0412 5
							Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
8443	21524		0.54		9.0E-03 AF223391.1	LN	peollosed
10050	ł				9.0E-03 P28011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
10068	23104	36707	1.47		9.0E-03 P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
	ı						

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					,		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	201	8.0E-03	8.0E-03 BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo saplens; cDNA clone IMAGE:3878405 5'
11231			2.79		8.0E-03 Z49852.1	Ŋ	S.cerevisiae chromosome X reading frame ORF YJR152w
11883		38433			8.0E-03 AA828817.1	EST_HUMAN	od80809,s1 NCI_CGAP_Ov2 Homo septents cDNA clone IMAGE:1374232
11683	1			80	0E-03 AA828817.1	EST_HUMAN	od80a09.s1 NCI_CGAP_Ov2 Homo saplens cDNA clone IMAGE:1374232
12015	1	ľ		80	8.0E-03 AF064589.1	NT	Homo capiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12205	1	l		L	0E-03 M69035.1	NT	Oryctolagus cuniculus elF-2a kinase mRNA) complete cds
							Homo sepiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (W HI LE), member 1),
12252	25191		7.14	80	0E-03 AB038161.1	LN.	complete cds
13145	25959		1.18	- 40		EST_HUMAN	qm58c09.x1 Scares_placenta_8:c9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:18927523'
712	1	26930	12.35	7		NT	Cryptosporidium parvum HC-10 gene, complete cds
712			12.35	1	.0E-03 AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
666	L		3.26	7.	0E-03 AF243376.1	NT	Glycine max glutathione S-transferaco GST 21 mKNA, partial cds
1140				7	.0E-03 AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5
	<u>]</u>				090780	TOGGSSIMS	FORKHEAD BOX PROTEIN D3 (HNF3/FH) TRANSCRIPTION FACTOR GENESIS) (HEPALOCY LE INLICI EAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1395				\	00000	100 100	LAZONO e1 Stratanena fatal retina 837202 Homo septens cDNA clone IMAGE:853145 3
1428		27653			.0E-03 AA668298.1	ES HOMAN	BOT BUDG. S. LOUGHSHOTH FOR EA LAWS. CONTINUE CHINA PHONE MACRE 7813739 3.
1532	14685		3.28	7	.0E-03 AW303599.1	EST HOMAN	XX1DX_XI Soules Intelligence of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of
2332	16060	28598	2	7.0E-03	.0E-03 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROLEIN PRECURSOR
	Ì					1444	hn67h07.x1 NCI_CGAP_KId11 Homo saplens cunA cione inta dE, 3032808 3 efinita to community and
2695				`	.0E-03 AW.772132.1	ESI HUMAN	Legendre dienin, horin NILT Lowe conjone CONA Clone IMAGE 1751955 3
3648		29824		_	.0E-03 AI150273.1	ES! HUMAN	HOLINGAL OF THE AND COME SHEET OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
3863	17023		0.71		.0E-03 AW 444463.1	EST HUMAN	
3014	17073	30071	1.13	_	.0E-03 AF196344.1	N TN	Rattus norvegicus neuronal nicotinic acetylcitoline receptor subunit (Alpha10) mRNA, complete cds
4128	1				.0E-03 AW 444463.1	EST_HUMAN	Ut-H-Bi3-ekb-o-10-0-Ut.s1 NCI_CGAP_Suk5 Homo septens cUNA clone IMAGE:2/33691 3
4721	L			ľ	.0E-03 AW 630888.1	EST_HUMAN	hh89a05.y1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2869836 5
110	Ļ		8.54		0E-03 AL 163278.2	F	Homo saplens chromosome 21 segment HS21C078
	<u> </u>						y 62g01.rt Soares fotal liver spleen 1NFLS Home sapiens cDNA clone IMAGE:211824 5 similar to
5940			0.72		7.0E-03 H71106.1	EST HUMAN	190:X14723 CLUB IERIN PRECUNSOR (Inclinery),
6238			4.42		7.0E-03 AW861059.1	EST_HUMAN	KC1-C 10280-0-00400-010-000 C 10200 Fullipo Septemb CC1-C 10280-0-000 Figure 1444 CF 342475 5
6444				'`	7.0E-03 W68251.1	EST HUMAN	2005/110.F1 Soaries Tetal Theat John Figure Sapidas Cotto Saries Cotto
6667	19826	33213	3 2.92		7.0E-03 AA327129.1	EST HUMAN	EST 300/4 Colon I nomo sapiens culva o tim

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	Top Hit Descriptor	7g34b10.x1 NCI_CGAP_Bm23 Hamo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13397 HYPOTHETICAL PROTEIN 384D8_2, ;contains TAR1.t2 TAR1 TAR1 repetitive element :	CM2-CT0478-230800-347-b11 CT0478 Homo septens cDNA	S.cerevisiae chromosome il reading frame ORF YBL077w	S.cerevisiae chromosome II reading frame ORF YBL077w	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens 959 kb contig between AML:1 and CBR1 on chromosome 21q22, segment 3/3	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens serine paimitbyl fransferase, subunit II gene, complete cds; and unknown genes	yv49c10.s1 Soares fetal liver spleen 1NFLS. Homo saplans cDNA clone IMAGE:246066 3' similar to contains	Alu repetitive element;	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'	wc37e09:x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2320840 3'	PM3-HT0344-181199-002-g06 HT0344 Hcmo sapiens cDNA	Bos faurus mRNA for NDP52, complete cds	Homo sapiens partial MUC5B gene, exon 1;29	Homo sapiens partial MUC5B gene, exon 1;29	yv16h01.s1 Soares fetal liver spleen 1NFLS Home sapiens cDNA clone IMAGE:242833 3' similar to contains	Alu repetitive element;	601145154F2 NIH MGC 19 Homo septent; cDNA clone IMAGE:3160476 b	Homo sapiens LSFR2 gene, penultimate exon	Homo sapiens chromosome 21 segment HS21C100	hd22a05.x1 Soares_NFL_T_GBC_S1 Homb sapiens cDNA clone IMAGE:2910224 3' slmllar to SW:PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to swexp_HIMAN_O75489 ORPHAN NUCLEAR RECEPTOR PXR:	to the control transfer on the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the control to the contr	Danio reno cociani i eceptua gene ciuatari	ah/8e11.s1 Sogres_testis_NH   Hario sapians curin clone 1521/12.5	ah78e11.s1 Soares tests NHT Homo sapiens cUNA clone 13/21/1/2.3	y77h04,r1 Soares fetal liver spiech TNFLS Homo sapiens count cione invage: 211331 3
	Top Hit Database Source	EST_HUMAN Q	EST_HUMAN C	NT S.		NT		T_HUMAN	NT H	NT TN			SWISSPROT BE	SWISSPROT BE	EST_HUMAN A		-	Г		Ĭ.		$\neg$	T_HUMAN		H H	EST HUMAN S				HOMAN		EST_HUMAN IN
	Top Hit Acession No.	7.0E-03 BE857385.1	7.0E-03 BE928133.1	7.0E-03 Z35838.1	7.0E-03 Z35838.1	7.0E-03 AJ229043.1	7.0E-03 AJ229043.1	7.0E-03 BE175667.1	7.0E-03 AF281074.1	7.0E-03 AF111168.2		7.0E-03 N52378.1	7.0E-03 P48982	7.0E-03 P48982	7.0E-03 AV687379.1				7.0E-03 AJ004862.1	7.0E-03 AJ004862.1		7.0E-03 H94065.1	7.0E-03 BE263253.1	7.0E-03 Y17455.1	7.0E-03 AL163300.2	6.0E-03 AW511148.1	7 07 7 7 1 1 1 1 1	0.UE-US AW 311140.1	6.0E-03 AF112374.1	6.0E-03 AA759135.1	6.0E-03 AA759135.1	6.0E-03 H75690.1
S Park	Most Sumiar (Top) Hit BLAST E Value	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03		7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03		7.0E-03	7.0E-03	7.0E-03	7.0E-03	8.0E-03	1		8.0E-03	6.0E-03	6.0E-03	6.0E-03
	Expression Signal	1.05	1.93	4.76	4.78	0.59	0.59	2.48	0.58	0.64		0.68	2.72	2.72	7	0.80	0.47	2.41	1.86	1.66		1.95	1.46	1.78	1.68	8.78		8.70	0.04	3.29	3.28	227
	ORF SEQ ID NO:	33243	33550	34238	34239	34632	34633	34905	<b> </b>			38414	36548	36549			37456			١						27494			29054		29148	
	SEQ ID NO:	19853	20133	20754	20754	21114	21114	21384	21892	22852		22834	22961	22981	<u></u>			L	L	L	L	26189	l	1	i	1	<u> </u>					
	Probe SEO ID NO:	6695	7228	7689	7689	8031	883	8302	8813	9597		9794	9921	9921	10513	10704	10800	11065	11140	11140		12792	12800	12908	13058	1260		1269	2831	2956	2958	3318

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Probe SEQ ID NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No	Top Hit Database Source	Top Hit Descriptor
3378	16550		89:0	6.0E-03	5.0E-03 AF180338.1	TN	Notoncus sp. cytochrome c oddase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
848	16636	29655		6.0E-03		Į.	Fugu rubripes zinc finger protein, Isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3469	16836	22656		6.0E-03	8.0E-03 U90880.1	Ä	Fugu rubripos zinc finger protein, isotocin, fatty ecid binding protein, seplapterin reductase and vasotocin genes, complete cds
3838	16800			6.0E-03	1	EST_HUMAN	2013a11.r1 Scares_parathyroid_tumor_NbHPA Homo saplens oDNA clone IMAGE:322172 5
3760	16911	29914	3.73	6.0E-03	BF510986.1	T_HUMAN	UI-H-BI4-apm-c-06-0-UI-S1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:3087754 3
3877	17036	30034	1.31	6.0E-03	4029	NT	Mus musculus glucosamine-8-phosphate deaminase (Grpl), mKNA
4032	17188	30199	9.0	- !		EST HUMAN	RC0-CT0204-240999-021-b10 CT0204 Homo saplens cDINA
4067	17223		1.26		8.0E-03 BE250108.1	EST HUMAN	600942904F1 NIH_MGC_15 Homo saplens clune IMAGE:Z809013 0
484	17624		1.54		6.0E-03 AI016833.1	EST HUMAN	ov33011.x1 Soares_testis_NHT Homo sapiens cUNA cone iMACE:1039174 3
4817	17950	30835			8.0E-03 AA324242.1	EST_HUMAN	E3T27116 Cerebellum II Homo sapiens cDNA 5 and similar to EST containing Alu repeat
5305	18422	31392	9.0		AAB8997.	EST_HUMAN	495g09.s1 Soares_parathyroid_tumor_NbHPA Homo saptens culva cione invace:1404266 s
6281	25822	32803	99.0	6.0E-03	9627521 NT	LZ	Variola virus, complete genome
9969	20269	33707	0.8		6.0E-03   O14994	SWISSPROT	SYNAPSIN III
989 7689	18513	31505	260	6.0E-03	6.0E-03 BE253748.1	EST_HUMAN	601112363F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33531725
7389	20477	33944			6.0E-03 AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7399	20477	33945			AA299442.1	EST HUMAN	EST:1949 Uterus tumor I Homo sapiens cibNA 5 end
7824	20879	34380	8.0		6.0E-03 AF128894.1	L	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
							ow/3a04.x/ Soares_parathyroid_tumor_NbHPA Homo septens cDNA clone IMAGE:16466/0.3 Similar to
8042	1				-	EST HUMAN	Contains MERTULDI MERTU (appeading element)
8161		34763				EST HUMAN	RCO-UMBBOT-21030U-032-guz Omnus I maine septents const
8238	21318		1.65		-	EST_HUMAN	801454915F1 NIH, MGC, 90 HOMB SEPTING CONSTITUTION OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED OF THE INVITED
9754	22692	36262	7.03		6.0E-03 D10548.1	Ļ.	Subacule scienceing panencephalitis (SOPE) wins mixivA for rusion protein
					* *************************************	MANUTAL FOR	622602X1 NC_CGAP_Kid11 Home sapiens CUNA clone IMAGE:2131202 3 SIMIRATE DISVENTISA_HOWAIN PAGES SIMIRATED SWINTISA_HOWAIN PAGES SIMIRATED SOMENTISA_HOWAIN ED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRATED SOMENTISA SIMIRA
10249	┙				0.0E-03 A1432001.1	ATAMOL DE	Doubling Arthritis from
10365	23400	37011	0.75		6.0E-03 AJ011849.1	Ž	Datellius subuling telling general and an analysis and absent and a fabrical and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated and annulated annulated and annulated annulated and annulated annulated and annulated annulated and annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated annulated ann
						!	Homo sapiens okadaic acid-inducipie and cylvir-regulated pricepiropickan i.e. (Appril 1971) ili vira, caribidae
10503	23638		0.01		6.0E-03 AF084555.1	LN.	CGS
10615	53649	37258	0.64		6.0E-03 X68368.1	LN	M.thermoformicicum complete plasmid privi DNA
10661	23695		0.54		6.0E-03 AF245505.1	¥	Homo saplens adlican mKNA, complete cds
10983		37697			AW962	EST HUMAN	EST374237 MAGE resequences, MAGG Homo saplens cunA
11049	24126		1.94	6.0E-03	11545814 NT	Ę	Homo sapiens hypothetical zno linger protein FLV 140 11 (FLV 140 11), minus

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Single Exoll Plones Explessed III Flavelika	Top Hit Descriptor	Mus musculus zinc-finger protein mRNA, complete cds	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5	Rhodobacter capsulatus strain SB1003, partial genome	602151024F1 NIH_MGC_81 Hamo saplens cDNA clone IMAGE:4292212 5	Methanobacterium thermoautorrophicum from bases 429192 to 450296 (section 39 of 146) of the complete genome	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)	Brassica napus alg gene for S-locus glycopiotain, cultivar 12	R.norvegicus VEGP2 gene	7n38h11.x1 NCI_CCAP_Lu24 Homo sapieris cUNA clone IMAGE:33b85994 3	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA cynthase, complete cds; complete ORFA, and grpE- like protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-	ilke protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete ods; complete URFA, and grpE- litze zydaln cymplete ods	Purcey, compress one 1 Antin 1 1900 Antin Complete ade complete OREA and crof-	Chiamydia trachomatis partai Orkre, aminoexys-trovk symiassa, cumpress cus, complete cds.	Arabidopsis thaliana mRNA for DEAD box FINA helicase KH3	qd7ed05.x1 Soares_testis_NHT Homo sapians cDNA clone IMAGE:1735689 3	Homo capiens mRNA for KIAA1180 protein, partial cds	yo81f09.s1 Soares infant brain 1NIB Homo saplens cLINA cione IMAGE 22399 3	Arabidopsis thallana DNA chromosome 4, contigurations 3	vi86g02.81 Soares breast 2NbHBst Homo sapiens cuina cione invalve: 100000 3	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAAU631 gene	Pseudomonas aaruginosa strain PAO1 penicillin-binding protein 15 (pont) gene, complete cas	Citrus sinensis seed storage protein citrin mRNA, complete cos	EST12218 Uterus tumor I Homo sapiens cLiNA 5' end	Natrix domestica Zfx type gene	yu79g10.r1 Soares fetal liver spleen 1NrLS Homo sapiens cUNA clone IMAGE. 240000 3	Citus sinensis seed starage protein durin minny, compressions	Homo sayens o'ch gane locus
Exon Probes c	Top Hit Database Source	П	THUMAN	$\neg$	EST_HUMAN 60	NT PE		SWISSPROT S	NT Br	NT R.	EST HUMAN 7r	NT FN		NT IN	1 L		NT FI		T_HUMAN	$\neg$	EST HUMAN X		HUMAN				T HUMAN		HUMAN		L
Single	Top Hit Acession No.	3.0E-03 U14556.1	3.0E-03 BE737895.1		3.0E-03 BF671185.1	3.0E-03 AE000833.1	1	6.0E-03 Q62209	8.0E-03 AJ245480.1	8.0E-03 X74807.1	6.0E-03 BF110298.1	5 0F-03 L 25105.1		5.0E-03 L25105.1	, 20,20	6.0E-03 L25105.1	5.0E-03 L25105.1	5.0E-03 AJ010457.1	5.0E-03 A1138977.1	3.1		ci	5.0E-03 R71794.1	6.0E-03 AJ297357.1	5,0E-03 AF147449.2	5.0E-03 U38914.1	5.0E-03 AA299675.1	5.0E-03 AJ002125.1	5.0E-03 H78355.1	5.0E-03 U38914.1	5.0E-03 AJ131016.1
	Most Similar (Top) Hit BLAST E Value	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	8.0E-03	6.0E-03	6.0E-03	5 0F-03		5.0E-03	101	5.0E-03	5.0E-03	5.0E-03	6.0E-03	5.0E-03	5.0E-03	6.0E-03	5.0E-03	6.0E-03	5,0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03
	Expression Signal	4.1	2.68	2.04	1.8	4.65	2.48	1.63	2.41	1.61	1.19	ă.		98:1	-	3.08	3.08	1.47	1.08	2.43	3.87	2.72	1.17	0.84	5.28	0.81	1.64	0.65			0.92
	ORF SEQ ID NO:		37938									26003		26904		26903	26904	27367		28974	29392		29423		28957			30374			30848
	SEQ.ID NO:	24297	24208	26232	25998	25926	25983	26397	26822	26018	25748	1	L	13871	<u> </u>	13871	13871	14301		L	16381	16397	16409	1	L	L	L	17387	H		17888
	Probe SEO ID NO:	11228	11229	12321	12425	12451	12532	12590	12944	13095	13147	698	8	989		687	687	1136	1601	2748	3208	3223	3235	3351	3790	3854	4079	4241	4421	4423	4731

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Probe SEQ ID NO:	SEO ID	ORF SEQ ID NO:	Expression Signal	Most Smilar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
11818	24868		3.41	5.0E-03	5.0E-03 BE048055.1	EST_HUMAN	な46004-y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 6
12070	1	38759		5.0E-03		П	Mus musculus genamic fragment, 279 Kb, chromosome 7
12070				5.0E-03			Mus musculus genomic fragment, 279 Kb, chromosome 7
12467			Ξ	5.0E-03		NT	Gailus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616			21.79	5.0E-03		NT	Brugia malayi Y chromosome marker
12718	_		2.03	5.0E-03	5.0E-03 L10347.1	NT	Human pro-alphat type II collagan (COL2A1) gene exons 1-54, complete cds
12760	İ		1.94	5.0E-03	5.0E-03 AA456597.1	EST_HUMAN	zx75e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT;
12802			5,99	5.0E-03	5.0E-03 BF572332.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapients cDNA clone IMAGE:4252002 5
13002	L	31951	2.68	5.0E-03	5.0E-03 AW449109.1	EST_HUMAN	UI-H-Bi3-ald-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cUNA clone IMAGE:2734Z15 3
242	13464	26493	1.54	4.0E-03	4.0E-03 AW 500196.1	EST HUMAN	UI-HF-BNO-ake-h-04-0-UI-r/ NIM MGC 50 Homo saplens cDNA clone INM-GE 30 read 1 3
331	1_			4.0E-03	4.0E-03 R46482.1	EST_HUMAN	yg51e04.s1 Soares infant brain 1NIB Homo capiens cDNA clone IMAGE:33966 3
456	1	26889		4.0E-03 P54675	P54675	SWISSPROT	PHOSPHATIOYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PI DING-3-KINASE) (PI3K)
919	L			4.0E-03	4.0E-03 AAB3B339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1352366 3
8	ŀ			4.0E-03	4.0E-03 R46482.1	EST_HUMAN	yg51e04.s1 Soares infant brain 1NIB Homo saplens CDNA clone IMAGE:30986 3
934	1_			4.0E-03	4.0E-03 AW749101.1	EST_HUMAN	RCs-BT0338-110100-012-f01 BT0333 Homo sapiens cDNA
1174	14337		34.06		4.0E-03 AA099777.1	EST_HUMAN	z181a08.r1 Stratagene colon (#537204) Homo sapiens cDNA clone IMAGE: 310998 3
1188	!				4.0E-03 AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo septens dDNA
1331	L	27558	1.48	4.0E-03	4.0E-03 AA284374.1	EST HUMAN	2S59801.r1 NC_CGAP_GCB1 Homo sapiens cDNA cione IMAGE:701739 5
1783	14832	28028	2.68		4.0E-03 U33472.1	Ŋ	Rattus norvegicus type 1 astrocyte and olfactory-limble associated protein AT1-46 mRNA, complete cds
2075	15215	28334	17.33			EST_HUMAN	2/8/16/08/11 Strategene colon (#93/204) Homo sapiens con A cione in MCE.3 10350 3
2321	1		2.08			EST_HUMAN	601304161F1 NIH MGC 21 Homo septents convictions invices 300010 o
2352	15483	28615	1.53		4.0E-03 AW 794740.1	EST HUMAN	RCS-UM0014-170400-023-G01 UM0014 Homo sapiens CUNA
							Homo explens X28 region near ALD locus conteining dual expeditionly procedurates 9 (UOST-9), indosorned protein L18a (RPL18a), Cab-7-Calmoulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), contein L18a (RPL), creatine transporter (CRTR), contein L18a (RPL), creatine transporter (CRTR), contein L18a (RPL), creatine transporter (CRTR), contein L18a (RPL), creatine transporter (CRTR), contein L18a (RPL), creatine transporter (CRTR), contein L18a (RPL), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatine transporter (CRTR), creatin
2639	15762	28875	1.95		4.0E-03 U62111.2	₽	CDM protein (CDM), adrenolativodystropiny protein
							Homo sepiens X28 region neer ALD locus containing dual specificity phosphatase 9 (UUSY-9), noosomal protein L18a (RPL18a), Ce2+/Celmodulin-dispendent protein kinase I (CAMKI), creatine transporter (CRTR),
2639	15762	28876	1.95		4.0E-03 U52111.2	LN.	CDM protein (CDM), adrenaleukodystrophy protein >
2755	15872	28980	2.97		4.0E-03 AJ277365.1	Į,	Homo sapiens polyglutamine-containing cri-t-Crit gene
2755	15872	28981	1 2.97		4.0E-03 AJ277365.1	N <sub>T</sub>	Homo sapiens polygiutamine-containing C14OK14 gene
2761	1	7 28984			4.0E-03 AL163284.2	N	Homo sepiens chromosome 21 segment HS21C084
3297	16471	1 29491	1.09		4.0E-03 BE154134.1	EST HUMAN	PM1-HT0340-151289-003-n08 HT0340 Homo sapiens curva

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					0		
Probe SEQ ID NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
3297	16471	29492	1.09	4.0E-03	4.0E-03 BE154134.1		PM1-HT0340-151298-003-h08 HT0340 Hcmo sapiens cDNA
3619	16783	29798		4.0E-03	4.0E-03 AW 188426.1	EST_HUMAN	xy98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IWAGE:26652793
3619	16783	29799		4.0E-03	.0E-03 AW188426.1		x/98/04.x1 NCI_CGAP_Co18 Homo sapien's cDNA done IMAGE:26652793'
3714	16875		0.64	4.0E-03	.0E-03 Q13606		OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875			4	.0E-03 Q13606	ISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17186	30207			4.0E-03 AF060868.1	NT	Mus musculus tumor susceptibility protein ;01 (tsg101) gene, complete cds
4102	17256			4		NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5339	18452	31420		4	.0E-03 AW 500547.1	EST_HUMAN	UI-HF-BNO-akj-e-10-0-UI.r1 NIM_MGC_50 Hamo sapiens aDNA clane IMAGE:307/466 5
5390	18592					NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete ods
5516	18713	L		4	.0E-03 AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5914	19102	32416	3.1	4.0E-03	.0E-03 P04196	SWISSPROT	(HPRG)
5918	19106	32418	1.8	ь	.0E-03 P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
6003	19188			7	.0E-03 AL133871.1	EST_HUMAN	DKFZp76111014_r1 761 (syncnym: hamy2) Homo saplens cDNA clone DKFZp76111014 6
8208	19384			7	.0E-03 U22180.1	FZ	Rettus norvegicus opsin gene, complete cdis
8363	19533			7	.0E-03 AW590572.1	EST_HUMAN	hg45c07.x1 NCI_CGAP_GC6 Homo sapleris cDNA clone IMAGE:2948652 3
8439	19606	32969	1.78	4		EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens oDNA clone IMACE:3461854 5
6089	19983			7	.0E-03 AA813222.1	EST_HUMAN	4)32f11.s1 Soares_tests_NHT Homo saplens cDNA clone 1392045 3
6914	20229		1.41	4		N	Lycopersicon esculentum knotted 3 protein (TKn3) mRNA, complete ods
7217	20082		1.12	7	.0E-03 AL163278.2	NT ·	Homo sapiens chromosome 21 segment HS21C078
7217	20082				1.0E-03 AL 163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428			•	1.0E-03 Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20860	34138	0.98	<b>,</b>	.0E-03 A1881483.1	EST_HUMAN	637912x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:2271814 3
7591	20662	34138	0.62	7	1.0E-03 BE670170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sepieris cDNA clone IMAGE:3284043 3
7693	20758		0.85	7	1.0E-03 X92109.1	NT	H.sapiens hcglX gene
	1				20 20	TOGGGGWIG	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
27.50	ı				AE444044	TIN TOTAL	V V V V V V V V V V V V V V V V V V V
823	1		3		1.0E-03 AF 111841.1	LN	Homo sanlens KIAA0345 cene product (KIAA0345), mRNA
000	ŀ	36784	7 0 07		AF13082	Ę	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cdc
0704	07870	١			0E-03 Y12855 1	LZ	Homo saplens P2X7 gene, exon 12 and 13
3	ı.						to 49b11.x1 Soares NFL_T_GBC_S1 Home sepiens cDNA clone IMAGE: 2090013 3' similar to contains Alu
<u>8</u>		35529	7.06		4.0E-03 AI553983.1	EST_HUMAN	repetitive element;
0608	22169	l			4.0E-03 AL163209.2	M	Homo sapiens chromosome 21 segment HS21C009
9100	1	35723			4.0E-03 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
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Jenta	Top Hit Descriptor	Hamo saplens chromosome 21 segment HS21C007	Hamo sapiens chromosame 21 segment HS21C007	yp42g12.r1 Soares retina N2b5HR Hamo sapiens cDNA clone IMAGE:190150 5'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55	Hamo sapiens splicing factor, arginine/serrine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA	Homo saplens chromosome 21 segment H321C006	Ureaplasme urealyticum section 3 of 59 of the complete genome	PM4-BN0138-180600-002-b08 BN0138 Hcmo saplens cDNA	601118164F1 NIH_MGC_17 Homo saplens cDNA done IMAGE:3028095 5'	UI-HF-BNO-alp-g-04-0-UI.r1 NIH_MGC_80 Hamo septens cDNA clone IMAGE:3080822 5	7q74c09.x1 NCI_CGAP_Lu24 Homo sapieris cDNA cione IMAGE: 3' similar to contains Atu repetitive element;contains demont MER31 repetitive element ;	hrozco7.x1 NCI_CGAP_Kid11 Home sepiens cDNA clone IMAGE:2953932 3' cimilar to contains element		RC3-ST0281-240400-015-f03 ST0281 Horno saplens cDNA	Homo sapiens Grb2-associated binder 2 (KIAA05/1), mKNA	Homo saplens protein kinase CK2 catarytic subunit alpha gene, exon 1	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1	nc73c05.s1 NCI_CGAP_Pr2 Homo sapients cDNA clone IMAGE:782984 similar to contains Alu repetitive element.	S.cereale (cv. Halo) mRNA for triosephosphate isomerase	Mus musculus intestinal trefoll factor gene, partial cds	Mus musculus intestinal trefoil factor gene, partial cds	oMt gene	601237982F1 NIH_MGC_44 Homo sapient; cDNA clone IMAGE:3609933 6'	IL2-UM0076-240300-056-D03 UM0076 Homo saplens cDNA	Mus musculus alpha-1(XVIII) collagen (COI.18A1) gene, excn 1 and 2		AV762392 MDS Hamo sepiens cDNA clone MDSBS G01 51	AV762392 MDS Homo septens cDNA clone MDSBSG01 5'	ah04f09.y5 Gessler Wilms tumor Homo sapiens cDNA done IMAGE:1155689 5'	euaß	umo sapiens cDNA 3
Single Exon Probes Expressed in Placenta		Hamo saplens chramos	-cmo sapiens chromos	p42g12.r1 Soares retin	Arabidopsis thaliana DN	Homo saplens eplicing ( (SFRS8) mRNA	Homo sapiens chromos	Ureaplasme urealyticum	PM4-BN0138-180600-0	501118164F1 NIH MG	UI-HF-BNO-aip-g-04-0-1	7q74c09.x1 NCI_CGAF element;contains demo	HNO2c07.x1 NCI_CGAF	LIKo repetitive element	RC3-ST0281-240400-0	Homo sapiens Grb2-as	Homo saplens protein k	Homo sapiens protein k	nc73c05.s1 NCI_CGAF element	S.cereale (cv. Halo) mR	Mus musculus intestine	Mus musculus intestine	Arabidopsis thaliana rpoMt gene	601237982F1 NIH MG	IL2-UM0076-240300-0	Mus musculus alpha-1(	C.elegans camdc gene	AV782392 MDS Hamo	AV762392 MDS Homo	ah04f09.y5 Gessler Wi	Rattus norvegicus gdnf gene	xu8.P10.H3 conorm Homo sapiens cDNA 3
Exon Propes	Top Hit Database Source	NT	INT	T HUMAN	NT .		NT	П			EST_HUMAN	EST_HUMAN		П	LHUMAN	NT	NT	LN	EST HUMAN	Γ	۲	N⊤	N⊤	П	EST HUMAN	NT	LN	EST HUMAN	EST_HUMAN	T_HUMAN	П	EST_HUMAN
Single	Top Hit Acessian No.	4.0E-03 AL163207.2	4.0E-03 AL163207.2		4.0E-03 AL161555.2	4759101 NT	4.0E-03 AL183206.2	4.0E-03 AE002102.1	4.0E-03 BE815173.1	4.0E-03 BE 298290.1	4.0E-03 AW 504273.1	4.0E-03 BF224125.1		4.0E-03 AW614596.1	4.0E-03 AW819141.1	11436965 NT	3.0E-03 AF011920.1	3.0E-03 AF011920.1	3.0E-03 AA468110.1	3.0E-03 Z32521.1	3.0E-03 U46858.1	3.0E-03 U46858.1	3.0E-03 Y09006.1	3.0E-03 BE379296.1	3.0E-03 AW802687.1	3.0E-03 U34608.1	3.0E-03 Y12500.1	3.0E-03 AV762392.1	3.0E-03 AV762392.1	3.0E-03 AI792278.1	3.0E-03 AJ011432.1	3.0E-03 AI538141.1
	Most Similar (Top) Hit BLAST E Vatue	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	. 4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03		4.0E-03	4.0E-03	4.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03
	Expression Signal	0.47	0.47	0.63	1.35	1.36	3	1.57	5.84	1.35	1,85	3.33		2.18	1.34	1.23	125	4.87	388	6.37	1.14	1.14	0.77	3.65	2.63	2.16	7.5	7.78	7.76	1.67	5.53	4.62
	ORF SEQ ID NO:	36447	36448	36768	37229	37986	38117	38762								31918	26626				28824			26338		29681		30248				30759
	SEQ ID NO:	22865	1	1	23822	24349	24455	25053	26163	L	L	ł	ı	26053	25581	25784	L	14077	l			l	1		16394	L		L	L_		1	17777
	Probe SEQ ID NO:	8828	8825	10131	10587	11283	11394	12072	12434	12457	12641	12814		12858	12871	13202	382	805	48	2367	2368	2368	3058	3162	3220	3504	3513	4086	4086	4147	4515	4641

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Children Front Trucks Laborated and Company	Top Hit Descriptor	DKFZp76180712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712.5	ab18a08,x5 Strategene lung (#337210) Horito saptens cDNA clone IMAGE:841142 3' similar to contains Alu	repetitive element	601482715F1 NIH_MGC_68 Homo saplens cDNA dana IMAGE:3885483 5	Homo capiens RAP1, G1Pase activating protein 1 (KAP1CA1) mixiva	Homo sepiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA	qe80b10.x1 Sogres_fetal_lung_NbHL19W Homo saplens cDNA clone IMACE:1746275 3 Similar to SW:AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17 ;contains MSR1.t2 MER22	repetitive element;	Homo sapiens hypothetical protein PLJ10559 (PLJ10559), mrNA	Mus musculus mRNA for hypothetical protein (UKFZ ortnogg)	Mus muscultus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2- Mb1) gene, Iow molecular weight protein 2 limp2 (Imp2) gene, complete cds	aa13/10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5	Fugu rubripes mRNA for sodium channel apha subunit, partial cds	Kluyveromyces marxianus pcpd gene for purine-cytosine permease	Oryza sativa gene for bZIP protein, complete cds	RC0-BT0812-250900-032-e07 BT0812 Homo saplens cDNA	RC0-BT0812-250900-032-607 B10812 Home sapiens curva	2b27b04.s1 Soares_parathyrod_tumor_Northy home sapiens count cione invoce.304703 3	wi24d09.x1 NCI_CGAP_Ut1 Homo sapiens GUNA Clone IMMUE.2423041 3	S. cerevisiae UCA35 gene, complete cas	HETEROGENEOUS NUCLEAR KIBONOCLEOPROTEIN AZ HOMOLOG I (FINAN PARA)	Homo sapiens chromosome zi segment nazilovoo	NONSTRUCTURAL PROTEIN V	historio XI NCI_CGAP_GU1 Homo sapiens cuna ciche image: 2809 i 3 similar du cumanis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un un manis un 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second second second second second second second second second second second second second second second second second	(Exploops) mailana Ulva Ciroliosonie +, ciriug negimenta ve desegara 2, circilar to che X57438 met	ov@d12.x1 NCL_CGAP_Kid3 Home saptents GUNA clone IMAGE: 1030241 3 Silitinal in 195.251 135_1131 HISTONE H2B.2 (HUMAN);	602035980F1 NCI_CGAP_Brn64 Homo saplens cDNA clone IMAGE:4183938 5	Synechocystis sp. PCC6803 complete gename, 3/27, 271600-402289	PARS-HT0344-071299-003-d07 HT0344 Homo septens cDNA	OL POLYPROTEIN (CONTAINS: PROTEINSE; REVENSE TRANSCAR TACL, INDONCOLLING
E EXUIT LIGUES	Top Hit Database Source	EST_HUMAN [	3	EST_HUMAN I	T_HUMAN				T_HUMAN		NT	TN	T_HUMAN	NT	LN		$\Box$		П	HUMAN	$\neg$ r	SWISSPROT	_	SWISSPROT	1444	ESI HUMAN	Į.	EST HUMAN	EST HUMAN	N <sub>T</sub>	EST_HUMAN	SWISSPROT
All III	Top Hit Acession No.	3.0E-03 AL119067.1		3.0E-03 AI732754.1	3E787946.1	3.0E-03 4506414 NT	4508414 NT		3.0E-03 AI193880.1	8922499 NT	3.0E-03 AJ249981.1	3.0E-03 U35323.1	3.0E-03 AA456701.1	3.0E-08 D37977.1	3.0E-03 AJ011419.1	3.0E-03 AB021738.1	.0E-03 BF333058.1	3.0E-03 BF333058.1	.0E-03 N92580.1	3.0E-09 AIB86028.1	1.0E-03 M63498.1	.0E-03 P51989	.0E-03 AL 163268.2	3.0E-03 Q9QM81		3.0E-03 AW613774.1	3.0E-03 AL161589.2	3 0E-03 Al016731.1	3.0E-03 BF338078.1	3.0E-03 D90901.1	3.0E-03 BE154670.1	3.0E-03 P03355
	Most Similar (Top) Hit BLAST E Vatue	3.0E-03		3.0E-03	3.0E-03	3.0E-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03	3.05-03	3.0E-03	3.0E-03	3.0E-03
	Expression Signal	0.69		2.05	6.53	6.0	6.0		1.76	3.36	1.09	83.0	8.72	0.75	1.38	3.71	60	<b>60</b>	1.4	0.47	69.0	١.	1.5	1.45		10.8	4.28	98 6				0.58
	ORF SEQ ID NO:	30978		31061	31083		31342		31347	31451		32237	33231	33744			_				<u>.</u>	35276					35866	34808			34604	1
	SEQ ID	179971	1	18085	18107	1	1	1	18381	Ĺ	ľ		Ľ		20433	<u>L</u>	L	1	ı	1	21591	1	21759		1	22270		1	┸	22664		1 1
	Probe SEQ ID NO:	4858		4955	4978	5255	5255		5282	5380	5673	5744	6683	7168	7354	7891	8124	8124	8350	8490	8510	8655	8879	8786		9192	8245	900	2000		9848	9836

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Top Hit Descriptor	Mus musculus myelin expression factor-3-like protein gene, partial cds	Homo sapiens chromosome 21 segment HS:21C102	UI-H-BI1-adt-g-10-0-UI.S1 NCI_CGAP_Sub3 Home sepiens cDNA clone IMAGE:2717010 3'	zx42a10.rf Soares_total_fetus_Nb2HF8_9vi Homo sapiens cDNA clone IMAGE:789114 5	60218396011 NIH_MGC_42 Home captions CDNA clone IMAGE: 4300070 3	H.saplens DIMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and KINGS, 9, 13 and 14 genes	Rattus norvegicus mRNA for SREB1, complete cds	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]	과13h01.r1 Stratagene fetal relina 937202 Homo sapiens cDNA clone IMAGE:609361 6	Rettus norvegicus 5-hydroxytryptemine7 receptor gene, partial cds	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds	UI-H-BW0-eir-g-03-0-UI.s1 NCI_CGAP_3cb6 Homo sapiens cDNA clone IMAGE:2730413 3	HA0507 Human fetal liver cDNA library Homo saplens cDNA	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7:49, and partial cds, atternatively soliced	And Section and the India No. 14 HBSS VI Home services CDNA clone IMAGE: 180890 3	WALL ASSOCIATED PROTEIN PRECURSOR	Homo septons X-linked arhidrotite ectodermal dysplasta protein gene (EDA), exon 2 and flanking repeat	regions	601876385F1 NIH_MGC_55 Homo sapiens oDNA clone IMAGE:4104692 5	Homo saplens mRNA for KIAA0693 protein, partial cds	Xenopus lasvis xefiltin mRNA, complete cds	ATP-DEPENDENT NUCLEASE SUBUNITIE	ATP-DEPENDENT NUCLEASE SUBUNITIB	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)	601887434F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4121408 5	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIES 7) (ADAMTS-7) (ADAM-TS7)	AV709075 ADC Hamo sapiens CDNA clone ADCAEF09 5'	Peccilentiim mRNA for havi-tRNA swithstiss (LvsRS)	Tracellation in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract o
Top Hit Database Source		NT	EST_HUMAN		EST HUMAN	L		SWISSPROT	EST_HUMAN	NT	TN	EST_HUMAN	EST_HUMAN	NT	N	F	FOT UI MAN	CIATICODOT	CALCONO		T_HUMAN	NT	NT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	TORGREIME	EST HUMAN	EV.	Ž
Тф Hit Acession No.	2.0E-03 AF302691.1	2.0E-03 AL163302.2	2.0E-03 AW137782.1	2.0E-03 AA450138.1	2.0E-03 BF568955.1	2 0E-03 XB7344.1	2.0E-03 AB040802.1	P03374	2.0E-03 AA179693.1	2.0E-03 U68491.1	2.0E-03 L35079.1	2.0E-03 AW 297380.1	2.0E-03 AI064746.1	2.0E-03 L42512.1	2.0E-03 L42512.1	2 05 03 05 223301 1	AF 223391.1	2.0E-03 K8///3.1	1000	2.0E-03 AF003528.1	2.0E-03 BF241410.1	2.0E-03 AB014593.1	2.0E-03 U63711.1	P23477	P23477	2.0E-03 Q95203	2.0E-03 Q95203	2.0E-03 BF308187.1	20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO 20 PO	2.0E-03 AV709075 1	VC 1464 4	2.0E-03 X94451.1
Most Similar (Top) Hit BLAST E Value	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	20E-03	20E-03 P03374	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	20 20	2.05-03	2.0E-03	2.05-03 1.11000	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03 P23477	2.0E-03 P23477	<u> </u>					١	
Expression Signal	1.59	76.0	4.83	4.92	98.0	5.48	0,62	2.39	1.02	13.93	1.99	1.22	1.05	2.11	2.11		77	1.57	100	98.0	1.67	1.83	2.08	3,83				7,66		2.10		1.45
ORF SEQ ID NO:	28305			29880	29686	20019							30670				A PAR		31067	31223			32325						١		22030	
Exen SEQ ID NO:	15192	Ĺ	1				$\perp$	17378	17435	1_	1_	L	17689	L	L	<u> </u>			18091	18257	L	25810	19019	1			1		<u> </u>	8/981	1	19706
Probe SEQ ID NO:	2051	2324	2647	3503	3510	9776	4062	4228	4280	4336	4632	4547	4551	4668	4668		4828	4832	4962	5132	299	5745	5828	6236	6236	6476	6478	6478		6514	8	6544

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
6736	19892		1.36	2.0E-03	2.0E-03 AIB91089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgreefe_colon_NHCD Homo sepiens cDNA clone IMAGE:2522177 3' clmilar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
6775	L	33320	0.7		2.0E-03 AA677831.1	EST_HUMAN	zł3a11.s1 Scares fetal liver spleen_1NFILS_S1 Homo saplens cDNA cione IMAGE:4306523
7098	Ĺ				2.0E-03 AB038502.1		Ceanorhabditis elegans mRNA for galectin LEC-11, complete cds
7231					2.0E-03 BE087986.1		CM4-BT0386-061289-054-d01 BT0386 Homo saplens cDNA
7294	Ι.		0.65		2.0E-03 AI29883.1	EST_HUMAN	qm99d11.x1 NCI_CGAP_Lu5 Home sapiens cDNA clone IMA/dE:1896363 3
7444	j		0.8		2.0E-03 T86569.1	EST_HUMAN	yd77g10.r1 Soares fetal liver spieen 1NrLS; Hamo septens cultiva don't living population of
7784	20860	34342	1.41	2.0E-03	2.0E-03 P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8241	ŀ		2.97		2.0E-03 AW 592004.1	EST_HUMAN	h37b08x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2834039 3 similar to 1 K:Qb097e Q60978 JERKY ;
	_		  -  -			MANUEL TOP	yk42g06.s1 Soares melanocyte 2NbHM Horno capiens cDNA clone IMAGE:264442.3' similar to contains 11 hol 1 remetitive element:
8412	21483	35023	5.49	١	2.0E-03 N2028/.1	ES JOUNAIN	LIJOZ ELI Opcouro cicurioni,
8412	21483	35024	5.49		2.0E-03 N20287.1	EST_HUMAN	ykłygób; st. Soares metanocyte znonim notifo septetis como volie introduzonny o stilling. 30 domino L1 b2 L1 repetitive element ;
8450	l		0.84		2.0E-03 Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.65 IN CHROWDSOME I
8481	上	L			P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8636	L	L		2.0E-03	IN 6005855 NT	NT	Homo sapiens Retina-derived POU-domain/factor-1 (RPF-1), mRNA
8536	L	35154	1.04	2.0E-03	IN 6005855 NT	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPI-1), mKNA
8561			1,03		2.0E-03 AU136879.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5
	L						Homo saplens ASCL3 gene, CEGP1 gene, C11onf14 gene, C11onf15 gene, C11onf16 gene and C11on117
8614	21694		60		2.0E-03 AJ400877.1	뉟	gene
9386	19018	32323	8 0.79		2.0E-03 AW 796111.1	EST_HUMAN	MRZ-UM0025-300300-102-102 UM0U25 Hemo equens conva
9386	i_	32324	62.0		2.0E-03 AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM00250 Hemo segrens curva
	L					ļ	Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitn-conjugating enzyne EZU ง (กายอาวาจากละละ ออกแก่ปลายค่อ
9441	1				2.0E-03 AF224669.1	I N	(Contract) Variety Contract School 1NFLS Home senions CDNA clone (MAGE:194296 3)
9726	_ }				2.0E-03 H50832.1	ESI HOMAN	Spougos) out of the line spinor in the company of the line line of the line in the company of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line of the line
9726	3 22791	36363	3 0.71		2.0E-03 H50832.1	EST HUMAN	yposava, statistives spiecin invited nation supraise con a variation of the spiecin supraise control of the spiecin supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control of the spiecing supraise control
	<u>L</u> .	_					TENASCIN PRECURSOR (TN) (HEXABRACHION) (OYTOTACTIN) (NEURONECTIN) (GMEM) (JJ)
-					004004	TOGGSSIMS	(MICLENDINGOS ANTIGEN) (GELOMATASOCOCIATED CATACOCIATION CONTINUED CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATACOCIATION CATAC
9/28	⅃			1	2.0E-03   2.0E-1	TOCHOO!!!!	BETA DALACTORIDASE PRECIEDOR (I ACTASE)
9868					2.0E-03 P48982	SWISSPROT	BELY-GALACIOSIDAGE PUEDINGON (CACTASE)
8986	8 22908	36494			2.0E-03 P48982	SWISSPROI	BELA-CALACTOSIDASE TRECONSON (LACTOS)
8924	ļ		0.6		2.0E-03 AF097732.1	¥	Homo sapiens caspase reduitment domain-contaming protein (bout 10) gene, compress cas

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$\Gamma$	$\overline{}$	Т	٦	Т	Т	Т	Т	Т	1	шТ	Т		Т	T	Т		Т	T			T	Т		П	٦		$\neg$
	Top Hit Descriptor	Homo sapiens caspase recruitment domain; containing protein (BCL10) gene, complete cds	QV3-OT0064-060400-144-e01 OT0064 Hojmo saplens cD/VA	zs10g06.s1 NOL CGAP_GCB1 Hamo sapiens cDNA clone IMAGE:684754 3	MR2-GN0030-140900-001-e05 GN0030 Homo saplens cDNA	Human dystrophin gene	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)	RC3-BT0333-310800-115-g04 BT0333 Horino saplens cDNA	H.saplens variable number tandem repeat (VNTR) locus DNA	tyG5h03.x1 NCI_CGAP_Kld11 Homo sapleris cDNA clone IMAGE:2283889 3° similar to SW:VA I G_MANSE  Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G;	Hamo sapiens SEL1L (SEL1L) gene, partial cds	oy43g06.s1 Soares_parathyrold_tumor_Nbl;IPA Homo oxpiens cDNA clone IMAGE:1668834.3' similar to TR:P97s35 P97535 PS-PLA1 PRECURSOR.;	Camelus dromedarius cvhp19 gene for Immimoglobulin heavy chain variable region	AV897968 GKC Homo saplens cDNA clone GKCGXD05 5'	H. saplens M1 gene for muscarinic acetylcholine receptor	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G6c, G5b, G6d, G6a, G6f, BAT5, G5b, G5K2B, BAT4, G4, Apo M, BAT3, BAT2, Alf-1, 107, LST-1, LTB, TNF, and LTA genes, complete cds	AV697968 GKC Homo saplens cDNA clone GKCGXD05 5'	y08c08.r1 Soares_pineal_gland_N3HPG Homo saplens cDNA clone IMAGE:232334 5	es70b08.x1 Barstead colon HPLRB7 Homo copiens cDNA clone IMAGE:2334039 3' smiter to 1R:Q13825   Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE.;	as70b08.x1 Barstead colon HPLRB7 Horno saplens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE.;	wk86g06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3	wx83e10x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'	wd86e01x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu penditive element:	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)	Homo sapiens SCL gene locus	Homo sapiens mRNA for KIAA1291 protein; partial cds	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE)
	Top Hit Database Source	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	۲	SWISSPROT	EST_HUMAN	TN	EST_HUMAN	IN	EST_HUMAN	N	EST HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	DOT LIMAN	SWISSPROT	Ā	μN	SWISSPROT
,  -	Top Hit Acession No.	2.0E-03 AF097732.1	2.0E-03 AW884269.1	2.0E-03 AA251376.1	2.0E-03 BF367386.1	MB6524.1	207354	2.0E-03 BF330909.1	211740.1	2.0E-03 AI625745.1	2.0E-03 AF157516.2	2.0E-03 A1084325.1	2.0E-03 AJ245167.1	2.0E-03 AV697966.1	Y00508.1	2.0E-03 AF129756.1	2.0E-03 AV697966.1	1.0E-03 H96471.1	1.0E-03 AI720263.1	1.0E-03 AI720263.1	1.0E-03 Al865788.1	1.0E-03 Al9545721	00 00 00 00 00 00 00 00 00 00 00 00 00	P47808	1.0E-03 AJ131016.1	1.0E-03 AB033117.1	P18915
	Most Similar (Top) Hit BLAST E Value	2.0E-03 /	2.0E-03	2.0E-03	2.0E-03	2.0E-03 MB6524.1	2.0E-03 P07354	2.0E-03	2.0E-03 Z11740.1	2.0E-03	20E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03 Y00508.1	2.0E-03	2.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03				1.0E-03	
	Expression Signal	0.6	0.96	6.26	0.49	2.14	3.79	2.36	9.64	3.37	4.31	1.71	4.86	4	1.29	1.38	2.46	1.38	. 1.55	39:1	2.61	1.61	i c	2 42	9 52	1.37	2.81
	ORF SEQ ID NO:	36553	l		37270		34342		38526	<u> </u>	38833		L		32039			26684			l	l		21412			<u> </u>
	Exan SEQ ID NO:	22864	L	23283	1	l_		L			L	1		1	1	l _				1	ı		i	45534	_1_	L	
	Probe SEQ ID NO:	9924	10118	10248	10828	11265	11778	11836	11844	12180	12198	12222	12245	12482	12561	12897	13090	452	862	852	1119	1139		ZALL	2222	3044	3280

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Top Hit Descriptor	CARBONIC ANHYDRÁSE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Human MUC2 gene, promoter region	Hunan MUC2 gene, promoter region	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15	აი63407.x1 Sogres_NHCeC_cœrvical_tumoi Hamo sapiens cDNA clone iMAGE:2698381 3' similar to contains TAR1.11 TAR1 repetitive element ;	S.cerevisiae chromosome X reading frame (JRF YJR149w	RC1-TN0128-160800-021-g01 TN0128 Homo saplens cDNA	TCBAP1D4809 Pediatric pra-B cell acute lymphoblastic leukemia Baylαr-HGSC project=1CBA Homo sapiens cDNA clone TCBAP4809	Caenorhabditis elegans spliced leader RNA(SL3 alpha), (SL4), and (SL5) ganes	ov45c04.x1 Sogres_testis_NHT Homo sapions cDNA clone IMAGE:1640262 3'	ov45c04.x1 Soares_test(s_NHT Homo sapiens cDNA clone IMAGE:1640262 3'	PM0-HT0339-200400-010-D02 HT0339 Hcmo saplens cDNA	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)	M-51602x1 NCI_CGAP_Lu24 Homo saptens cDNA clone IMAGE:3178955 3	234401.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5	Homo sapiens KVLQT1 gene	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds	Epctein-Barr virus (AG876 isolate) U2-IR2 comain encoding nuclear protein EBNA2, complete cds	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IN/AGE:3943954 5	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)	yyO7h08.r1 Soares melanocyte 2NbHM Hono sapiens cDNA done IMAGE:270587 5' similar to contains element MER8 repetitive element;	уу07h08.r1 Soares melanocyte 2NbHM Honio sapiens cDNA done IMAGE:270587 5' similar to contains	element MER6 repetitive element;	602088042F1 NIH_MGC_68 Homo capiene cDNA clone IMAGE:4068907 5	Mouse nucleolin gene	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3	Homo sapiens T-cell lymphome invesion and metastasis 1 (TIAM1), mkNA	yd93a11.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:115772.5	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
Top Hit Database Source	SWISSPROT	SWISSPROT	NT	TN	TN	EST_HUMAN		EST_HUMAN	EST HUMAN	Г	EST HUMAN	Г	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	NT	NT.	NT	EST_HUMAN	SWISSPROT	EST HUMAN	1	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	NT	EST_HUMAN	EST HUMAN
Top Hit Acession	18915	208547	J68061.1	J68061.1	1.0E-03 AB044400.1	1.0E-03 AW170552.1	249849.1	1.0E-03 BE939162.1	1 0E-03 BE248538 1	129449.1	1.0E-03 AI073485.1	1.0E-03 AI073485.1	1.0E-03 BE154087.1	048409	1.0E-03 BE219340.1	1.0E-03 AA290951.1	1.0E-03 AJ006345.1	1.0E-03 K03332.1	1.0E-03 K03332.1	1.0E-03 BE796491.1	Q02388	1 0F-03 N41974 1		1.0E-03 N41974.1	1.0E-03 BF541639.1	1.0E-03 X07699.1	1.0E-03 BE963939.2	11526176 NT	1.0E-03 T87761.1	1.0E-03 AW902585.1
Most Similar (Top) Hit BLAST E Value	1.0E-03 P18915	1.0E-03 P08547	1.0E-03 U68061.1	1.0E-03 U68061.1	1.0E-03 /	1.0E-03	1.0E-03 Z49849.1	1.0E-03	1 05-03	1.0E-03 U29449.1	1.0E-03	1.0E-03	1.0E-03	1.0E-03 O46409	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03 Q02388	1 DF-03		1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03
Expression Signal	2.81	0.75	0.94	96.0	1.43	0.98	0.91	2.34	08.7	0.0	2.54	2.54	9	15.5	4.73	7	3.57	1.64	1.64	0.95	1.7	8	?	9.0	95.0	2.75	0.85	8.77		1.68
ORF SEQ ID NO:	29452					30200		30673						31276			İ_	L	31810		32181	_		32245			32708		32992	
SEQ ID	18434	1	ı	ı	ı	l		ı	1	265	1	1		L	i .	ı	١.	ı	18768	ı	18890	18043	L	18943	L	19322	19360	<u> </u>		19702
Probe SEQ ID NO:	3260	3374	3632	3632	3755	4034	404	4556	6097	4785	4045	2 8 8 8	4948	5188	5324	5423	5518	5572	5572	2690	5696	£7£4	3	5751	6033	6144	6184	6321	6484	6239

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WO 01/57272

	Homo seplens DiGearge syndrome critical region, centromeric end	Humen gene for fourth sometostatin receptor subtype	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3	Homo eqpiene X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrendeukodystrophy protein >	Human TRPM-2 protein gene, exons 1,2 and 3		Hamo sapiens prolactin-releasing peptide receptor gene, 5' flanking region	Homo sapiens partial steerin-1 gene		1	Rattus norvegicus plasma membrane Ca2+/ATPase isoform 3 (PMCA3) gene, 5' flanking region	V.carteri gene encoding valvaxopsin		Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dépendent protein kinase I (GAMKI), creatine transporter (CRTR),	CDM protein (CDM), adrenoleukodystrophy protein >	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds	Human class III alcohol dehydrogenasa (ADH5) chi subunit mRNA, complete cds		П	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds			Homo capiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds			Pseudomonas aeruginosa PA01, section 323 of 529 of the complete genome
Top Hit Database Sœurce	N	IN	NT	ΤΝ	P	EST_HUMAN	N	M	EST HUMAN	Z	LZ	IN	EST_HUMAN		<u>k</u>	N	NT	EST HUMAN	TN	N		SWISSPROT	NT	TN	EST HUMAN	L	۲
Top Hit Acession No.	0E-03 L77570.1	0E-03 D16826.1	0E-03 AJ229042.1	0E-03 U52111.2	0E-03 M83378.1	0E-03 BE880044.1	0E-03 AF274581.1	0E-03 AJ251973.1	0E-03 AA122270.1	0E-03 AF153980.1	.0E-03 U29397.1	0E-03 Y11204.1	.0E-03 AW840353.1		.0E-03 U62111.2	0E-03 M30471.1	.0E-03 M30471.1	0E-03 AI247482.1	.0E-03 AF011400.1	.0E-03 AF011400.1		.0E-03 Q0112B	.0E-03 AF003529.1	.0E-03 AF097485.1	0F-03 A1024350.1	.0E-03 AE004782.1	1.0E-03 AE004782.1
Most Similar (Top) Hit BLAST E Value	1.0E-03	1.05-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03		1.0E-03	1.0E-03	1.0E-03		_	_						_	1.0E-03	-			
Expression Signal	1.41	281	1.12	1.98	3.44	0.79	99.0	5.02	1.05	2.36	0.75	1.48	0.65		0.65	3.89	3.89	0.47				0.88	9.37				
ORF SEQ ID NO:		33843		34370							İ		35791			35947			L	38425		36660		l	97185	1	
Exon SEQ ID NO:	20046	.L_	1_		1	20984	1	1	l	1	1		ı	1_	22367	1	22395	i i	1	22847	1_		23401	1	1		23856
Probe SEQ ID NO:	6895	7302	7658	7817	7885	7934	8073	8136	0227	3 8	RRZS	9144	9470		0284	840	8319	9020	2000	9807		10025	10366	10372	6	10823	10823

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	Top Hit Descriptor	ag93/12.s1 Stratagene hNT neuron (#837233) Homo sepiens cDNA clone IMAGE:1142083 3' similar to contains Alu repotitive element;	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA	RC1-CT0279-181099-011-a09 CT0279 Homo saplens cDNA	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA	tt73612.x1 NCI_CGAP_HSC3 Homo saplens cDNA clone IMAGE:2246446 3' similar to TR:026195 0.26195	PVA1 GENE.	AV759949 MDS Homo sapiens curva clone MUSUUTTT 9	PROTEIN-TYROSINE PHOSPHALASE DEL LA PRECURSOR (R+11-DEL LA)	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELIA)	PROTEIN GRAINY-HEAD (DNA BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY)	(TRANSCRIPTION FACTOR NTF-1)	601433087F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3918524 5	to05h11x1 NCI_CGAP_Co16 Homo saplers cDNA clone IMAGE:2063013 3' similar to contains Alu	repetitive element;	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5	Nicotiana tabacum chloroplast, complete genome	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)	Homo sapiens KVLQT1 gene	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1	Glycynthiza glabra GgbAS1 mRNA for beta-amyrin synthase, complete cds	X.læavis mRNA far C4SR pratein	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Homo saptens prion protein (PrP) gene, complete cds	#24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3	th85a08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2176310 3	Homo saplens CYP17 gene, 5' end	Homo sapiens prion protein (PrP) gene, complete cds	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome X open reading irame o (CAURFO) mRIVA
	Top Hit Database Source	EST_HUMAN co	EST_HUMAN R	EST_HUMAN R	EST_HUMAN Q		Т	П			PI SWISSPROT (T	Т	SWISSPROT (1	EST_HUMAN 6	8	UMAN	UMAN		SPROT			ISSPROT	NT		SWISSPROT			T HUMAN				
	Top Hit Acession No.	.0E-03 AA706202.1	_	.0E-03 AW362303.1				.0E-03 AV759949.1						.0E-03 BE894488.1		.0E-03 Al347355.1	.0E-03 BE780572.1	11465934 NT			3.0E-04 AJ006345.1		1.1	3.0E-04 X96469.1		1	8.0E-04 AA777084.1	8.0E-04 AI571099.1	7.0E-04 L41825.1	7.0E-04 U29185.1	AL 16321	4885170 NT
Most Similar		1.0E-03	1.0E-03 /	1.0E-03/	1.0E-03		1.0E-03 /	1.0E-03 /	1.0E-03 P23468	1.0E-03 P23468	1 0F-03 P13002		1.0E-03 P13002	1.0E-03		1.0E-03	1.0E-03	1.0E-03	9.0E-04 P08548	9.0E-04 P06727	9.0E-04	9.0E-04 P02381	9.0E-04	8.0E-04	8.0E-04 P08547	8.0E-04	8.0E-04	8.0E-04	7.0E-04	7.0E-04	7.0E-04	7.0E-04
	Expression Signal	0.53	2.01	2.01	2.40		2.03	2.63	2.17	2.17			1.53	. 5.51		7.37	3,83	1.17	0.7	2.08	0.58	1.27	1.46	1.07	4.4	2.5	2.59	1.87	1.11	1.45	1.33	1.4
	ORF SEQ ID NO:		37617						38543				38612				31551		31409			33166	L			31002			28127			
	SEQ ID NO:	i i	ı	23988	1		24138	24486	1		i i	21247	24910	L	1	26118	<u>l_</u>	L		L	ļ_	1	١.	L	L			L		Ł	L.	16526
	Probe SEQ ID NO:	10830	10902	10902	10989		11062	11426	11858	11858	***	1761	11824	12175		12679	12812	12889	6327	5789	6388	6615	9843	1517	4298	4887	11412	11578	1874	2472	2778	3353

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Top Hit Descriptor		QVO-CT0225-021099-030-607 CT0225 Homo sepiens cDNA	nk27e11.s1 NCI_CGAP_Co11 Home sapie;is cDNA clone IMAGE:1014764 3' similar to contains Alu	repaired defining a spirit of the said Metal Oppose MITH TUBOMBOSDONDIN	ADAM-IS / PRECURSOR (A DISIN EGRIN AND METALLOPROTEINASE WITH TRINGWISON ONE). MOTIFS 7) (ADAMTS-7) (ADAM-TS7)	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	zo33b08.r1 Stratagene colon (#937204) Homo sapiens cDNA done IMAGE:588663 5'	Gorilla gorilla involucrin gene medium allele, complete cds	dd13f06x1 Soares_placenta_8to9weeks_2\bHP9to9W Homo saplens cDNA done (MAGE:17236193' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element,	cobsects.s1 NCI_CCAP_CCB1 Homo capions cDNA clone IMAGE:1339226 3' similar to contains element MED22 contains element	MENZZ repeture centralit. a55th03.st Soares, tests. NHT Homo septens cDNA clone IMAGE:1394357.3'	AND STATE IT. SALE LONG 1 MANUAL TAND STATES HOME COND. CHOOSE KK2745 5' SIMILATO	KKZ745F Human retai neart, Lambda 24F Express noine saprens corrollar and a common and REPETITIVE ELEMENT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR	xs06e02.x1 NCI_CGAP_Kid11 Homo capiens cUNA clone IMAGE:2700833 3	Human familial Alzheima's disease (STMZ) gene, complete cos	DKFZp586MZ024_71 386 (synonym: nuter) Homo sapiens count clone out choosings.	Bos taurus micromdar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	m15h02.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clane II/AGE:913875	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cas	601876534F1 NIH_MGC_55 Homo sepiens cDNA clone IWAGE:4104887 3	Haemophilus Influenzze Rd section 63 of 163 of the complete genome	se70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to 1 K:Q13825 Q13825 AU-BINDING PROTEIVENOYL-COA HYDRATASE. ;	as70b08.x1 Barstead colon HPLRB7 Homo capieno cDNA clone IMAGE:2334039 3' similar to TR:013825 013825 AU-BINDING PROTEIV/ENOYL-COA HYDRATASE.;	RC3-CT0254-130100-023-f01 CT0254 Honio sapiens cDNA	Homo saplens chromosome 21 segment HS21C078	DKFZp434D059_r1 454 (synonym: niess) riamo sapiens cuiva cione un rzy4540059 5
Top Hit		EST_HUMAN C		ESI_HUMAN	SWISSPROT N	B FA	EST_HUMAN z		EST HUMAN		EST HUMAN	Т			T HUMAN	П	EST_HUMAN		T_HUMAN		T_HUMAN	NT	EST HUMAN		П	П	EST HUMAN
Top Hit Acession	o N	.0E-04 AW851844.1		5.0E-04 AA548931.1	5.0E-04 Q9UKP4	3.0E-04 AF248054.1	5.0E-04 AA156080.1	5.0E-04 M23604.1	B 0F-04 A 188382 1		5.0E-04 AA814519.1	A404040.	5.0E-04 N83765.1	6.0E-04 P29128	5.0E-04 AW270938.1	5.0E-04 U50871.1	6.0E-04 AL048507.2	5.0E-04 AF248054.1	5.0E-04 AA568513.1	5.0E-04 U63834.1	4.0E-04 BF241482.1	4.0E-04 U32748.1	4.0E-04 A 720263.1	4.0E-04 AI720263.1	4.0E-04 AW753356.1	4.0E-04 AL163278.2	4.0E-04 AL048704.1
Most Similar (Top) Hit	BLAST E Value	5.0E-04		5.0E-04	5.0E-04	3.0E-04	5.0E-04	5.0E-04	20F-04			3.05-04	5.0E-04	6.0E-04	5.0E-04	5.0E-04	6.0E-04		5.0E-04	5.0E-04	4.0E-04	4.0E-04		<u> </u>			
Expression	Signal	2.03		1.6	0.94	2.51	7 08	9.01	4. 4.	33	0.95	70.	0.58	0.64	4.78	9.0	1.9	15	2.39	1.33	0.75	1.36	1.55				1.1
- 0	Ö Q			29677	28972					1	35115				ŀ			31830				26907	<u> </u>	1			
Exam	S S	14884	l	16667	16969		1	١.		1	- 1	22534	22713	١_	L	23619	24289	18784			L	L		1	1		15337
Probe	S S S	1531		3200	3809	6580	6785	7534	0	2	8468	9477	9571	9718	6086	10484	11220	12012	12301	12872	£63	69	RZ0	978	1493	2148	2202

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					į		Children Exolitioned Explored III I lacorina
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	4.0E-04 O98815	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
3233	L	29420		4.0E-04	4.0E-04 AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, attematively spliced
4397	<u> </u>			4.0E-04	4.0E-04 A1720263.1	EST HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sepiens cDNA clone IMAGE:2334039 3' similar to 1 R:Q13825 Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE.;
3443				4.0E-04	4.0E-04 AV696624.1	EST HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFFH07 5
4443	<u> </u>			4.0E-04	4.0E-04 AA578331.1	EST HUMAN	rh10a10.s1 NCI_CGAP_Co1 Homo sapleris cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4443	<u> </u>		i.	4.0E-04	4.0E-04 AA576331.1	EST_HUMAN	rh10a10.s1 NCI_CGAP_Co1 Homo sapien's cDNA clone IMAGE:951930 3' sImilar to gb:M21121 T-CELL speciFIC RANTES PROTEIN PRECURSOR (HUMAN);
4669	١_	30781	2.33	4.0E-04	4.0E-04 AA086324.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cUNA done iMAGE:302070 3
5199	1			4.0E-04	4.0E-04 BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5
7418	``		1.55	4.0E-04	4.0E-04 P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7705				4.0E-04	4.0E-04 AL161566.2	·	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7898	1	34456		4.0E-04	4.0E-04 AU122079.1	EST_HUMAN	AU122078 MAMMA1 Homo saplens cDNA/clone MAMMA1001620 6'
8733	L			4.0E-04	4.0E-04 BF240712.1	EST_HUMAN	G01876985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5
8741	L			4.0E-04	4.0E-04 N25507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2NbHM Homo sepiens cDNA clone IMAGE::264142.5
9892			3.37	4.0E-04	4.0E-04 A1025699.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3
10045	1_		1.12	4.0E-04	4.0E-04 AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12691	_		1.56	4.0E-04	4.0E-04 AF254822.1	TN	Homo sapiens SMARCA4 Isoform (SMARCA4) gene, complete cds, alternatively spliced
5	L	26415	3.21	3.0E-04	3.0E-04 AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) (Homo sapiens cDNA clone DKFZp761J2Z1 5
200	13423	28454	1.7	3.0E-04	3.0E-04 P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE AZ RECEPTOR PRECURSOR (PLAZ-K)
883	l		1.63	3.0E-04	3.0E-04 U83991.1	NT	Human short chain acyl CoA dehydrogenasis gene, exons 1 and 2
1886	I	28137	1.7	3.0E-04	3.0E-04 AI262100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kid11 Home saplens cDNA clone IMAGE::2028197 b
190	L		26'0	3.0E-04	3.0E-04 AI399674.1	EST_HUMAN	ht23a02.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2119082 3
3383			4.35		3.0E-04 P25147	SWISSPROT	INTERNALIN B PRECURSOR
4071	17227	30234	4.94		3.0E-04 P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4167			1.36		3.0E-04 AJ271735.1	NT	Homo saplens Xq pseudoaufosomal region; segment 1/2
4205	17354		1.06		3.0E-04 BE140609.1	EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens CDNA
4635	L.,		1.16		3.0E-04 BE148546.1	EST_HUMAN	MR0-HT0241-030200-008-e01 HT0241 Homo capiens cDNA
4937	L		5.2			EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Hano sepiens cDNA
5004	18133	31107			3.0E-04 AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Hamo sapiens cDNA
6271	1				3.0E-04 AL163281.2	닏	Homo sapiens chromosome 21 segment HS21C081
6929	1	33611		L		NT	Homo seplens chromosome 21 segment HS21C078

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Top Hit Descriptor	RC4-NN0027-060400-011-b08 NN0027 Hamo saplens cDNA	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)	zx48408.r1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:785471 5' similar to gb:M82762 VACUOLAR ATP SYNTHASE 16 KD PROTECUPID SUBUNIT (HUMAN);	wt76a11.x1 Soares_thymus_NHFTh Homo saplens cDNA clone IMAGE:2513276 3'	ajz4g05.s1 Soares_testis_NHT Homo sapiens cDNA cione 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);	nc38e04.r1 NCI_CGAP_Prz Homo saplenii cDNA done IMAGE:1010430 similar to contains L1.tz L1 repetitive element;	Homo saptens mRNA for KIAA0749 protein, partial cds	DKFZp647L186_r1 647 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp647L186 5'	Homo saptens SCG10 like-protein, helicast-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'	Human dystrophin gene	Human dystrophin gene	qh99e11.x1 Soares_NFL_T_GBC_S1 Horrio septens cDNA clone IMAGE:1858052 3' similar to contains MER3.b2 MER3 repetitive element;	Homo saplens chromosome 21 segment HS21C003	Mus musculus 5' flanking region of Plb/3 gene	zu39b05.s1 Soares ovary turnor NbHOT Homo sepiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element,	Human germilne T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1, TCRBV14S1,	TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA done IMAGE:1539760 3	Homo capiens tubulin, beta, 4 (TUBB4) mRNA	QV2-BT0636-070500-194-b07 BT0636 Hamo capiens cDNA	EST390550 MAGE resequences, MAGP Homo sapiens cDNA	Phaseolus vulgaris nitrate reductase (PVNR2) gane, complete cds	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE 732555	w01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cunA cione inracci.cscope o
Top Hit Database Source	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT.	EST HUMAN	FZ	EST HUMAN	TN	NT	EST_HUMAN	NT	NT	EST_HUMAN		NT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	Ŋ	EST_HUMAN	EST HUMAN
Top Hit Acession No.	3.0E-04 AW893981.1	23468	22807	3.0E-04 AA454055.1	3.0E-04 Al992139.1	3.0E-04 AA781201.1	3.0E-04  AA228301.1	3.0E-04 AB018292.1	3.0E-04 AL134483.1	2.0E-04 AF217796.1	2.0E-04 AU146707.1	2.0E-04 M86524.1	2.0E-04 M86524.1			١.	2.0E-04 AA478980.1		2.0E-04 U68061.1	2.0E-04 AI124529.1	5174736 NT	2.0E-04 BE082317.1	2.0E-04 AW978441.1	2.0E-04 U01029.1	2.0E-04 H96265.1	2.0E-04 H96265.1
Most Similar (Top) Hit BLAST E Value	3.0E-04 /	3.0E-04 PZ3468	3.0E-04 P22807	3.0E-04/	3.0E-04	3.0E-04	3.0E-04	3.0E-04	3.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04		2.0E-04	2.0E-04	2.0E-04					
Expression Signal	79'0	0.73	2.16	128	0.46	1.98	2.39	2.54	4.81	1.33	2.67	5.02	5.02	2.78	2.6	1.71	1.21		6.42		0.82	2.58	0.98	5.5		1.76
ORF SEQ ID NO:	31471			l			<u> </u>	L		26432									28878	L	L	29697	L.			
Exch SEQ ID NO:	18556		1_	<u> </u>		I	١.	L	ı	L	上	L	L		L	L	1		15764	上	1	L	L	17408	_	17926
Probe SEQ ID NO:	7130	7765	8454	10124	10384	10676	12240	12848	13114	180	169	930	830	1208	1213	1879	2267		2641	3052	3415	3622	4022	4261	4791	4791

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		_		_	_	_	-,-		_	-	_	-	-	_		1		-		-	$\neg$	7	т	T		Т	т	Т	7	$\overline{}$	٦.
Top Hit Descriptor	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds	Danko rerio hagoromo gene, exons 1 to 6, partial cds	Dictyostelium discoldeum Interaptin (abpD) gene, complete cds	AV654352 GLC Homo sapiens cDNA clane GLCDUH10 3	Iq03b11x1 NCI_CGAP_Ut3 Homo septens;cDNA clone IMAGE:22077093	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene	AU121712 MAMMA1 Homo seplens cDNA clone MAMMA1000798 3	QV0-CT0387-180300-167-e10 CT0387 Hamo sapiens cUNA	UNE-1 REVERSE TRANSCRIPTASE HOWOLOG	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN- JASSOCIATED PROTEIN)	Scienum lycopersicum phytochrome F (PHYF) gene, partial cds	Scienum Iyoopersicum phytochroma F (PHYF) gene, partial cds	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	Conjugació das)	nome segments Drive, Decor to Great British agon, control of the case)	Homo sapiens FRA3B common fragile region, diadenosine trphosphate hydrolase (FHIT) gene, exon 5	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)	at22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3	GASTRULA ZINC FINGER PROTEIN ALCGF28.1	RC3.HT0264-161099-011-505 H10254 Homo sapiens GUNA	ZIGGC11.1 Soares testis NH1 home suprems and in increase the source of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the suprementation of the 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Top Hit Database Source	L	Þ	N	EST_HUMAN	<b>EST_HUMAN</b>	EST HUMAN	N	NT NT	EST_HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	NT	N.	ļ	Z	NT	TN	TN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	뉟	뒫
Top Hit Acession No.	J09226.1	2.0E-04 AB037997.1		_		2.0E-04 AA296652.1	4758179 NT	2.0E-04 AF140708.1	2.0E-04 AU121712.1	2.0E-04 AW860963.1	208548	P54286	2 0F-04 U32444.2	2.0E-04 U32444.2		2.0E-04 AB026898.1	2.0E-04 AB026898.1	2.0E-04.AF020503.1	2.0E-04 X57331.1	2.0E-04 AA725700.1	P18715	2.0E-04 BE149303.1	2.0E-04 AA405777.1	2.0E-04 AV730373.1		2.0E-04 A1440282.1	2.0E-04 AW136740.1	2.0E-04 BE065781.1	2.0E-04 P21733	2.0E-04 L19248.1	2.0E-04 D87675.1
Most Similar (Top) Hit BLAST E Value	2.0E-04 U09226.1	2.0E-04	2.0E-04	2.0E-04	2.0E-04/	2.0E-04	2.0E-04	2.0E-04 /	2.0E-04	20E-04	2.0E-04 P08548	2.0E-04 P54298	2 OF 04	20E-04		2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04	2.0E-04 P18715										
Expression Signal	1.22	1.47	0.92	1:11	1.83	0.83	0.92	1.01	2.57	0.84	13.68	1 45	1 00	1.02		1.24	124	214	0.67	89.0	0.47	1.16		3.88		2.68		271	32.04	2.05	1.29
ORF SEQ ID NO:		31256	L			L						34357				35094	35095	<u> </u>				36808	36847			38318			38790	38806	6
Exon SEQ ID NO:	18046	L		١.	1	1_	١.		1	L	į .	1	ı	1	Į	21560	21560		上	1	ı	ļ	23259	L	l	24638		L	ı		1 26179
Probe SEQ ID NO:	4916	5174	5216	5661	5874	5868	9909	6369	7378	7478	7798	1000	200	8442		8479	8479	8368	8044	9535	9619	1018	10223	11088		11585	11710	11859	12106	12121	1319

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acessian No.	Top Hit Database Source	Тор Hit Descriptor
788	13987	27018	96.0	-	.0E-04 H99646.1	EST HUMAN	yx26c09.s1 Soares melanocyte 2NbHM Horno sepiens cDNA clone IMAGE:262864 3' similar to contains L1.t1 L1 repetitive element;
						1000000	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE;
2 3	- 1	27322			0E-04 P11369	EST HIMAN	UI-H-BIG-eab-6-09-0-UI:s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	2027		97.6			EST HUMAN	UI-H-BIO-aab-0-09-0-UI.s1 NCI_CGAP_Sub1 Homo saplens cDNA clone IMAGE:2708825 3'
1383	L				0E-04 U62918.1	Ę	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcome associated herpesvirus O/RF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosyflormytilychamidine synthase, and LAMP
1657	14810	27894	4.23	_	.0E-04 AF148805.1	L	(LAMP) genes, complete cds
	L						Keposi's sercome-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosyformylglycinamidine synthase, and LAMP
1667	14810		4.23		.0E-04 AF148805.1	N	(LAMP) genes, complete cds
1909	1_				.0E-04 AB048342.1	LN	Equus caballus DNA, chromosome 24q14, inicrosatellite TKY36
2752	1	28978			.0E-04 BE218833.1	EST_HUMAN	hv46c08.x1 NCI_CGAP_Lu24 Homo saptens cDNA clone IMAGE:3176366 3'
2762	ı	ŀ	1.08		.0E-04 BE218833.1	EST_HUMAN	hv45c08.x1 NCI_CGAP_Lu24 Homo sapients cDNA clone IMAGE:3176368 3'
3356	16528		1.18	1	.0E-04 Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 34 SUBUNIT 2) (SPSABO)
	1			. `	0000	HOL	#01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repeditive
3829					1.0E-04 A1440282.1	ESI_HUMAN	Marion date 4 tree IV colleges mBNA
4171		30314			1.0E-04 M14042.1	2	Wobse spire I type-to compart in the Coppose 2
4192					1.0E-04 AV647727.1	EST HOMAN	AV64//2/ GLC Horno Saptens GLNA Glandis GLCDBOUGH S
5207	18328		1.24			LN.	Homo eaplens KIAAU237 gene product (KIAAU237), mrNA
5207	1			1.0E-04	7662015 NT	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mKNA
5980	١.	32485			1.0E-04 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9269	19731	33109			1.0E-04 AA177111.1	EST_HUMAN	no02e12.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:252
9077		33633	990		1.0E-04 AA564561.1	EST HUMAN	nj25a04.61 NCI_CGAP_AA1 Homo sapiens' cDNA done IMAGE:99348B 3' similar to gb:M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN);contains Alu repetitive element;
7336	3 20417				1.0E-04 AI251980.1	EST_HUMAN	qv67d10.x1 NCI_CGAP_Ov32 Homo septens cDNA clone IMAGE:1985683 3'
7744	1				1.0E-04 AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_0v32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	ı				1.0E-04 AA630453.1	EST_HUMAN	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3
9538	L		2.75		1.0E-04 AI806220.1	EST_HUMAN	wr26e08.x1 Soares_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE:2356/42 3
9548		L			1.0E-04 088969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSUR (CYSTATIN 6)
9625	5 22680		0.76		T77153.	EST_HUMAN	yd72c08.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA cione IMAGE:113774 5
9846	8 22888	36468		1.0E-04	10863876 NT	NT.	Homo sapiens phospholipid scrambase 1 (FLSCR1), mRNA

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Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Percent   Perc	r		7	_,	_	7	7		Т		-		Т	т		7	7		т		┑		7	7	7	T	т	丁		T	T	٦
Expn SEQ 1D ID NO:         Expression Signal         (Top) Hit LOP) Hit Value         Most Similar Value         No. Pub. Pub. Pub. Pub. Pub. Pub. Pub. Pub	ל באדי פסטינים	Top Hit Descriptor	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	ZINC FINGER PROTEIN 157	Mouse alpha leukocyte Interferon gene, complete cds	Hamo sapiens mRNA for KIAA1142 protein  partial cds	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:2816518 3'	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	an45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'	WiS4c11.X1 NCI_CGAP_CO16 Homo sapieris cDNA clone IMAGE:2394068 3' similar to contains MER6.t1 MER8 repetitive element :	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR	UI-H-BI1-aer-d-05-0-UI.c1 NCI_CGAP_Suk3 Homo capiens cDNA clone IMAGE:2720289 31	UI-H-BI1-acr-d-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'	Homo sapiens gene for cholecystokinin type. A receptor, complete cds	Homo saplens methyl-CpG binding protein 1 (MBD1) gene, exon 15b	xa34g05.x1 NCI_CGAP_Br18 Homo saplens cDNA clone iMAGE:2568728 3' similar to contains L1.t2 L1 renetitive element :	ov23f08x1 NCI CGAP Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element	MIR repetitive element;		Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6b, G6d, G6e, G6f, BAT6, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds	Pisum sativum mRNA for beta-1,3 glucanasə (gns2 gene)	Pisum sativum mRNA for beta-1,3 glucanasi (gns2 gene)	Human platelet-derived growth factor A chain (PDGFA) gene, exons only	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2554638 3'	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	2588h01.s1 NCI_CGAP_GCB1 Home sapiens cDNA clone IMAGE:704683 3' similar to contains Alu	Perfective defined hydrollights eventually represented the second of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect of the perfect	The Strong grows At EACTORS Lower analyses CONT.	NOST INCOME TO THE TOTAL OF THE SECOND SECOND
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Expn SEQ 1D NO:         ORF SEQ ID NO:         Expression Signal Signal D NO:         Most Signal Signal NO:         Most Action           22447 23456         37050 37431         1.12 2.3         2.3 2.45           24673 24673         3.59 3.473         2.3 3.59 3.473         2.3 3.59 3.473           24673 3880 3880 3870 3870 3870 3870 3870 38	9110	Top Hit Acessian Na.	P08547	P08548	P51786	M28587.1	AB032968.1	AW269081.1	<b>ට</b> ගැනෙන	Q03696	AA718933.1	A1762208 1	060716	AW 204958.1	AW 204958.1	D85606.1	AF120982.1	AW073078 1		AI287878.1	Q60716	AF129756.1	AJ251648.1	AJ251646.1	M83575.1	AW044605.1	Y11668.1	M69197.1	1 000000	AAZ/8333.1	AVV OPT 1990.	AW84/443.1
Exon ORF SEQ Express SEQ ID NO: Sigma NO: 224477 37451 24678 38837 24678 38830 24678 38830 24678 38127 22839 38127 22839 38127 22839 38127 22839 38127 22839 38127 22839 38127 22839 38127 22839 38127 22839 38127 22839 38130 22839 38146 22827 38148 22827 38158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158 28158			1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	9.0E-05	0.50	9.0F-05	9.0E-05	9.0E-05	9.0E-05	9.0E-05	20 DE 08		9.0E-05	9.0E-05	9.0E-05	8.0E-05	8.0E-05	8.0E-05			8.0E-05	Lo	1	١	
Evan SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	3.59	1.12	0.46	2.3	1.81	1.94	1.57	1.67	2.44	4.18	137	2.44	2.44	3.03	3.3			1.61	3.41	3.37	1.22	3.11	1.01	0.78	0.51	2.58	,			S.TO
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		Probe SEQ ID NO:	10382	10420	10775	11622	11960	11991	12024	12024	718	4108	9084	7781	7751	2/196	6/96	11,000	7	11518	11918	12469	\$	887	3015	4604	8948	11419		13108	ğ	357

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Top Hit Descriptor		HUM072014F Human fovea cDNA Homo sipiens cDNA clone EST HFD072014	HUM072014F Human fovea cDNA Homo saptens cDNA crone EST HFUU72014	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)	Homo sepiens chromosome 21 segment HS210078	Dictyostellum discoldeum gene for TRFA, complete cds	Homo sepiens jun dimerization protein genej partial cds; cfos gene, complete cds; and unknown gene	Hamo saplens chromosome 21 segment HS210001	Rat cytomegalovirus Maastricht, complete genome	nh93g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:988096 3	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HrbED60	Homo saplens sarcoglycan, epsilon (SGCE), mRNA	Homo saplens chromosome X open reading frame 6 (CXORF6) mRNA	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA	wb54h06.x1 NCI_CGAP_GC6 Homo sapiers cDNA clone IMAGE:2309331 3' simitar to gp:JU3230 UNA TOPOISOMERASE I (HUMAN):	Home contact many define throbit electers inhibitor dens. complete cds	Train september inches Variation of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of	CONTACTION PRECURSOR (GLYCOPROTEIN GP 139)	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)	yy50g11.r1 Soares fetal liver spieen 1NFLS 10mo septens civily digite liwing E. 240212.0	oj80s03.s1 Soares_NFL_T_GBC_S1 Homo Sapiens culva cione IMA GETTO 4500 3	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDINA	RC4-BT0311-141199-011-h06 BT0311 Homo saplens cUNA	zi08c08.e1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA cione IMAGE:491726 3: similar to contains element MER28 repetitive element ;	PM4-NN0050-310300-001-f10 NN0050 Horno saplens cDNA	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR	C4B-BINDING PROTEIN PRECURSOR (C4BP)	C4B-BINDING PROTEIN PRECURSOR (C4BP)	yez8c12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5	hi37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:2974444 3	y159408.s1 Soares placenta Nb2HP Homo sepiens cDNA dons IMAGE:143635 3' similer to contains Alu repetitive element contains LTR7 repetitive element;
	Somos	П	EST_HUMAN		LN L	TN	FN	۲		EST_HUMAN	T HUMAN	TN	NT	NT	EST HIMAN		Z	SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	FST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession		.0E-05 L49075.1	.0E-05 L49075.1		78.2		.0E-05 AF111167.2	.0E-05 AL183201.2	15300	2.1		10835046 NT	4885170 NT	4885170 NT	AC OF AIRECOAL A	A1000241.1	3.0E-05/AF053630.1	Q12860	3.0E-05 Q12860	3.0E-05 N72829.1	3.0E-05 AA897680.1	3.0E-05 BE054410.1	3.0E-05 BE084410.1	8 0E-05 AA150482 1	8 OF 05 AW896829 1	8.0E-05 Q60401	8.0E-05 P08807	P08607	6.0E-05 T94149.1	6.0E-05 AW627985.1	6.0E-05 R75639.1
Most Similar (Top) Hit BLAST E	Value	7.0E-05 L	7.0E-05	7.0E-05 Q22949	7.0E-05/	7.0E-05 /	7.0E-05/	7.0E-05/	7.0E-05	7.0E-05	7.0E-05	7.0E-05	8.0E-05	8.0E-05	20 20 0	0.05-03	8.0E-05					6.0E-05	6.0E-05	A 0 H 0	8 OF -05	6.0E-05					
Expression Signal	,	12.	1.14	1 07	5.16	3.9	0.85	1.88	0.68	1.24	3.6	5.87	1.59	1.59		8	254	3.26	3.26	1.5		1.03		2	20.02	2 93	55-				
ORF SEQ		26793					_	30614		<u> </u>	36261			28345		ļ							Ì							36550	
SEQ ID	ë	13773	13773	Ĭ	1	1	1	1		١.	1	ı	1		<u> </u>	- 1		19217	1	l	t	21358	ı	ŀ	24722	L		L			1
00	ġ	£8	88	Cac	2783	3227	4168	2649	56	88	9753	11430	2083	2083		2655	2875	8034	<b>603</b>	6533	7073	8276	8278		200	8787	9653	PAES	27.21	9922	10987

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4501 17641 30625 7.91 3.0E-05 BE169211.1 EST HUMAN PM1-HT0521-120200-001-e10 HT0521 Homo saplens cDNA 4501 17641 30628 7.81 3.0E-05 BE169211.1 EST HUMAN PM1-HT0521-120200-001-e10 HT0521 Homo saplens cDNA 4501 17641 3.0E-05 AA388679.1 EST HUMAN EST79998 Placenta I Homo saplens cDNA similar to p53-associated protein
17641 30628 7.81 3.0E-06 BE169211.1 EST HUMAN 47755 30707 1.11 3.0E-05 AA388679.1 EST HUMAN
1777 3.0E-05 AA368679.1 EST HUMAN
111 3.0E-05 AA368679.1 EST HUMAN
10/05

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	·	ed protein		ле IMAGE:1849458 3' similar to	. mRNA				701841 3	3,					IB IMAGE:2367209 3	(E PROTEIN 2)	(E PROTEIN 2)				855052 3' similar to contains		MAGE:632734 5' similar to						p5661084 5			nd trypsinogen gene families
Single Exon Propes Expressed in Pracenta	Top Hit Descriptor	EST79996 Placenta I Homo saptens cDNA similar to similar to p53-associated protein	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	qn84c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo septens cDNA clone IMAGE:1849468 3' similar to contains Alu repetitive element contains element KER repeditive element;	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myc2pl), mRNA	Homo sapiens SYBL1 gene, exons 6-8	Homo sapiens SYBL1 gene, exons 6-8	601567451F1 NIH_MGC_21 Homo saplenis cDNA clone IMAGE:3842292 5	2360b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3	hi94e08.x1 NCI_CGAP_Lu24 Homo sapieris cDNA clone IMAGE:3009638 3*	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	wg36f09.xt Soares_NSF_F8_9W_OT_PA!P_S1 Homo saplens cDNA clone IMAGE:2387209 3	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	PROTEIN KINASE C-BINDING PROTEININELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	Homo saplens DiGeorge syndrome critical region, centromeric end	Homo sapiens Xq pseudoautosomal region; segment 1/2	xs89d06.x1 NCI_CGAP_Ut2 Homo saplens cDNA clone IMAGE:2776811 3	qh8e11:x1 Soares_NFL_T_GBC_S1 Homb sapiens cDNA clone IMAGE:1855052 3' similar to conteins MER3.b2 MER3 repetitive element;	Human adenosine deaminase (ADA) gene, complete cds	zq48a12.r1 Stratagene hNT neuron (#937233) Homo saplens cDNA done IMAGE:632734 5' similar to	contains Alu repetitive element; contains element L1 repetitive dement;	RC3-BT0319-120200-014-h08 BT0319 Homo seplens cDNA	Homo saptens p47-phox (NCF1) gene, complete cds	H.sapians DNA for endogenous retroviral like element	S.cerevisiae 12.8 Kbp fregment of the left arm of chromosome XV	DKFZp5881084_r1 588 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5881084 5	Homo saplens SCL gene locus	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	Homo sepiens chromosome 9 duplication of the T cell receptor beta focus and trypsinogen gene families
on Propes Ex	Top Hit Database Source	EST_HUMAN ES	Į.	中B EST HUMAN con	Т	Har				EST_HUMAN his		SWISSPROT ME		EST_HUMAN ES	HUMAN		SWISSPROT PR	Ho	Hol	EST_HUMAN xs8	EST HUMAN ME	<b>T</b>			EST_HUMAN RC	ЭН	H	3.0	EST_HUMAN DK	He	오	H
e EX		EST	눌	EST	崖	Ę	ΙN	EST	EST	EST	노	3MB	Z	EST.	EST	SWI	SWI	ΙN	N	EST	EST	Ę		EST	EST	Ę	Ę	ž	EST	Ā	호	뒫
Sing	Top Hit Acession No.	3.0E-05 AA368679.1	3.0E-05 AF149773.1	3.0E-05 AI248061.1	11072102 NT	3.0E-05 AJ225782.1	3.0E-05 AJ225782.1	3.0E-05 BE733157.1	3.0E-05 AA284049.1	3.0E-05 AW 770982.1	6912431 NT	P43361	3.0E-05 X03273.1	3.0E-05 AA372562.1	3.0E-05 AI768331.1	Q62918	Q62918	3.0E-05 L77570.1	3.0E-05 AJZ71735.1	3.0E-05 AW518689.1	2.0E-05 AI286021.1	2.0E-05 M13792.1		2.0E-05 AA160562.1	2.0E-05 BE066036.1	2.0E-05 AF184814.1	2.0E-05 X89211.1	2.0E-05 X95465.1	2.0E-05 AL039107.1	2.0E-05 AJ131016.1	2.0E-05 AJ011712.1	2.0E-05 AF02B308.1
	Most Similar (Top) Hit BLAST E Value	3.0E-05	3.0E-05	3.0E-05	3.0E-06	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05 P43361	3.0E-05	3.0E-05	3.0E-05	3.0E-05 Q62918	3.0E-05 Q62918	3.0E-05	3.0E-08	3.0E-05	2.0E-05	2.0E-05		2.0E-05	l			2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05
	Expression Signal	1.11	0.93	0.7	1.72	121	121	2.28	1.55	1.58	9.1	62.0	15.0 .	4.4	3.62	26.0	0.82	1.61	1.37	1.28	149	14.63		6.89	1.28	1.04	1.12	0.87	0.81	9.0	1.84	0.87
	ORF SEQ ID NO:	30708	30859	26014	32155	33456	33457	34681	35166	35718	35721	35726		36154		37403					28658				28393	L				31106		
	SEQ ID NO:	17725	17876	13881	18869	20047	20047	21164	21628	22173	22177	22181	22407	22586	22903	23788	23788	25255	25374	26198	15531	15773		15893	16382	16597	16622	16748	17068	18132	19068	19222
	Probe SEQ ID NO:	4588	4741	4050	5875	6897	6897	8082	8547	88 76 88 76 88	8608	9102	833	9521	8883	10755	10766	12353	12551	12913	2400	2650		2777	3207	3429	3455	3583	3908	888	5878	6039

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	Top HIt Descriptor	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	qo72a02x1 Soares_placenta_8tb9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715114.3' similar to contains L1.t3 L1 repetitive element;	nw06d12.s1 NCI_CGAP_SS1 Hamo sapieris cDNA clone IMAGE:1238519 3'	P.falciparum mRNA for AARP1 protein, parital	qz47b08.x1 NCL_CGAP_Kld11 Homo espiens cDNA clone IMAGE:2030003 3' similet to TR:002711 O02711 PRO-POL-DUTPASE POLYPROTEIN;	wd35h07xf Soares_Dieckgraefe_colon_NHCD Homo sepiens culva crone IMACE.2522077 3	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA0), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA4, HoxA4, HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	Homo sapiens indolethylamine N-methyltransferase (INMT) mKNA, INMT-2 allele, complete cos	tg20h05x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE::2109369 3	COMPLEMENT DECAY-ACCELERATINGIFACIOR (CUSS)	COMPLEMENT DECAY-ACCELERATINGINACION (CDSS)	Home saplens chromosome 21 segment H3/1/LUU/	7175g09.y1 NCI_CGAP_Brn20 Homo capiens cDNA clone IMAGE:3340576 5	we1a08.r1 Soares_placenta_3tc9weeks_2NbHP8tc9W Horno sapiens cDNA clone IMAGE:259570 61	w81a08.r1 Sogres_placenta_8tcSweekg_2\VbHP8tc8W Homo sapiens cDNA clone IMAGE:259570 5'	wit35h07 x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3	RC5.HT0562-280300-012-E12 HT0582 Homo septens cDNA	we12h05x1 NCI_CGAP_Lu24 Homo captens cDNA clone IMAGE:2340921 3	hw21a03.x1 NCI_CGAP_X011 Homo sepiens cDNA clore IMAGE:3183532.3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2;	xe89a03.x1 NCI_CGAP_Co17 Homo septents cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element;
בייין ויייין פּ	Top Hit Database Source	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	ΤN	EST_HUMAN	EST_HUMAN	TN	L N	NT	EST_HUMAN	SWISSPROT	SWISSPROT	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	QH3183	213183	2.0E-05 AI149272.1	2.0E-05 AA714330.1	2.0E-05 Y08926.1	2.0E-05 A1492860.1	2.0E-05 A1991025.1	2.0E-05 AF224262.1	2.0E-05 AF224262.1	2.0E-05 AF128847.1	2.0E-05 AI381040.1	P49457	P40457	2.0E-05 AL163207.2	2.0E-05 BF055939.1	2.0E-05 N41751.1	2.0E-06 N41751.1	2.0E-05 AI991026.1	2.0E-05 BE175801.1	2.0E-05 AI912713.1	2.0E-05 BE348229.1	2.0E-05 AW074604.1.
	Most Similar (Top) Hit BLAST E Vatue	2.0E-05 Q13183	2.0E-06 Q13183	205-05	2.0E-05	2.0E-05	2.0E-06	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05 P49457	2.0E-05 P49457	2.0E-05	2.0E-05	2.0E-05	2.0E-06					
	Expression Signal	0.91	0.91	0.79	2.11	1.69	-	7.24	2	2	11.0	1.58	95.0	99'0	0.0	0.94	3.53	3.53		1.55		3.7	8.13
	ORF SEQ ID NO:	32601		_	33311	l			33844	33845		34671			36764		37472	37473		37549			
	Exan SEO ID NO:	19273	1	1	1	<u> </u>	20107	20115	20385	20385	20597	21151	22524	22524	23165	L	23850	23850		L			i
	Probe SEQ ID NO:	6092	6092	6286	6760	7042	7054	7062	7303	7303	7524	8069	9467	9467	10127	10339	10817	10817	10881	11738	11081	12477	12592

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	<u> </u>					_						_						_		,—			_				_		-	_	
	Top Hit Descriptor	Homo sapiens ABCA1 (ABCA1) gene, complete cds	AU131513 NT2RP3 Hamo sapiens cDNA clane NT2RP3002707 5	qf68g11x1 Soares_tests_NHT Homo sepiens cDNA clone IMAGE:1755236 3'	Homo saplens chromosome 21 segment HS210082	Drosophila melanogaster strain Lamto 120 Suppressor of Halriess (Su(H)) gene, partial cds	Homo sapiens calcium channel alpha (E subunit (CACNA1E) gane, exons 7-49, and partial cds, alternatively	boliced	MOSAIC PROTEIN LGN	Hamo saplens chromosome 21 segment HS21C003	zw69g04,r1 Sogres_tests_NHT Homo septens cDNA clone IMAGE:781494 5	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 31	Hamo sapiens chromosome 21 segment HS21C046	H.sapiens repeat region	Homo sapiens Spast gene for spastin protein	Ins19902.81 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1	L1 repetitive element;	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products	7p57d01.x1 NCJ_CGAP_P728 Homo saplens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3 MER10 repetitive element:	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	Homo saplens chromosome 21 segment HS21C027	2/35/12.s1 Soares_total_fetus_Nb2HF8_9v/ Homo sapiens cDNA clone IMAGE:788519 3' similar to Inhi rozza PEROXISOME PROI IFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN):	2505611.11 NCI_CGAP_GCB1 Hamo sepleris CDNA clone IMAGE: 684332 5' similar to contains Alu	repetitive element;contains element TAR1 repetitive element;	AV732190 HTF Hamo saplens cDNA clone HTFBIH01 5	hd41b02x1 Scares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.tt OFR repetitive element	hd41b02.x1 Soaros_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:2912043 3' similar to contains	OFR.t1 OFR repetitive element;	UI-H-BIZ-egk-e-08-0-UI:s1 NCI_CGAP_Sub4 Homo sepiens CDNA clone IMAGE:2724398 3'	UI-H-BIZ-egk-a-08-0-UI.s1 NCI_CGAP_Sub/ Hamo sepiens cDNA done IMAGE:2724398 3'	he07c10.x1 NCI_CGAP_Kid12 Homo capteris cDNA clone IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element;
	Top Hit Database Source	TN	EST_HUMAN	EST_HUMAN	N	N-		L	SWISSPROT	NT	EST_HUMAN	EST_HUMAN	TN	TN	TN		EST HUMAN	INT	EST HUMAN	SWISSPROT	NT	MAN III	10000	EST_HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN
.B	Top Hit Acession No.	2.0E-05 AF275948.1	2.0E-05 AU131513.1	2.0E-05 AI200970.1	1.0E-05 AL163282.2	1.0E-05 AF088273.1		1.0E-05 AF223391.1	P81274	1.0E-05 AL163203.2		1.0E-05 AW419134.1	1.0E-05 AL163248.2	1.0E-05 Z18943.1	1.0E-05 AJ246003.1		1.0E-05 AA641846.1	4505844 NT	1 OF OR BE222848 1	P19474	1.0E-05 AL 163227.2	A O TO A A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO TO A CO	100000	1.0E-05 AA236110.1	1.0E-05 AV732180.1	1 0E-05 AW510902 1		1.0E-05 AW 510902.1	1.0E-05 AW291521.1	1.0E-05 AW 291521.1	1.0E-05 AW 466995.1
	Most Similar (Top) Hit BLAST E Value	2.0E-05	20E-05	2.0E-05	1.0E-05	1.0E-05		1.0E-05	1.0E-05 P81274	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05		1.0E-05	1.0E-05	1000	1 0F-05 P19474	1.0E-05	10.0	20-30.1	1.0E-05	1.0E-05	1 0F-05			1.0E-05		
	Expression Signal	3.24	2.01	1.62	1.86	1.71		0.97	11.86	1.45	2.14	2.24	0.86	0.64	1.13		4.24	5.19	2 6	2.03	230	6	2.33	12.29				67.0	1.18	1.18	2.04
	ORF SEQ ID NO:		32014	<u> </u>	28083	L			30236	30420	30514	31080		l	33451			l	1			_	70000	36107			L	36683		38757	1
	Exan SEQ ID NO:	25905	25551	25787	16071	16901		17074	17230	17433	17535	18104	18207	18212	20043		20135	20316	COBC	21008	22105		75577	22544	22708	23084	3	23081	ı	23158	ł
	Probe SEO ID NO:	12850	12825	13206	2769	3740	T	3915	4074	4288	4392	4975	5079	5084	1688		7230	7232	1627	202	94.48		0078	9487	9998	10043	2	10043	10120	10120	10387

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		6.49	7.0E-08	1.1	П	QV2-OT0062-250400-173-h01 OT0062 Hcmo saplens cDNA
5925	١.	32424	0.83	7.0E-08	.0E-08 N98645.1	EST_HUMAN	W6507.11 Sogres, multiple, sciencels, ZN671MSP Homo sapiens colna cione invage, 210412.5
G	1	[	0.83	7.05-08	TN 60702411	Ę	Hamo saplens DNA segment, numeraus coples, expressed praces (GS1 gene) (DXF68S1E), mRNA
10808	1			7.0E-06	Q81147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	1	31547		7.0E-08	72.1	EST_HUMAN	601881522F1 NIH_MGC_67 Homo sapients cDNA clone IMAGE: 4093972 5
2984	1		1.17	8.0E-06	8.0E-06 BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-011 B10379 Hamo sapiens curvA
3784				8.0E-06	8.0E-06 BE069189.1	EST HUMAN	QV3-BT0379-010300-103-011 B1 03/9 Hamo sapiens curva
4876	١.			8.0E-06	8.0E-06 Q01456	SWISSPROT	OVARIAN ABUNDAN I MEGGAGE PROTEIN (CAM PROTEIN)
4887	L	30997	2.19		Af040099.1	EST_HUMAN	code02.x1 Scares_fetal_liver_spieen_Tivitus_51 namo septats curva datre involutivo o crimena contains MER8.t2 MER8 repetitive element;
5465	1_				8.0E-06 AF167441.1	TN	Mus musculus E-cedherin binding protein E7 mRNA, complete cds
5525	1		1.16		8.0E-06 Q02040	SWISSPROT	PROTEIN XE7
10060	<u></u>		1.98		6.0E-08 AW801912.1	EST_HUMAN	IL5-UM0070-110400-083-002 UM0070 Homo sapiens curvin
13142	1_	31948			11418157 NT	N.	Homo sapiens calcium channel, votage-dependent, alpha 11 subunit (Chorton), minus
6188			3.74		5.0E-06 AL163246.2	۲N	Homo sapiens chromosome 21 segment H321 CU40
6467	19634	32895	1.94		5.0E-06 U07581.1	LΝ	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	20460	33923	1.18		5.0E-06 AB007546.1	Ā	Homo sapiens gene for LECTZ, complete cus
8654	<u></u>		99'0		5.0E-06 AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 C-10302 Homo sapiens CDIVA
8654		35275			5.0E-06 AW856972.1	EST HUMAN	RC1-CT0302-120200-013-102 CT0302 Figure Septemble CD17A
10307	L_	36947	6.96		5.0E-06 AA313620.1	EST_HUMAN	EST 185498 Colon carcinoma (no.c.) ceu mie nomo sepiena con o sero
10731	<u> </u>		0.51		5.0E-06 P06681	SWISSPROT	COMPLEMENT CZ PRECURSOR (CS/CS/CS/CS/CS/CS/CS/CS/CS/CS/CS/CS/CS/C
13011	$\Box$	31957	r 5.49		5.0E-06 A1085045.1	EST HUMAN	HADS// Human retailiner conveniorery more sequents works  And the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of
90	13950	78877	547		4.0E-06 R16267.1	EST HUMAN	yaqooosin soares iniani baliin mib homo appala oo oo oo oo oo oo oo oo oo oo oo oo oo
	1				4 OF OR AW 103354 1	FST HUMAN	xx66912.x1 NC_CGAP_Eso2 Homo sapleris cDNA clone INA GE:2589574 3' similar to contains Alu repetitive element ;
600	14040	27110		L	4 NF-08 A1334928 1	EST HUMAN	Ib33e09.x1 NCI_CGAP_HSC2 Homo saplens cDNA clone IMAGE:2056168 3'
200	1				4 0E-06 Al334928.1	EST HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo septens oDNA done IMAGE:2056168 3'
35	Ŧ.				4.0E-06 BF365612.1	EST HUMAN	QVZ-NT0046-200600-250-h07 NT0046 Homo saplens cDNA
2000					4.0E-06 AW015401.1	EST HUMAN	UI-H-BIO-aat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo saptens cONA clone IMAGE:Z/10420 3
200	1		0 80		4 0E-06 AF198349.1	칟	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
1818	$\perp$ L	20321			4.0E-06 AW848295.1	EST HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo saplens cDNA
- 2054					O DANGERON		

PCT/US01/00663

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Top Hit Descriptor	wi94c10.x1 NCI_CGAP_Brn25 Homo sepiéns cDNA clone IMAGE:2432562.3' simitar to contains element MER22 repetitive element ;	TRANSMEMBRANE PROTEASE, SERINE 2	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV1232 region	Hamo saplens SPP2 gene for secreted phosphoprotein 24 precursor, exans 1-6	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486	xs53e01.x1 NCL_CGAP_Kid11 Homp sapiens cDNA clone IMAGE:27/3368 3	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saptens cDNA clone IMAGE:432663 3* similar to contains L1.11 L1 repetitive element;	<u>a34b08.s1</u> Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;	Homo canions DP1200 mRNA complete cits	Mile Suprime Annual Marie Management of the Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Marie Mari	ak48g11.s1 Scares_tests_NH   Homo applens outwh clone invide: 140e252 5 stilling to contain the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains 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ippetitive element ;	hq84d12.x1 NCI_CGAP_HN13 Homo sepiens cDNA clone IMAGE:3124151 3	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3	yb78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5 similar to contains L1 repetitive element	Homo sapiens gene for alpha-1-microglobulin-bilunin, exons 1-5 (encoding alpha-1-microglobulin, N-	tarminus.)	AU159412 THYRO1 Hamo sepiens CDNA clone THYRO1001602 3	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	601336213F1 NIH MGC 44 Hamo seplens cDNA clone IMAGE:3050314 3	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)	Rco-L10001-261199-011-A03 LT0001 Homo saptens cDNA	HOMEOBOX PROTEIN GOOSECOID	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)	wa04e03,x1 NCI_CGAP_KId11 Homo capitato cDNA done IMAGE:2297068 3' similar to contains MEK30.b1	MER30 repetitive element;	HISTIDINE-RICH GLYCOPROTEIN PRECORGON	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECONSON (NAMA)	AV63/333 GLC Hamo sepiens alive GLC/2000 s
Top Hit Database Source		ISSPROT		NT TA		EST_HUMAN x	EST HUMAN 0		111	7	EST_HUMAN L	EST_HUMAN L	Г	EST HUMAN h	FST HUMAN	Т	NT TN					EST_HUMAN 'F	SWISSPROT	SWISSPROT	Г	$\neg$		Т	EST HUMAN
Top Hit Acession	4.0E-06 AI886939.1	4.0E-06 O15393	4.0E-06 AF009860.1	4.0E-06 AJ272265.1	4.0E-08 AB007955.1	4.0E-06 AW 299734.1	3.0E-06 AA700562.1	3 0E.08 AA200562 1	A 1700001 A	3.0E-06 AFZ0Z635.1	3.0E-06 AAB68218.1	3.0E-06 AI857779.1	3.0E-06 BE047094.1	3.0E-06 BE047094.1	3 0F-08 T50268 1		3.0E-06 X54816.1	3.0E-06 AU159412.1	3.0E-06 P08548	3.0E-06 BE562964.1	3.0E-06 P07743	3.0E-06 AW385262.1	2.0E-06 P54366	2.0E-08 P21414		2.0E-06 AI672138.1	2.0E-06 P04929	2.0E-06 P08719	2.0E-06 AV657555.1
Most Similar (Top) Hit BLAST E Value	4.0E-08	4.0E-06	4.0E-06	4.0E-08	4.0E-08	4.0E-06	3.05-08	90506	0.01.0	3.05-00	3.0E-06	3.0E-06	3.0E-08	3.0E-06	80-70 s		3.0E-06	3.0E-08	3.0E-08	3.0E-08	3.0E-08	3.0E-06				2.0E-06	2.0E-06	2.0E-06	
Expression Signal	1.89	0.68	4.49	1.28	3.89	1.33	1.31		151	1.48	0.84	2.67	1.47	1.47	č	2	5.52		2.14	0.81		12.07	222	6.39		2.58	1.69	1.81	0.9
ORF SEQ ID NO:	31041	35308			37546		28494	1	20463		29180		30040	L			30807	L	L	34874		L				28707			29786
Exan SEQ ID NO:	18059	21776	1	1	1	1	1		- 1	15471	16164				l		17819	L	上		L		L	L	<u> </u>	15579	15862	15755	16771
Probe SEQ ID NO:	4929	8698	8	6068	11736	13149	6866.	1	7837	2340	2988	9440	388	3883	7503	1004	4884	6288	7377	8274	8883	12856	207	1599		2451	2537	2832	3607

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	Top Hit Descriptor	2p02e05.rl Stratagene overtan cancer (#937219) Homo saplans cDNA clone IMAGE:595232 5	UI-H-BI3-aky-g-05-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2/36176 3	Mus musculus gene for odorant receptor A16, complete cds	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3. similar to contains Alu repetitive element	annun,	te31f03.x1 Soares_NFL_1_GEC_S1 Home Repents curve crare Invest.Coo.x1 to cirring to the constant stands of the constant constant sequence.;	wjeobo4.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410053 3	nv59c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.ts L1 repositive element '	reportune current.	K3-SNOOO7-120400-002-102 SNOOO7 HOLLS CONT	A447R Heart Homo sapiens cDNA Glone A447	zh27c11.s1 Soares_pineal_gland_N3HPO Homo saptens cDNA clone IMAGE:413300 3' cimilar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;	yu37c04.r1 Scares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:235974 5' similar to gb:X74929	KERALIN, 1YPE II CYTOSNELETAL 8 (HUWANY),	Homo saplens glypican 3 (GPC3) gene, partial cos and rianking repeat regions	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	tribg10.x1 NCL CGAP_Gas4 Homo sapiens cUNA clone IMAGE:2141730 3	yw65e03.s1 Soares_placente_8tc9weeks_2NbHP8tc9W Homo saplens cDNA clone IMAGE:257212.3"	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'	PROTEIN MOV-10	hs9202.x1 NCI_CGAP_Kid13 Homo saplens cDNA done IMAGE:3144699 3' similar to contains L1.02 L1	OBCANIC CATIONICAPAITINE TRANSPORTER 2/SCITTE CARRIER FAMILY 22 MEMBER 5/(HIGH	AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)	Mus musculus D6MM5E protein (D6Mm5e) mRNA, complete cds	MEROZOITE SURFACE PROTEIN CMZ-8	Homo sapiens chromosome 21 segment HS210078	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapkans cDNA clone IMAGE:428982.3' similar to contains Alu repetitive element;	206s12.s1 Soares_fotal_liver_splean_1NFLS_S1 Homo sepiens cDNA clone IMAGE:429982 3' sImilar to contains Alu repetitive element;	
-	Top Hit Database Source	EST_HUMAN 2	T_HUMAN	NT		ESI HOMAIN B	EST_HUMAN C	EST_HUMAN w	u Martin Foo	Т	٦	EST HUMAN A	EST_HUMAN T		HOMAN		1	EST_HUMAN (		EST HUMAN /	SWISSPROT		ESI HOMAN	SWISSPROT	Г	SWISSPROT		EST HUMAN		٦
ŝ	Top Hit Acession No.	П		2.0E-06 AB030896.1	, 0007207	0E-06 AAB/4932.1	A1539448.1	2.0E-06 AI819424.1	7 000 100 1	QA688423.1	2.0E-08 AW 869223.1	T12238.1	2.0E-06 AA772497.1		2.0E-06 H62051.1	2.0E-06 AF003529.1	2.0E-06 AF003529.1	.0E-06 A1473450.1	2.0E-06 N30576.1	2.0E-06 AV748969.1	P23249		2.0E-06 BE328232.1	0E-08 076082	.0E-06 AF084384.1	0E-06 P09125	.0E-06 AL163278.2	OF-08 AA034141 1	0E-08 AA034141 1	
	Most Similar (Top) Hit BLAST E Value	2.0E-08/	2.0E-06	2.0E-06	100	2.0E-08/	2.0E-08	2.0E-08	20.0	2.05-08	20E-08	2.0E-06	2.0E-06		2.0E-06	2.0E-06	2.0E-08	2.0E-06	2.0E-08		2.0E-06 P23249		2.0E-06	•				_	'	
	Expression Signal	1.54	89'0	1.7		0.92	0.62	5.64		0.63	1.02	97.0	1.05		1.59	6.0	6.0	95.0	98'0	0.7			5.94	7				7		
	ORF SEQ ID NO:	30017			١		32766			34183		34882					36057		36527	L	31649			97090		27719	L			
	Exon SEQ ID NO:	17018	l	17035		19389	18420	ı	1		21184	21383	1	1_		22491	L	L	i	L	L	1	25473	43970	1	Į.	1		1	14/30
ı	Probe SEQ ID NO:	3858	3868	3876		6214	6246	6571		7635	8102	8281	9038		8046	8417	9417	9436	8802	10123	12548		12711	5	874	1482	1553	609	200	1603

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Top Hit Descriptor		ql82g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)	Homo sapiens UDP-glucuronosyltransferació gene, complete ods	EST05660 Fetal brain, Stratagene (cat#939206) Homo sepiens cDNA clone HFBEN89	Homo sapians chromosome 21 segment HS21C080	Homo saplens membrane Interfeukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11	Horno sepiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA	Homo saplens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mKNA	CM3-CT0277-221099-024-e11 CT0277 Home septens cDNA	Homo septens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), end_oomplement component C2 (C2) genae,>	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION	7994f07.x1 NCI_CGAP_Co16 Hamo septens aDNA clone IMAGE:3314149 3' similar to TR:075920 075920	4F5L.;	CM0-BT0281-031199-087-e03 BT0281 Homo sapiens cDNA	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA	hu11h05.x1 NCI_CGAP_Lu24 Homo sapiers cDNA clone IMAGE:3166329 3' similar to contains L1.b2 L1 L1	repeality element,	Wh64/10.X1 NCI_CGAP_Kid11 Homo expiens CDNA cigne IMAGE: 2303347.3	ES (83815 Supt cells Homo sepiens CUNA 3 end	wh84f10.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:23855473	Hamo saplens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cas	Mus musculus OG-2 homeodomain protein (OG-2) gene, partal cas	tgocbo5x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element contains element A3R repetitive element ;	tg06b05x1 NCI_CGAP_CL1 Homo sepiens cDNA clone IMAGE;2107953 3' stmilar to contains Alu	repetitive element contains element A3R repolitive element ;	xa31e02.x1 NCI_CGAP_Br18 Homo capiem; cDNA clone IMAGE:2568362 3' similer to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);	ADAM-TS 1 PRECURSOR (A DISINTEGRÎN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIES 1) (ADAMTS-1) (ADAM-TS1)	S. ANTIGEN PROTEIN PRECI RSOR	
Top Hit Database	Source	EST_HUMAN q	SWISSPROT P	H	T_HUMAN	П	_ I			EST_HUMAN C	1 E S	TORPROT	Т	EST_HUMAN 4	EST_HUMAN C	EST_HUMAN C		Т	П	П	T HUMAN		E L	EST HUMAN	T	EST_HUMAN r	EST HUMAN		Т	٦
Top Hit Acession	ż	3.0E-07 AI288598.1	P21414	8.0E-07 AF135416.1	8.0E-07 T07770.1	8.0E-07 AL163280.2	7.0E-07 AF167341.1		F005700 NT	6.0E-07 AW855558.1	A DE 07 DE010413-1	D44470	071	8.0E-07 BF001867.1	6.0E-07 BE063509.1	6.0E-07 AW903222.1		6.0E-07 BE222380.1	5.0E-07 AI831893.1	AA380630.1	5.0E-07 AI831893.1	5.0E-07 AF149774.1	6.0E-07 U65067.1	5 0F-07 At393981 1		5.0E-07 Al393981.1	5.0F.07.1AW070885.1	E OF 07 OOIWIIO4	20,000	5.0E-07 P09593
Most Similar (Top) Hit	Value	8.0E-07	8.0E-07 P21414	8.0E-07	8.0E-07	8.0E-07	7.0E-07	7.0E-07	7.0E-07	6.0E-07	10 W	A DE 07 DA4470	0.00	8.0E-07	6.0E-07	6.0E-07		6.0E-07	5.0E-07	6.0E-07	5.0E-07	5.0E-07	6.0E-07	5.05-07		5.0E-07	5.05.07	100	3.05-07	2.05-07
5	350	4.23	8.17	8.44	5.84	6.1	0.97	0.86	0.88	3.47	245	7.4.2	-	1.31	1.45	1.72		1.32	1.04	2.39	0.73	0.97	1.33	1 74		1.71	18 09	60,	1.02	0.89
ORF SEQ		31009					28167	31806	31907			١		35972	38800							30886	32767	33487		33488	34050		Lencs	
Exon SEQ ID	ö	18023	19192	21273	24907	25143	15057	18830	18830	15105	2000	13000	1/230	22418		26087			13549	14248	ı	17904	19421	20078		20075	Į	ı		21767
Probe SEQ ID	ö	4893	6007	818	11921	12183	1814	9836	5636	1962	9000	1007	4080	8342	12115	12444		13229	336	1082	3086	4769	6247	137		7210	7503	3	\$	8687

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Single Exoli Flores Explessed in Floresina	Top Hit Descriptor	GM-BT178-220499-014 BT178 Homo septens cDNA	COLLAGEN ALPHA 1(1) CHAIN PRECURSOR	Homo sapiens Xq pseudoautoscmal region; segment 1/2	Hamo sapiens chromosame 21 segment HS21 CO85	QV0-CT0383-210400-204-512 CT0383 Homo sapiens cUNA	ws84h05.x1 NCI_CGAP_Co3 Homo capiens cDNA clone IMAGE: 25046547 3	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, excits 1-9	HISTONE DEACETYLASE 8 (HDS) (HISTONE DEACETTRASE WINDAY)	HISTONE DEAGETYLASE 5 (HD5) (HISTONE DEAGETYLASE MIDAL)	Homo sepiens chromosome 21 segment HS21000/	xy49g11,x1 NC  CGAP Lu34,1 Homo sapiens cuna done invaria 2500046 5	601676748F1 NIH MGC 21 Homo sapiens cDNA clone IMACE 3408001 3	601876748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3939531 3	Homo sapiens chromosome 21 segment HS21C018	wi81508.x1 NCI_CGAP_Kid12 Homo sapiens cunA cione liwA cel. 2339703 3	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cUNA cione liva dE: 2389703 3	PM1-BN0083-030300-003-612 BN0083 Homo sapiens CUNA	601649083F1 NIH_MGC_73 Homo saplens cDNA clone IMAGE:3932924 5	Homo sapiens deleted in lymphocytic feukemia, 1 (DLEU1), mKNA	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced	untranslated exons	Homo sepiens Xq paeudogutosoma region; segment 1/2	Human polymorphic microsatellite UNA	Human igK subgroup i germline gehe, exons 1 and 2, v-region 0 to slicite	n(56809.s.) NCI_CGAP_OVZ Homo septens cund cione invage: Secos23 similiar to contains four repressive alement.	Human polymorphic microsofallita DNA	Time payor program of a billion of the contact of NA	MRX-BN0119-02030-01-11 BN0119-0-1-10 General PN14	MRO-BN0115-020300-001-111 BN0115 Home septens contra	YOUTIZITY SORIES TEEM INTO SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR OF THE SOLITOR O	HYPOTHETICAL 63.8 KD PROTEIN IN GUTT-RIMT INTERGENIO REGION FREGUENCE	OVOSTATIN PRECURSOR (OVOMACROGLUBOLIN)	AV650201 GLC Homo saprens curve donle cuccedor i s	Wedge 12.X1 Source and a facility septical source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility source and a facility s
EXOIL FIGUES	Top Hit Database Source	EST_HUMAN (	SWISSPROT			_	T_HUMAN		SWISSPROT	$\neg$	- 1			EST_HUMAN		$\neg$	╗	EST_HUMAN	THUMAN					Ν	NT		בים שמייים	- N	EST HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST HUMAN
Single	Top Hit Acession No.	7.1	•	5.0E-07 AJ271735.1		5.0E-07 AW862537.1	4.0E-07 AW009602.1	5.1			1	4.0E-07 AW 419134.1		4.0E-07 BE901976.1	4.0E-07 AL163218.2	4.0E-07 AI785528.1	4.0E-07 AI765528.1	4.0E-07 BE001828.1	4.0E-07 BE967557.1	11437071 NT		3.0E-07 U19719.1	3.0E-07 AJ271735.1	3.0E-07 M99149.1	3.0E-07 M64857.1	A 400000 A	3.0E-07 AA520763.1	3.0E-07 M89148.1	3.0E-07 BE005077.1	3.0E-07 BE005077.1	3.0E-07 T84704.1	3.0E-07 P38739	3.0E-07 P20740	3.0E-07 AV650201.1	3.0E-07 AI797238.1
	Most Similar (Top) Hit BLAST E Value	5.0E-07	5.0E-07 P11087	5.0E-07	5.0E-07	5.0E-07	4.0E-07	4.0E-07	4.0E-07 Q9Z2V6	4.0E-07 Q9Z2V6	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07		3.0E-07	3.0E-07	3.0E-07	3.0E-07	10 10 0	3.05-07	3.05-07	3.0E-07	3.0E-07	3.0E-07	3.0E-07	3.0E-07		
	Expression Signal	5.47	6.69	2.08	1.2	3.08	1.68	8.0	76.0	26.0	0.51	4.9	0.63	0.53	0.58	3.88	3.88	89.	1.33	1.71		5.38	3.59	1.43	3.62		232	1.14	4.99	4.69	0.97	1.78	0.64	۳	0.7
	ORF SEQ ID NO:	37217	38493				30261		33983	33364		35875	36976				37882					26686	26806				١		28789	28790	29289			30970	
	SEQ ID	23612	24796	24868	25968	25966	17280	20410	20485	20495	l	I_	23367	1_	<u> </u>	24248	L_	L	1.	L	L	13650	13786		14808		ı	15492		L	16275	16402	17937	17982	18015
	Probe SEQ ID NO:	10577	11805	11880	12256	12918	4108	7328	7417	7417	8107	9251	10332	10332	10531	11179	11179	11495	11919	13207		454	596	1405	1655		20K	2361	2540	2540	309	3228	4802	4849	4885

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Probe SEQ ID NO: 6175 6783 6095 6095 7678	SEO ID NO: 18297 18295 19276 20743	ORF SEQ ID NO: 31259 32281 32805	Expression Signal 1.43 1.43 12.39 5.09 5.09 5.09 5.09	Most Section 1	Similar Top Hit Acession No. 3.0E-07 T57850.1 3.0E-07 T67850.1 3.0E-07 C88807 3.0E-07 C42280 3.0E-07 ANY107168.1	Top Hit Delabase Source Source EST_HUMAN SWISSPROT SWISSPROT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN	Top Hit Describtor  ye14h09.s1 Stretagene Iurg (#337210) Horio sapiens cDNA clone IMAGE:80705 3' similar to similar to gb.M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)  ye14h09.s1 Stratagene Iurg (#337210) Horio sapiens cDNA clone IMAGE:80705 3' similar to similar to gb.M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)  ye14h09.s1 Stratagene Iurg (#337210) Horio sapiens cDNA clone IMAGE:80705 3' similar to similar to gb.M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)  PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)  (PEPTIDYLARGININE DEIMINASE TYPE/ALPHA)  WWIT-14 PROTEIN PRECURSOR  co04-10.s1 NCI_CGAP_GCBI Horio sapiens cDNA clone IMAGE:1339890 3'  QV1-LIM0036-200300-116-g02 LIM0038 Horio sapiens cDNA (done IMAGE:2261037 3' similar to contains Alu repetitive alement in MSR1 repetitive element i.
8330 8330 8330	22406 22408 25777 13267				3.0E-07 P33240 3.0E-07 P33240 3.0E-07 AJ132352.1 2.0E-07 AF262988.1	SWISSPROT SWISSPROT NT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT) CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT) Rattus norvagicus mRNA for 45 kDa secretory protein, partial Homo septions TREZ-interating telement FAPT) protein (RAPT) mRNA, complete cds
158 168 186 767 779	11111 _				2.0E-07   L77669.1 2.0E-07   L77669.1 2.0E-07   U38849.1 2.0E-07   AF003530.1 2.0E-07   AF003530.1	NT NT NT NT SWISSPROT	Homo saplens DiGeorge syndrame critical region, teloment end Homo saplens DiGeorge syndrame critical region, teloment end Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds Homo saplens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeal regions Homo saplens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeal regions Homo saplens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeal regions RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
966 987 1189		27200 27201 1 27409	2.32		2.0E-07 AA223260.1 2.0E-07 T63042.1 2.0E-07 Q28768	EST_HUMAN EST_HUMAN SWISSPROT	z/08b07.s1 Stratagene NT2 neuronal precursor 697230 Homo saplens cDNA clone IMAGE:650869 3' similar to do:L31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element yof 5904.s1 Stratagene lung (#637210) Homo saplens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1630 3708 3779 5238	14782 16869 16940 18360				2.0E-07 Q09701 2.0E-07 BF131397.1 2.0E-07 AF125348.1 2.0E-07 AW902219.1	SWISSPROT EST HUMAN NT EST HUMAN	HYPOTHETICAL 72.5 KD PKO LEIN CZP7.10 IN CANCONACIONE I 601818916F1 NIH_MGC_58 Homo sapiens: cDNA clone IMAGE:4044891 5' Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial ods QV3-NN1023-280400-168-h11 NN1023 Homo sapiens cDNA

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Top Hit Descriptor	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA	UI-H-BI3-ake-b-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE::2/34008 3	qg56d05.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1839177 3'	AV728380 HTC Homo sapiens cDNA done HTCAEG02 5	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clane IMAGE:471808 3	Homo sapiens chromosome 21 segment HS21C103	CM4-NN0003-280300-124-e06 NN0003 Homo sapiens CDNA	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA CLYCOPROTEIN) (GBG) (PBF2)	PM0-HT0339-260100-006-H07 HT0339 Homo sepiens dDNA	zn85h11,x5 Strategene lung carctnoma 937218 Homo saptens cDNA clone IMAOE:505029 3' similar to	contains THR.b2 THR repetitive element;	Hano sapiens chromosame 21 segment HS:21 C082	GLYCOPROTEIN GPV	Homo saplens chromosome 21 segment HS21C082	AV718882 GLC Homo sapiens cDNA clone GLCFNF04 5'	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5	Homo sapieno chromosome Xq28 melanom'a antigen family AZa (MAGEAZA), melanoma antigen family A12 (MAGEA12), melanomo antigen family AZb (MAGEAZB), melanoma antigen family A3 (MAGEA3), caltractin	(CALT), NAD(P)H dehydrogoneso-like protein (NSDHL), and LI>	tz43d08.y1 NCI_CGAP_Brn52 Homo sapleits cDNA clone IMAGE:2291339 5	1243d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5	yv43c07.s1 Soares fetal liver splean 1NFLS Homo saplens cDNA clone IMAGE:245484 3	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA	PM4-TN0024-030800-002-b05 TN0024 Hoino sapiens cDNA	Homo sapiens chromosome 21 segment HS210081	ENTEROPEPTIDASE (ENTEROKINASE)	ENTEROPEPTIDASE (ENTEROKINASE)	zi51e10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cONA clone IMAGE 434346 3	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBUSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
Top Hit Database Source	П	EST_HUMAN I	EST_HUMAN		T_HUMAN	TN	EST_HUMAN	SWISSPROT		EST HUMAN	Г	EST_HUMAN	LN	SWISSPROT	NT		EST_HUMAN		NT	EST_HUMAN	<b>EST_HUMAN</b>			EST_HUMAN	NT	SWISSPROT	SWISSPROT	EST HUMAN	SWISSPROT
Top Hit Acession No.	:0E-07 AW898066.1	2.0E-07 AW448968.1	2.0E-07 AI208715.1	2.0E-07 AV729390.1	2.0E-07 AA035198.1	2.0E-07 AL163303.2	2.0E-07 AW 892507.1	P00751	P00751	20E-07 BE153717.1		2.0E-07 AI732462.1	1.0E-07 AL163282.2	1.0E-07 P09258	1.0E-07 AL163282.2	1.0E-07 AV718662.1	1.0E-07 AV718662.1		1.0E-07 U82671.2	1.0E-07 BE047871.1	1.0E-07 BE047871.1	1.0E-07 N55081.1	1.0E-07 BF375909.1	1.0E-07 BF375909.1	1.0E-07 AL163281.2	1.0E-07 P97435	1.0E-07 P97435	1.0E-07 AA693576.1	1.0E-07 P57110
Most Similar (Top) Hit BLAST E Value	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07	2.0E-07 P00751	2.0E-07 P00751	2.0E-07		2.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07		1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	
Expression Signal	1.52	0.73	3.39	3.87	1.11	1.4	6.34	1.01	1.01	2.96		2.38	0.76	2.08	1.24	2.91			0.8	4.60	4.69	7.8	0.69	0.68				2.7	1.05
ORF SEQ ID NO:	31638	33229			35508		37122	37342						27784		30534		<u> </u>	33180	33560	33561		34382		L	L		L	36090
Exan SEQ ID NO:	18680	25829	19957		l	1_	L		1	1		25967		1	1	ì	1	1	19791	Ľ	L		١.	<u>l_</u>	上	L		22233	22527
Probe SEQ ID NO:	5460	6681	6802	8664	8893	8883	10474	10708	10706	4243R	3	12226	1128	2888	3838	4408	4408		6632	7008	7006	7662	7826	7826	7854	8410	8410	9155	9470

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Single Exon Probes Expressed in Placelita	Top Hit Descriptor	hu <u>z8h06.x1 NCI_CGAP_Mel15 Ho</u> mo sapians cDNA clone IMAGE:3171419 3' similar to contains MER18.t3 MER18 repetitive element ;	602137714F1 NIH_MGC_B3 Home sapiens cDNA clone IMAGE:4274426 5	EST185054 Brain IV Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21 CO82	qx89e03.x1 NCI_CGAP_GC6 Homo septerts cDNA clone IMAGE:2009692 31	hr53c11.x1 NCI_CGAP_Kld11 Homo sepiens cDNA done IMAGE:3132212.3' similar to TR:095722 095722 DJ1163J1.1;	H. saplans ALAD gene for porphobilinogen synthase	Human lambda-immunoglobulin constant rėgion complex (germline)	te51b06.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'	AV734819 cdA Homo sapiens cDNA clone cdABFB06 5'	windba07.x1 NOI_COAP_Gas4 Homo septens cDNA clone IMAGE:2446632 3' aimitar to containe OFR.t2	OFR repetitive element;	Homo sapiens chromosome 21 segment HS21C101	Homo sapiens partial steerin-1 gene	wd16b05x1 Soares_NFL_T_GBC_S1 Horro sapiens cDNA clone IMAGE:2328273 3'	601590133F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943976 5	601590133F1 NIH_MGC_7 Home saplens oDNA clone IMAGE:3943976 5	on15c02.x1 Normal Human Trabecular Bonis Cells Homo septens cDNA done NHTBC_cn15c02 random	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sepiens cDNA clone NHTBC_cn15c02 random	EST382776 MAGE resequences, MAGK Homo sapiens cDNA	Homo saplens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	Homo sapiens microsomal epoxide hydrolass (EPHX1) gene, complete ods	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)	Rat mRNA for ribosomal protein L31	DYNEIN HEAVY CHAIN (DYHC)	DYNEIN HEAVY CHAIN (DYHC)	yc11e12.r1 Stratagene lung (#937210) Homb saplens cDNA clone IMAGE:80398 5	corg3.P11.A5 conorm Homo septens cDNA 3	Rattus norvegicus Munc13-1 mKNA, complete cds
Exon Propes E	Top Hit Database Source	EST_HUMAN ME	EST_HUMAN 602	EST_HUMAN ES		EST_HUMAN   ox	EST HUMAN DJ	Г		EST_HUMAN te5	EST_HUMAN AV	Π	T HUMAN		OH IN	EST_HUMAN  wd		EST_HUMAN 60	EST_HUMAN on	EST_HUMAN an	EST_HUMAN ES	-H	NT H	SWISSPROT A			1	- 1	EST HUMAN CO	
Single	Top Hit Acession No.	.0E-07 BE327843.1	1.0E-07 BF674524.1	1.0E-07 AA386311.1	1.0E-07 AL163282.2	1.0E-07 AI341136.1	1.0E-07 BE048770.1			9.0E-08 AI539362.1	9.0E-08 AV734819.1			9.0E-08 AL163301.2		8.0E-08 AI911352.1	8.0E-08 BE795469.1	8.0E-08 BE795469.1	8.0E-08 AI752367.1	8.0E-08 AI752387.1	8.0E-08 AW970893.1	8.0E-08 AF111167.2	8.0E-08 AF253417.1	7.0E-08 Q02357	7.0E-08 X04809.1	7.0E-08 P15305	7.0E-08 P15305		-	7.0E-08 U24070.1
	Most Similar (Top) Hit BLAST E Value	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.05-07	1.0E-07	1.0E-07	9.0E-08	9.0E-08		9.0E-08	9.0E-08	9.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08	7.0E-08
	Expression Signal	0.0	2.35	1.23	1.22	2.35	3.37	1.45	2.1	0.75	2.04		1.92	2.38	2.51	2.09	1.01	1.57	6.35	5.35	3.03	0.48	1.73	3,94	19.51	0.88	0.88	0.62	1.73	4.1
	ORF SEQ ID NO:	38438	36778	36784		38771	34764			33982	36732		38185	38656					36667	35558	38449	37445		26345	27622	29839		31413		38658
	SEQ IO	22856	23178	23187	23716	25065	25030	25438	25508	20510	23129	,	24517	24850	L	1	ł	16798	22018	22016	L	23821	l_		<u> </u>		_	18445	)	24955
	Probe SEQ ID NO:	9816	10140	10149	10682	12085	1250R	12659	12852	7433	10091		11457	11965	12458	622	1075	3634	8937	8937	9827	10788	11523	82	1392	3666	3666	6332	11052	11970

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					, [		
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslan No.	Top Hit Database Source	Top Hit Descriptor
12978	16823		1.84	7.0E-08	0E-08 P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	ı		1.84		.0E-08 P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073			3.0E-08 AL163248.2	Ŋ	Homo saplens chromosome 21 segment HS21C048
8	ı				6.0E-08 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	1		1.77		6.0E-08 BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-409 HT0166 Homo saplens cD:\A
3129	ı		0.68	8.0E-08	7662473 NT	۲	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4383	L		1.15	<u> </u>	6.0E-08 AL163248.2	F	Hamo sapiens chromosome 21 segment HS21C048
8137	L	ļ	0.69		.0E-08 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3	<u></u>		200		2 OC 00 A 8 02 70 75 4	NAMINANI	obsecos s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1335368 3' similar to contains MFR13 N3 MFR12 reposititive element
82CB	\$677		0.33		AMOZIOTO.	NCMO!	PETERSON DEL VIETE DEL VEBOTEIN FONTAINS. DEVEBOE TRANSCORPTASE
11701	24698	38390	2.16			SWISSPROT	REIROYRUS-RELATED POLITINOTEIN (CONTRINS, NEVENSE TISMOSOM, 1905.) ENDONUCLEASE]
11823	1		1.43		3.0E-08 AL163209.2	LY	Homo sapiens chromosome 21 segment HS21C009
87	1	26350		Ĺ	5.0E-08 AL163303.2	NT	Homo saplens chromosome 21 segment HS21C103
	L			L			nh03b09.s1 NCI_CGAP_Thy1 Homo saplers cDNA clone IMAGE:943193 similar to contains Alu repetitive
2309	15441	28576	3.93		5.0E-08 AA493851.1	EST_HUMAN	element;
12185	25144		4.55		5.0E-08 P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C6 CONVERTASE)
12382	25271	32077	1.77		5.0E-08 AW851878.1	EST_HUMAN	QVo-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1789	L.,		1.03	`	4.0E-08 P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1790	L.	28041			4.0E-08 P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2960	L				4.0E-08 ALD79581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 51
							co05e02x1 Soares_fetal_liver_spleen_1NFILS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to
3132	16308		1.01	Ì	4.0E-08 AI078417.1	EST HUMAN	contains Alu repetitive element;
4024	17180		0.65	,	4.0E-08 U82868.1	NT	Homo sapiens shox gene, alternativaly spliced products, complete ods
6535			1.07	Ĺ	4.0E-08 P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8998	1		6.0	Ľ	4.0E-08 O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9340	1	36969			4.0E-08 L42571.1	FN	Oricetulus griseus ribosomal transcription fector (UBF2) mRNA, complete cds
9845		ļ	1.66	ľ	4.0E-08 P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10536	23571		0.85		4.0E-08 AI016342.1	EST_HUMAN	d78d12.s1 Soares_total_fetus_Nb2HF8_9w; Homo saplens cDNA clone IMAGE:1622903.3'
	<u>.                                    </u>					200	er22d10.xt Gessler Wilms tumor Homo oppiene cDNA clone IMAGE:1699411 3' similar to contains Atu
10597	23632	37241	4.75		4.0E-US AIUSUUZZZ	ESI TOWN	repoulte deliterischen vermen vermen vermen vermens.
4132B	24301	38037	5.18		4.0E-08 AA393627.1	EST HUMAN	Z76C08.r1 Soares_testis_nh i Homo septiens cuna cione invace: 726247 3 similiar to in cocos78 G505579 NA/CA,K-EXCHANGER.;
1	1			1			

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Dafabase Source	Top Hit Descriptar
11328	24391	38038	5.16	4.0E-08	4.0E-08 AA393627.1	EST_HUMAN	z/76b08.r1 Soares_testis_NHT Homo sapiéns cDNA clone IMAGE:728247 5' similar to 11R:G505579 G505579 NA/CA,K-EXCHANGER.;
11349	1_			4.0E-08	4.0E-08 BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 6
11349	L	L		4.0E-08	4.0E-08 BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo saplens cDNA clone IMAGE:4333300 5
42400	1			4.0E-08	4.0E-08 W76159.1	EST HUMAN	zd85g03.r1 Soares_fetal_heart_NbHH19Wi Homo sapiens cDNA clone IMAGE:34555 5' similar to contains L1.t1 L1 repetitive element;
3	<u> </u>					ı	tb95a11.x1 NCI_CGAP_Co16 Homo sapieris cDNA clone IMAGE:2062078 3' sImilar to contains MER18.b3
12904	25598		2.01	4.0E-08	1.0E-08 AI343353.1	EST_HUMAN	MER18 MER18 repetitive element;
5728	18921	32216	2.27	3.0E-08	3.0E-08 BE018348.1	EST HUMAN	bb79a10.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:30485/0 5 similar to TR:U92158 U92158 SYNTAXIN 17.;
7115	L	L		3.05-08	3.0E-08 AI792737.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:1944045 5'
711	L	L		3.0E-08	3.0E-08 AL 163246.2	Z	Homo sapiens chromosome 21 segment HS21C046
							th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Home saplens cDNA clone IMAGE:2128273 3! similar to
7928	20978		3.32		3.0E-08 AI436352.1	EST_HUMAN	TR:013537 013537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSOS SECTIONS.
10102	23140		0.63	3.0E-08	3.0E-08 AF055066.1	. LN	Homo sapiens MHC class 1 region
11276	L	37983	1.64	3.0E-08	3.0E-08 AI218001.1	EST_HUMAN	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMACE:1840284.3
11957	l	38646	1.32		3.0E-08 AF111167.2	LN	Homo sapiens jun dimerization protein gene, partial cds; cfcs gene, complete cds; and unknown gene
	ł						yg02f04.r1 Scares infant brain 1NIB Homo saplens cDNA done IMAGE:30948 5' similar to contains Alu
12156	28125		33.85		3.0E-08 R18420.1	EST_HUMAN	repelitive element;
211	l		4.16		2.0E-08 AW302996.1	EST_HUMAN	xr87f05x1 NCI_CGAP_Lu26 Homo septent; cDNA clone IMAGE:2/6/139 3
236	13458		5.76		2.0E-08 AA425588.1	EST HUMAN	zwe6f07.11 Soares, total_(etus_Nb2HF8_9w Homo sapiens cDNA cione IMAGE:773317 5 similar to contains. Au repetitive element,contains element MER16 repetitive element ;
509	L	28732			2.0E-08 AF198349.1	Ā	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
977	L				2.0E-08 AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Hamo saplens cDNA
677	1	L			2.0E-08 AW888438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1014	L		7.78		2.0E-08 BE280477.1	EST HUMAN	601155321F1 NIH_MGC_21 Homo septens cDNA clone IMAGE:3138693 5'
1373	L	3 27602			2.0E-08 AL163247.2	N FN	Homo sapiens chromosome 21 segment HS21C047
177.	L	L			2.0E-08 AW841890.1	EST_HUMAN	IL5-CN0024-030300-026-C01 CN0024 Homo sapiens cDNA
1780	L				2.0E-09 BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Hamo saplens cDNA clone IMAGE:3845199 5
ğ	L		8.7		2.0E-08 AW270271.1	EST HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo septiers CDNA clone IMAGE:2743149 3'
	ł		1.86		2.0E-08 K00218.1	NT	Sheep His-tRNA-GUG
0000	1			l	2 0F-08 042280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
327	16453	29474			3 042200	3W1001 NO.	

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		Т	╗	-	Г	Т	٦	<sub>2</sub> T	7		П		co .	Т	T	Т	T			$\Box$	Ţ				Т	٦
Top Hit Descriptor	WNT-14 PROTEIN PRECURSOR	RC3-ST0197-161099-012-b03 ST0197 Homo capiens cDNA	Homo sapiens shox gene, alternatively spliced products, complete cds	aa26c07.rt NC _CGAP_GCB1 Homo sapiéns cDNA clone INAGE:814380 5' similar to contains L1.t2 L1 repetitive element ;	he17h08,x2 NCI CGAP CML1 Homo septions cDNA clone IMAGE:2919327 3' similar to contains Atu	repetitive element	ai80h11.s1 Soares_testis_NHT Homo sepiens cDNA clone 1377189 3	xd32c04.x1 NCI_CGAP_Ovz3 Horno seplens cDNA done IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839874 3'	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 6'	W72f02.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;	w72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' sImilar to contains	LTR1.b3 LTR1 repetitive element;	Homo saplens chromosome 21 segment HS21C084	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT HBINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)	Homo sapiens caveclin 1 (CAV1) gene, exon 3 and partial cds	PM2-HT0130-150999-001-f12 HT0130 Homo saplens cDNA	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukernia Baylor-HGSC project≃TCBA Homo sapiens cDNA clone TCBAP5232	TCBAP1D5232 Pediatric pre-B œil acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sepiens oDNA clone TCBAP5332	Homo saplens hyperion gene, exons 1-50	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	Homo sapiens chromosome 21 segment HS21C102
Top Hit Dafabase Source	SWISSPROT	EST_HUMAN	TN	FST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	NT	NT	SWISSPROT	SWISSPROT	SWISSPROT	NT	EST HUMAN	EST HUMAN	EST HUMAN	LN.	SWISSPROT	\ V
Top Hit Acessian No.	042280	2.0E-08 AW813620.1	2.0E-08 U82668.1	2 NE-08 AA458040 1		2.0E-08 AW 572881.1	2.0E-08 AA813204.1	2.0E-08 AW088924.1	P10272	2.0E-08 AA490121.1	2.0E-08 AU139978.1	2.0E-08 N78097.1		2.0E-08 N78097.1	2.0E-08 AL163284.2	11431676 NT	P31792	P13002	P13002	1.0E-08 AF125348.1	1.0E-08 BE141959.1	1.0E-08 BE246844.1	1 0E-08 BF246844.1	1.0E-08 AJ010770.1	P19474	1.0E-08 AL163302.2
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AL163279.2           30481         4.17         8.0E-08 AL163279.1           30482         4.17         8.0E-08 AL163279.1           30481         4.17         8.0E-08 AL163279.1           30482         4.17         8.0E-08 AL163279.1           30481         2.54         8.0E-09 AL163270.1           30508         2.54         8.0E-09 AL163270.1	ORF SEQ         Expression Signed         (Top) Hit Top Hit Acesslon Database Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         Top Hit Top Hit Acesslon Signed         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Probe SEQ ID NO: 6496 8777 10483 12089 12089 1447 1900	σ	g	Express Signs	Most Similar (Top) Hit BLAST E Value 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09 6.0E-09	Similar Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single Single S	Top Hit Database Source Source T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	Top Hit Describtor Tobos Lyprosocu in Facoritia Top Hit Describtor Source Source  1 EST HUMAN xn88h08.x1 Scares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3°  1 EST HUMAN MR3-HT00446-260300-201-h12 HT0446 Homo sapiens cDNA clone IMAGE:2701311 3°  1 EST HUMAN MR3-HT00446-260300-201-h12 HT0446 Homo sapiens cDNA clone image of the mono sapiens fibroblast growth factor receiptor 3 (achondroplasia, thanatophoric dwarfsm) (FGFR3) mRNA NT Homo sapiens fibroblast growth factor receiptor 3 (achondroplasia, thanatophoric dwarfsm) (FGFR3) mRNA NT Homo sapiens fibroblast growth factor receiptor 3 (achondroplasia, thanatophoric dwarfsm) (FGFR3) mRNA Contains MER29.b2 MER29 repetitive element;  EST HUMAN HUMGS0003762 Human adult (K. Okubo) Homo sapiens cDNA EST HUMAN RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA EST HUMAN RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA Human sapiens chromosome 21 segment HS210084
6988 8785 10300	18703 18507 21884 23335		0.86	6.0E-09 6.0E-09 6.0E-09 6.0E-09	6.0E-09 AA359464.1 6.0E-09 U66059.1 6.0E-09 P37071 6.0E-09 AW 799867.1	EST_HUMAN NT SWISSPROT EST_HUMAN	ES 108749 Fetal lung il nomo saptens curva o eno Human gentine, TRY1, TRY2, TRY3, Human germline T-cell receptor beta chein Dopamine-beta-hydroxylass-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV2ZS1A2V1T, TCRBV3S9, TCRBV2S1A1T, TCRBV3S9, TCRBV7SSA1N4T, TCRBV3SSA1SS> OLFACTORY RECEPTOR-LIKE PROTEIN COR5 PM2-UM0053-240300-005-c09 UM0053 Homo saplens cDNA
11944 634 887 1497 2500 8030				4.0E-09 4.0E-09 4.0E-09 4.0E-09	4.0E-09 AA460142.1 ES 4.0E-09 AL163282.2 NT 4.0E-09 AL163285.2 NT 4.0E-09 AA163285.1 NT 4.0E-09 AA360878.1 ES 4.0E-09 AA360877.1 ES	EST_HUMAN NT_ NT_ EST_HUMAN EST_HUMAN	zóbed9. st Soares_testis_NHT Homo sapièns cDNA cione IMAGE:795880 3' Homo sapiens chromosome 21 segment H\$210082 Homo sapiens chromosome 21 segment H\$210085 Homo sapiens chromosome 21 segment H\$210085 Homo sapiens hypothetical protein (AF038169), mRNA EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa zw04006.rf Soares NHHMD_S 1 Homo sapiens cDNA clone IMAGE:788288 5' zw04006.rf Soares NHHMD_S 1 Homo sapiens cDNA clone IMAGE:788288 5' zw04006.rf Soares NHHMD_S 1 Homo sapiens cDNA clone IMAGE:788288 5'
11330	24393 24440 15559	38041	1.02		4.0E-09   184942.1 4.0E-09   A1886401.1 4.0E-09   AA185142.1 3.0E-08   BE22239.1	EST_HUMAN EST_HUMAN EST_HUMAN	MINIOR NO. CGAP LU2 Homo septents cDNA clone IMAGE:2443627 3' 2734412.1 Scares_NHMPu_S1 Homo septents cDNA clone IMAGE:265278 6' stmilar to gb:L07807 DYNAMIN-1 (HUMAN): httd9609.x1 NCI_CGAP_Lu24 Homo sapleris cDNA clone IMAGE:3186120 3' similar to contains MER18:3 MER18 repetitive element;
2619 2716 3408	1111		0.89		3.0E-09 BE222239.1 3.0E-09 P23249 3.0E-08 BE222239.1	EST_HUMAN SWISSPROT EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapieris cDNA clone IMAGE:3166120 3' cimitar to contains MER18.t3 MER18 repetitive element; PROTEIN MOV-10 hu09e09.x1 NCI_CGAP_Lu24 Homo sapieris cDNA clone IMAGE:3168120 3' simitar to contains MER18.t3 MER18 repetitive element;

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SWISSPROT  EST_HUMAN  NT EST_HUMAN  EST_HUMAN  NT EST_HUMAN  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  EST_HUMAN  NT EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  TOTHUMAN  EST_HUMAN  EST_HUMAN  TOTHUMAN  EST_HUMAN  TOTHUMAN  TOTHUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  TOTHUMAN  EST_HUMAN  TOTHUMAN  TOTHUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  TOTHUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN  EST_HUMAN	30666 3.47 3.0E-09 AF175325.1		AF17532			lamo saplens eukaryotic initiation factor 4AI (EIF4A1) gone, partial cds
EST_HUMAN NT EST_HUMAN NT NT NT NT NT EST_HUMAN SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT NT EST_HUMAN NT EST_HUMAN NT EST_HUMAN STEATHUMAN NT EST_HUMAN NT EST_HUMAN NT EST_HUMAN NT	30751 1.19 3.0E-09 Q9Y3R5		O9Y3R5			558.1 KDA PROTEIN C210RF5 (KIAA0833)
NT SWISSPROT SST HUMAN EST HUMAN NT EST HUMAN SWISSPROT SWISSPROT SWISSPROT EST HUMAN NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN STEST HUMAN EST HUMAN EST HUMAN EST HUMAN STEST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN	34682 1.1 3.0E-09 BE465780.1		BE465780			hx80e02x1 NCI_CGAP_Kid11 Hamo sapiens cDNA clone IMAĢE:3194090 3' similar to TR:O53091 O55091 IMPACT PROTEIN ;
SWISSPROT EST_HUMAN NT NT NT NT SWISSPROT SWISSPROT SWISSPROT EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN EST_HUMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN STATEMAN	37096 1.87 3.0E-09 AL163247.2		AL163247.		П	domo saplens chromosome 21 segment HS21 C047
EST_HUMAN  NT  NT  NT  NT  NT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  EST_HUMAN  NT  EST_HUMAN  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  ST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  ST_HUMAN  NT  EST_HUMAN  NT  ST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  NT  EST_HU			Q10940	Ť	1 I	1YPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
EST_HUMAN  NT  NT  NT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT  SWISSPROT	37978 3.15 3.0E-09 BF109843.1		BF109943.		1	172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:3527030 3'
NT NT EST HUMAN SWISSPROT SWISSPROT SWISSPROT EST HUMAN NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN ST EST HUMAN ST EST HUMAN ST EST HUMAN ST EST HUMAN ST EST HUMAN ST EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT	37979 3.15 3.0E-09 BF109943.1		BF109943.1			172c08x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:3527030 3'
NT EST_HUMAN SWISSPROT SWISSPROT EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN NT EST_HUMAN NT EST_HUMAN NT	0.98 2.0E-09 X16674.1		X16874.1			4.saplens PADPRP-I gene for NAD(+) ADP-ribosytransferase
T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	27511 4.7 2.0E-09 AL 163284.2	L	AL163284.2	Ī		dano sapiens chromosome 21 segment HS21 C084
ISSPROT ISSPROT THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN	10.71 2.0E-09 AL118573.1		AL118573.1	Ĺ		JKFZp761B1710_r1 781 (synonym: hamy2) Homo oapiene cDNA clone DKFZp761B1710 5
THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN THUMAN	28661 2.24 2.0E-09 Q9Y3R5	,	O9Y3R5			58.1 KDA PROTEIN C210RF5 (KIAA0933)
T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN	3.01		060241	Ť		SRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN	6.0 ·		AI263479.1	Ī	T_HUMAN	ji07d09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN			M23161.1			⊣uman transposon-like element mRNA
T_HUMAN T_HUMAN T_HUMAN T_HUMAN T_HUMAN	32333 0.67 2.0E-09 AI004062.1		A1004062.1			0147b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN NT EST_HUMAN AT EST_HUMAN S1624 NT 31624 NT	0.75 2.0E-09 AL163249.2		AL163249.2	Ì		damo sapiens chromosame 21 segment HS21C049
EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN 31624 NT	0.88 2.0E-09 AA357407.1		AA357407.1			EST66142 Kidney IX Homo sapiens cDNA i3 end similar to EST containing L1 repeat
EST_HUMAN NT EST_HUMAN NT EST_HUMAN ST EST_HUMAN EST_HUMAN 31624 NT	34155 8.81 2.0E-09 AA461430.1		AA461430.			zx83h06.r1 Soares_(otal_fetus_Nb2HF8_9¼ Homo sapiens cDNA clone IMAGE:786187 5' sImilar to contains Alu repetitive element;
EST_HUMAN  NT  EST_HUMAN  NT  EST_HUMAN  EST_HUMAN  EST_HUMAN 31624 NT	0.66		W28834.1			52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN 1624 NT	34534 0.59 2.0E-09 AI243732.1		AI243732.			th88g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18541143'
EST_HUMAN NT EST_HUMAN EST_HUMAN 1624 NT	35528 1.2 2.0E-09 AJ271736.1		AJ271736.1			нато sapiens Xq pseudoautosomal region; segment 1/2
EST_HUMAN EST_HUMAN 1624 NT 1924 NT	0.85		AV688642.1			4V688642 GKC Homo saplens cDNA clone GKCACA11 5'
EST_HUMAN EST_HUMAN 31624 NT 31624 NT	20.08 2.0E-09 X16674.1		X16674.1	Ī		4. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
EST_HUMAN EST_HUMAN 31624 NT						nc11c02.r1 NCI_CGAP_Pri Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive
T_HUMAN	1.86 2.0E-09 AA226070.1		AA226070			yement,
031624 NT 031624 NT	1.19 1.0E-09 W 78152.1		W781521			zz/9403.s1 9cares_feta _heart_NbHH19W_Homo sepiens cDNA clone IMAGE:346863 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
				031624		Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
	27354 1.43 1.0E-09			5031624	LN	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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			DNA-DIRECTED RNA POLYMERASE II L'ARGEST SUBUNIT	Hano sapiens presentiin-1 gene, exons 1 and 2	Homo sapiens presentiin-1 gene, exons 1 and 2	Home sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17	Т	1	П			Г	П		$\Box$				HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III	Macaca tonkeana isolate 669tonkpeona NADH dehydrogenase subunit 4L gene, complete cds; and NADH	dehydrogenase subunit 4 gene, mitochondrial genes encoding mucchondrial provents, partal cos				Homo saplens chromosome 21 segment HS21C103	Homo septens mannosidase, beta A, fysosomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds		I aqS3h11 x1 Stanley Frontal SN pool 2 Homo caplene cDNA clone IMAGE:2035653
	EST_HUMAN	EST_HUMAN	SWISSPROT	TN	NT	F.V	EST HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	EST_HUMAN	SWISSPROT	SWISSPROT		Į.	EST_HUMAN		EST_HUMAN	NT NT	NT	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	7.0E-10 AA345220.1	7.0E-10 BF352883.1	P35084	7.0E-10 AF029701.2	7.0E-10 AF029701.2	14000T	6.0E-10 A34008/7.1	002817	6.0E-10 AW853719.1	P33730	P33730	P88073	6.0E-10 AW971923.1	5.0E-10 AL046804.1	5.0E-10 Q01033	5.0E-10 AF181897.1	5.0E-10 BF105159.1	5.0E-10 P34678	5.0E-10 P34678		5.0E-10 AF091415.1	4.0E-10 AI221083.1		4.0E-10 AW 594709.1	4.0E-10 AL163303.2	4 0E-10 AF224689.1	4.0E-10 AW293243.1	4.0E-10 AI287342.1
Most Similar (Top) Hit BLAST E Velue	7.0E-10	7.0E-10	7.0E-10 P35084	7.0E-10	7.0E-10	000	8.0E-10	6.0E-10 Q02817	8.0E-10	6.0E-10 P33730	6.0E-10 P33730	6.0E-10 P88073	6.0E-10	5.0E-10	5.0E-10	5.0E-10	5.0E-10	5.0E-10	5.0E-10								l	
Expression Signal	4.06	1.37	1.85	1.54	1.54		9.44	1.88	3.15	96'0	96.0	0.48	1.95	5.29	1.14	1.4	1.85	2.24	2.24		131	1.09		1.4	6.79	17.76		
ORF SEQ ID NO:		34124	L	34764			17172			35602		1				31202		36374			38725				28877		L	37305
Exan SEQ ID NO:	19486	20848	20889	21245	21246	<u> </u>	14111	1	ł	22062		1_	_	L	L	L	l_	22801	22801		25021	13345	1	15193			İ	1.
Probe SEQ ID NO:	6314	7574	7834	8163	8163	- 5	9836	4815	4861	8983	8983	9834	12223	780	3564	5105	7475	92.26	9236		12040	114		2062	2040	7227	10398	10862

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						חוואים העמון ו ומשכה באלווים	
Probe SEQ ID NO:	Ewn SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827			4.0E-10	.0E-10 BE169208.1	EST HUMAN	PM1-HT0521-120200-001-008 HT0521 Horino sapiens cDNA
10794	23827	37451	0.54	4.0E-10	.0E-10 BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-008 HT0521 Homo sapiens cDNA
							y/32f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains
88	14112	27173	2.24	3.0E-10	.0E-10 N36113.1	EST_HUMAN	L1.t1 L1 repetitive element;
1382	14537		5.3		3.0E-10 AY005160.1	NT	Homo sapiens extracellular glycoprotein lacriffin precursor, gene, complete cos
4657	17783	30777		3.0E-10	3.0E-10 AL163203.2	TN	Homo sapiens chromosome 21 segment HS210003
4657	17783		0.94	3.0E-10	.0E-10 AL163203.2	NT	Hano sapiens chromosome 21 segment HS210003
6360	18463			3.0E-10	3.0E-10 1.34079.1	NT	Human XRCC1 DNA repair gene, genomic
5571	18767		0.78	ľ	3.0E-10 N50109.1	EST_HUMAN	yz11g08.s1 Sogres_multiple_scierosis_2NtHMSP Homo sepiens cDNA clane IMAGE:2827823
8332	1958				3.0E-10 P20350	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
88	ı		3.62		3.0E-10 BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sepiens cDNA done IMAGE:2906318 5
7837	1		1.42		3.0E-10 AV743302.1	EST_HUMAN	AV743302 CB Hamo sapiens cDNA clone CBFBGD08 5
7837	1	L		ľ	3.0E-10 AV743302.1	EST HUMAN	AV743302 CB Homo sepiens oDNA clono CBFBGD08 6
	1	L					ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA done IMAGE:220511 3' similar to contains MER29
8928	22007	35546	1.57		3.0E-10 H87208.1	EST_HUMAN	repetitive element;
9248	1		1.52		3.0E-10 AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Horrio saplens cDNA
9249	22326				3.0E-10 AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo saplens CDNA
9541			0.78		3.0E-10 AF020503.1	K	Homo sapiens FRA3B common fregile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10879			1.95		3.0E-10 T65891.1	EST_HUMAN	yc11e12.r1 Stretagene lung (#937210) Honjo sepiens cDNA clone IMAGE:80398 5
10820	L	ŀ	96'0		3.0E-10 AA769294.1	EST_HUMAN	nzaegoa.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3
12941	l l	31977			3.0E-10 BE179517.1	EST_HUMAN	IL3.HT0618-110500-136-E07 HT0618 Hamo septens CDNA
8		١.			2.0E-10 P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN 3 (CENTROMERE PROTEIN B) (CENF-B)
98	1	_	2.08		2.0E-10 P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN 3 (CENTROMERE PROTEIN B) (CENP-B)
							Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal gooptosis innibitory
1946	15089					N	protein (rigip) and survival motor neuron protein (smiri) genes, complete cos
3051	16227		0.84		2.0E-10 BF675047.1	EST_HUMAN	802136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:42/3377 5
5924	1_		2.3		2.0E-10 Q28640	SWISSPROT	(HPRG)
	1						Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gane, partial ode; oytochrome P450 polypeptide
							4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P460
6380	18549	32905	1.56		2.0E-10 AF280107.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
7537	20810	34084	6.41		2.0E-10 BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3840824 5
8203	L				2.0E-10 P26809	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; KIBUNUCLEASE H ]
8203	1	l	0.58		2.0E-10 P26809	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H J

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2171

12165

8855

7860 8434

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protein L18a (RPL18a), Ca2≁/Celmodulin-d'spendent protein kinese i (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy/protein > protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinaso I (CAMKI), creatine transporter (CRTR), Homo saplens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 7078408.x1 NCI\_CGAP\_Kid11 Homo sepiens cDNA clone IMAGE:3642303 3' similar to contains L1.t3 L1 qm04e10x1 NCI\_CGAP\_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.t1 L1 zn23g08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clane IMAGE:548314 5 we82f04.x1 Sogres\_NFL\_T\_GBC\_S1 Homb saplens cDNA done IMAGE:2347615 3' similar to contains Homo sapiens X28 region near ALD loous containing dual opecificity phoophatase 9 (DUSP9), ribosomal Homo sapiens X28 region near ALD focus containing dual specificity phosphatase 9 (DUSP9), ribosomal oy85h03.x1 Soares\_fetal\_liver\_splean\_1NFI,S\_S1 Homo septens cDNA clone IMAGE:16726613 AV662123 GLC Homo sepiens cDNA clane GLOCXA11 3'
[QV0-CT0225-191199-058-c08 CT0225 Homo sepiens cDNA
[QV2-TT0003-161199-013-g10 TT0003 Homo sepiens cDNA
[DX2-TT0003-161199-013-g10 TT0003 Homo sepiens cDNA
[DKFZp434N1317\_r1 434 (synonym: htes3) Homo sepiens cDNA clane DKFZp434N1317 6'
[DKFZp434N1317\_r1 434 (synonym: htes3) Homo sepiens cDNA clane DKFZp434N1317 5' 210f12.x1 Soares\_total\_fetus\_Nb2HFB\_9w Homo sapiens cDNA clone IMAGE:2043695 3 Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5 Top Hit Descriptor MR0-SN0038-290300-001-101 SN0038 Homo saplens cDNA CDM protein (CDM), adrenoleukodystrophy protein > LINE-1 REVERSE TRANSCRIPTASE HOMOLOG TB\_6A4 Fetal brain library Homo septens cDN MER31.t1 MER31 repetitive element; Single Exon Probes Expressed in Placenta repetitive element repetitive element EST\_HUMAN EST\_HUMAN EST\_HUMAN NT EST\_HUMAN EST\_HUMAN EST\_HUMAN EST HUMAN SWISSPROT SWISSPROT EST\_HUMAN EST\_HUMAN EST HUMAN **EST HUMAN** EST\_HUMAN EST HUMAN HUMAN EST\_HUMAN Top Hit Database Source 눋 Ę 닐닐보 Top Hit Acesslan 1.0E-10 XB7344.1 9.0E-11 BE145600.1 9.0E-11 AL134395.1 9.0E-11 AL134395.1 1.0E-10 AW652123.1 1.0E-10 AW652001.1 1.0E-10 AW832912.1 1.0E-10 A1797745.1 1.0E-10 P08548 1.0E-10 AU128584.1 1.0E-10 AW 408990.1 1.0E-10 AL041685.1 2.0E-10 BF434565.1 2.0E-10 AI862153.1 1.0E-10 AW867767. AL041685.1 1.0E-10 AF213884.1 1.0E-10 AA081868.1 1.0E-10 AI038280.1 ġ AI268340. 1.0E-10 U52111.2 1.0E-10 U52111.2 M30829.1 1.0E-10 / 1.0E-10 (Top) Hit BLAST E Value Most Similar 1.8 6.02 18.24 16.24 0.58 1.62 6.24 0.69 .06 3.09 7.33 9 1.33 3.37 6.0 0.67 Expression Signal 30379 34419 20521 28433 30378 30388 29768 ORF SEQ ΘŃΟ 21834 23441 18503 15306 SEQ ID 17391 20713 20914 13490 2468<u>2</u> <del>1</del> 14789 15772 16753 1739 17380 18398 16793 17277 17430

4123

4245

4245 4253 4285 724 4485

1637 2849

3589

1600

9502

Probe SEQ ID

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					>		
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	29657	2.98	9.0E-11	9,0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sepiens cDNA clone DKFZp547D225 5'
3470	L		2.98	9.0E-11	9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo saplens cDNA clone DKFZp547D225 5'
4622	17759	30741	9.0	9.0E-11	9.0E-11 AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo eapiens cDNA clone IMAGE:970297 3'
5692	ı		3.05	9.0E-11	9.0E-11 BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	9.0E-11 AA324960.1 1	EST_HUMAN	EST27872 Cerebellum II Homo saplens cD/VA 5' end
10357		37003	1.17	9.0E-11	9.0E-11 AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	<u> </u>		2.45	9.0E-11	9.0E-11 C16635.1	EST_HUMAN	C16335 Clontech human acrta cdyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-506B08 5
							yn53f11.s1 Scares adult brain N2b5HB55Y.Homo sapiens cDNA clone IMAGE:172173 3' similar to contains
3185	16360		10.53	8.0E-11	8.0E-11 H19971.1	EST_HUMAN	L1 repetitive element;
4164	17306	30300	5.37	8.0E-11	8.0E-11 N23712.1	EST_HUMAN	yw46e08.s1 Wefzmann Olfectory Epithelium Homo saplens cDNA clone IMACE:255288 3
5913	L	32415		8.0E-11	8.0E-11 AW674318.1	<b>EST_HUMAN</b>	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982.3'
	L	L					2/45h11 x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.t1
6811	19965		0.62	8.0E-11	8.0E-11 AW 166158.1	EST_HUMAN	MER10 repetitive element ;
1478	ı	27717	2.09	7.0E-11		EST_HUMAN	EST34392 Embryo, 6 week I Hamo sapiens cDNA 5' end
8698	21775		2.61	7.0E-11	7.0E-11 AF163864.1	IN	Homo septens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
10434	23469	•	1.37	7.0E-11	7.0E-11 P11369	SWISSPROT	ENDONUCI.EASE)
425	13820	26661	6.19		6.0E-11 M55270.1	L	Human matrix Gla protein (MGP) gene, complete cds
425	l_				6.0E-11 M55270.1	NT	Humen matrix Gla protein (MGP) gene, complete cds
		L					Hamo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
6862	20014	33424	16.0	8.0E-11	8.0E-11 L44140.1	NT	(GGPD) gene, complete cds's
7870	L	34431	3.5	6.0E-11 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8559		35179	66.9		6.0E-11 AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5
9514	<u>L</u>	36145	0.5	_	6.0E-11 BE063509.1	<b>EST_HUMAN</b>	CM0-BT0281-031199-087-a03 BT0281 Homo saplens oDNA
15	13250		1	5.0E-11	5.0E-11 AL163283.2	NT	Homo saplens chromosome 21 segment HS:21C083
3450	L	L	1.24		5.0E-11 AL163283.2	۲N	Homo sapiens chromosome 21 segment HS21C083
6646	L				5.0E-11 AL163213.2	TN	Homo saplens chromosome 21 segment HS21C013
7699	20764	34248	11.67	L	11416789 NT	NT	Homo sapiens protocadherin beta 3 (PCDHB3), mRNA
. 1433	14586		1.38		4.0E-11 AA436042.1	EST_HUMAN	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5
2851	15965	29074	9.84		4.0E-11 BE885900.1	EST HUMAN	601507531F1 NIH_MGC_71 Homo capiens cDNA clana IMAGE:3909235 5
3034	16210	29233	1.26		.2	NT	Homo sapiens chromosome 21 segment HS21C047
4740	17875				_	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo saplens cDNA clone 069
6605	5 19765	33154	3.29		4.0E-11 P20095	SWISSPROT	PRE-MRNA SPLICING FACIOR RNA HELICASE PRPZ

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		İ					
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7141	20276	33718	0.82	4.0E-11	4.0E-11 AA442630.1	EST_HUMAN	zv59f10.r1 Soares_testis_NHT. Homo sepiens cDNA clone IMAGE:757963 5' similar to TR:G1055250 G1055260 PHEROMONE RECEPTOR VN4.;
7532	1		3.66	4.0E-11		LΝ	Homo sapiens mannosidase, beta A, lysoscimal (MANBA) gene, and ubiquitin-conjugating enzyme EZU 3 (UBE2D3) genes, complete cds
9898	1		1.56	4.0E-11	4.0E-11 BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-f08 HT0256 Homo sapiens cDNA
CRRC		36487		4.0E-11	4.0E-11 Al609753.1	EST_HUMAN	tf82g12.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMACE::2105830 3' similar to WP:2K353.1 CE00385 ;
10859	1	1_		4.0E-11		П	MR0-GN0024-180900-008-h09 GN0024 Homo septens cDNA
12784	1			4.0E-11	1	NT	Homo saplens SH3-domain binding protein 1 (SH3BP1), mKNA
1521		27758	4	3.0E-11	TN 7709789	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (NM82), mKNA
4391	17534		1.35		3.0E-11 AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinome Homo sepiens CUNA of end
882		27215			2.0E-11 AI150502.1	EST_HUMAN	ব্যওভে4.x1 Sogres_testis_NHT Homo capions CDNA clone IMAGE:175/102 3 similar to contains MER io.to MER10 repetitive element ;
1212	١.			1	2.0E-11 R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1NIB Homo septens cDNA clone IMAGE:35144 5
1212			20.98		2.0E-11 R24807.1	EST_HUMAN	yg43e12.r1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:35144 5
1644	L			İ	2.0E-11 L17432.1	LN.	Galtus gallus rhoglobin, beta-H globin, beta-A globin, epsilon-globin, and offactory receptor-like protein COR3 beta (COR3 beta) ganes, complete cds
7,87	1			<u> </u>	2.0E-11 L17432.1	LN	Gailus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and offactory receptor-like protein COR3'bala (COR3'beta) genes, complete cids
2823					2.0E-11 AF087913.1	N⊤	Human endogenous retrovirus HERV-P-T47D
3266	L				2.0E-11 P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3403	1		0.92		2.0E-11 AI478617.1	EST_HUMAN	tm54c09.x1 NCI_CGAP_Ktd11 Hame sapiens cDNA clone IMAGE:2161938 3
3448		l			2.0E-11   Q10473	SWISSPROT	POLYPEPTIDE N-AGETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
	1	l			2 0F-41 AF020503 1	Ę	Homo sapiens FRA3B common fragile región, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3707	┸	29862			2.0E-11 P70213	SWISSPROT	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
4566	ı			L	2.0E-11 BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo septens cDNA
4728			0.8		2.0E-11 AL163227.2	ħ	Homo saplens chromosome 21 segment HS21C027
505	1_		1.85		2.0E-11 BE062658.1	EST_HUMAN	QV2-BT0258-261099-014-e01 BT0258 Homo sepiens cDNA
6142	18265	31234	0.82		2.0E-11 AA307331.1	EST_HUMAN	EST178228 Colon carcinoma (HCC) cell line Homo sapiens CDNA 5 end similar to similar to dipriezz- macroglobulin
0000	ı	ł			2 0F-11 AW877808.1	EST HUMAN	QV2-PT0073-280300-109-h09 PT0073 Homo sapiens cDNA
020	- 1						

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6440	19607	32970	2			EST_HUMAN	nc83h05.r1 NCI_CGAP_GC1 Homo sepieris cDNA clone IMAGE:797433 5' sImilar to SW:PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16. ;
7346	ſ		0.85		45.1	EST_HUMAN	7/97c03x1 NCI_CGAP_GC6 Homo sapiens cDNA clane IMAGE:34425653
9908	1		0.69		2.0E-11 P37072	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN CORG
9424	i .		1.39	2	.0E-11 AF029308.1	Ę	Hane suplens chromosome 9 duplication of the T cell receptor beta locus and trypshogen gene familles
10491	1	37135	5.13	ľ	ll	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	l	37376	1.09		20E-11 AW885874.1	EST_HUMAN	RC4-DT0072-170400-013-c11 OT0072 Homo seplens cDNA
10734	乚	37377	1.09			EST HUMAN	RC4-OT0072-170400-013-c11 O10072 Homo sapiens cD/VA
11375	24436		1.64		2.0E-11 AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens dUNA cione iMAGE:4/1/94 3
11375	24436	38095	1.84		2.0E-11 AA035369.1	EST_HUMAN	z/27g02.s1 Soares_pregnant_uterus_NbHPU Homo septens dDNA done IMAGE:471794 3
11408	24469	38133	1.4	, ,	2.0E-11 AA261956.1	EST HUMAN	23/18b04.rf NCI_CGAP_GCB1 Homo sapiens cUNA clone IMAGE:083319 3
12122	25102		12.19		2.0E-11 AL163278.2	NT	Hamo sapiens chromosome 21 segment H5210078
12297	ı		1.85		2.0E-11 AA704195.1	EST_HUMAN	2/77e03.s1 Scares_fetal_liver_spiecn_fNFILS_S1 Homo sapiens cDNA clone IMAGE:450924 3
12328	26237		1.44		2.0E-11 AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo septens cDNA
12354	ı	32115	2.15		2.0E-11 BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo saplens cDNA
12841			1.43		2.0E-11 D25217.2	TN	Homo saplens mRNA for KIAA0027 protein, partial cds
12813	L		3.62		2.0E-11 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	l		2.5	2.0E-11	11417988 NT	LN	Homo saplens SEC14 (S. cerevisiae) Hike 2 (SEC14L2), mRNA
88	13876	58909			1.0E-11 AJ131016.1	LN T	Homo saplens SCL gene locus
88	L		1.72		1.0E-11 AL163209.2	NT	Home sapiens chromosome 21 segment HS21C009
1244	L				1.0E-11 AL163279.2	TN	Homo sapiens chromosome 21 segment HS21C079
1628	14681		1.82		1.0E-11 AF119914.1	NT	Homo saplens PRO3078 mRNA, complete cds
2085	15235	28356	0.94		1.0E-11 P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2195	L				1.0E-11 AF000573.1	NT	Home sapiens hamogentisate 1,2-dloxygenrise gene, camplete cds
2228	15363	28492	1.1		1.0E-11 AA309318.1	EST_HUMAN	EST180186 Liver, hepatocellulær carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3588	L				1.0E-11 BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-412 BN0105 Homo saplens cDNA
5447	Ł.				1.0E-11 AL163247.2	ΙN	Homo sapiens chromosome 21 segment HS21C047
	L						7p57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAQE:3649945 3' similar to contains MER10.b3
5953	19139	32455	0.78		BF22264	EST_HUMAN	MER10 repetitive element;
8388	21477	35004			1 4885546 NT	INT.	Homo sapiens PHD finger protein 2 (PHF2),mKNA
8781	l	35403			1.0E-11 R13174.1	EST HUMAN	yf73d08.r1 Soares Infant brain 1NIB Homo (apiens cDNA done IMAGE:28165 5
9248	1	35870	1.49		1.0E-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo saplens cDNA

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•					ויייניווס	ביים וחיים	טוופס דאףוסססם ווון ומסטונים
Probe SEQ ID NO:	Exen SEQ ID NO:	OŖF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9248	22325	35871	1.49	1.0E-11	.0E-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Hcmo seplens cDNA
10626	23660		0.54	1.0E-11	1.0E-11 AL163302.2	NT	Homo sapiens chromosome 21 segment HS:21C102
11566		38302		1.0E-11	.0E-11 BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4285977 5'
12903	26879		1.37	1.0E-11	I,0E-11 Z20377.1		HSAAACADH P, Human foetal Brain Whole tissue Homo saplens cDNA
3017	16183		0.75		3.0E-12 P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002					9.0E-12 AL163300.2	NT	Hamo sapiens chromosame 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	9.0E-12 AL163300.2	NT	Homo saplens chromosome 21 segment HS21C100
9539	L	L	0.88	8.0E-12	8.0E-12 BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Horrio saplens cDNA
12408			4.68	8.0E-12	8.0E-12 AJ271738.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4783	L	30802		7.0E-12	7.0E-12 Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11831	24711	38402	6.8		.0E-12 AA704735.1	EST_HUMAN	223g01.s1 Scares_fetal_liver_splean_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152.3'
13225	25903		1.18	_	.0E-12 D16473.1	LN	Human mRNA, Xq terminal portion
3637	<u></u>		0.86		B.0E-12 AV730554.1	EST_HUMAN	AV730554 HTF Hano saplens cDNA clane/HTFAWF08 5'
	١						rz8871.51 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1302573 3' similar to contains Alu
4468	17608	30586	9.23	9	1.0E-12 AA732518.1	EST_HUMAN	repetitive element;
	<b>I</b>	L					#66g12.x1 Soares_NSF_F9_9W_OT_PA_F_S1 Homo sapiens cDNA clone IMAGE-2146438 3' similar to
5336	18449	31418	5.12		8.0E-12 AI459161.1	EST_HUMAN	contains MER10.tz MER10 MER10 repetitive element :
9188	22274	35811	1.09		6.0E-12 AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
0	2000		70.7	C 10 40	6 OE 42 0 0 0 4 7 8 9 8 1	ECT HIMAN	od10g11.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1387688 similar to contains MER29.02 MFR29 renetitive element
13206			1 25		G.0E-12 AW86846 1	EST HUMAN	RC4-OT0072-080400-012-f11 OT0072 Harro saplens cDNA
4068	1	277000			5 0F-12 T06573 1	EST HUMAN	EST04462 Fetal brain, Stratagene (cat#638,206) Homo sapiens cDNA clone HFBDV33
3477	1				5.0E-12 BE047779.1	EST_HUMAN	1242b05.y1 NCI_CGAP_Brn52 Homo sepiens cDNA clone IMAGE:2291217 6
3821	1	29984		Ĺ	5.0E-12 AJ271736.1	IN	Homo sapiens Xq pseudoautosomal reglon; segment 2/2
6145	ı				3.0E-12 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6145	19323		6.13	Ĺ	5.0E-12 AL163278.2	NT TA	Homo saplens chromosome 21 segment HS21C078
8820	19780	33168			5.0E-12 AW974760.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo saplens cDNA
7178	L			ľ	5.0E-12 AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (syncnym: hiss3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20022		0.83	"	5.0E-12 AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synanym: htes3) Hamo sapiens cDNA clone DKFZp434B1615 3'
	1						201912.s1 Soares_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:375718.3' similar to contains
8424	- 1	35038			5.0E-12 AA033745.1	ESI_HUMAN	L1.3 L1 repetitive element
8867			0.65		_	EST_HUMAN	RC1-010086-220300-011-b07 010086 Horno sepiens cDNA
9195			0.77	)		EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clane DKFZp434J0426 6'
9308	22384	35936			5.0E-12 AJ271735.1	N	Homo saplens Xq pseudoautosomal region; segment 1/2

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9623	22678	36247	1.22		5.0E-12 P34982	SWISSPROT	<u>OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)</u>
104B2	23517		4.8		5.0E-12 AL163303.2	L	Hamo sepiens chromosome 21 segment HS21C103
10573	23608	37213	0.69		5.0E-12 AL163302.2	NT	Homo sapiens chromosome 21 segment H321C102
10793	23823		9.0		6978754 NT	Ŋ	Rattus norvegicus Deleted in colcorectal cancer (rat homolog) (Dcc), mRNA
254		28505	3.29		4.0E-12 AA700326.1	EST_HUMAN	274g11.s1 Soares_fatal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:460676 3
285	i	28505	3.42		4.0E-12 AA700326.1	EST HUMAN	274g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4606763
4742	1		0.88		4.0E-12 AI889984.1	EST HUMAN	b26h05x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:22707453' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
787	20853		0.71		4.0E-12 BF445140.1	EST_HUMAN	nad21b03.x1 NCI_CGAP_Lu24 Hamo sapirans cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element;
					, F000017	<u> </u>	Homo explens S164 gene, partial cds; PS1 and hypothetical probein genes, complete cds; and S171 gene,
8437					4.0E-12/AF109907.1		Put to 200
11338	24401	38050	4.33		4.0E-12 AJ229043.1	Ę	Home sapiens 959 kb contig between AML1 and CBR1 on chromosome 21422, segment 3/3
1			3		A FOODE	Ė	Homo sapiens Bruton's tyrosine kirase (BTIK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein III ad I and ETD2 (FTD2) nemas complete rids
12684	25458		2.11		4.0E-12 U/802/.1	ž	THE TOTAL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
	4284B	26830	2.58		3 0F-12 AW341683 1	EST HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homb sapiens cDNA done INACE:2909377.3 5Imilar to 1 R:O14617 [O14617 SMRP.;
3	2						HA13401 to Source NET T GBC S1 Homb septens cDNA clone IMAGE:2808377 3' similar to TR:014517
831	13816	26840	2.58		3.0E-12 AW341683.1	EST_HUMAN	014617 SMRP.;
5276	18305	31363	0.78		3.0E-12 AL163268.2	NT	Homo sapiens chromosome 21 segment HS210068
9299	Į.		1.44		3.0E-12 AF111168.2	TN	Home sapiens serine paintiby transferase, subunit II gene, complete ods; and unknown genes
8570	21651				3.0E-12 035453	SWISSPROT	SERINE PROTEASE HEPSIN
10891	23975		2.32		3.0E-12 U37872.1	TN	Human prostate specific antigen gene, 5' flanking region
10891	23976	37607	2.32		3.0E-12 U37872.1	NT.	Human prostate specific antigen gene, 5' flanking region
1685					2.0E-12 AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-e05 UM0071 Horio saplens cDNA
3558	18721			2.0E-12	6754495 NT	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4230					2.0E-12 J01884.1	LN	Rat U3A small nuclear RNA
4230	L	L			J01884.1	R	Rat U3A small nuclear RNA
454	L				2.0E-12 BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Horino saplens cDNA
5018	L	31123		L	070306	SWISSPROT	TBX16 PROTEIN (T-BOX PROTEIN 16)
5018	l	31124	0.71		2.0E-12 070306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
9099			2.08		2.0E-12 AW971857.1	EST_HUMAN	EST383946 MAGE resequences, MAGL Homo sapiens cDNA
7328	20408	33870	3.85		2.0E-12 T08169.1	EST_HUMAN	EST06050 Infant Brain, Bento Scares Home sapiens cUNA done HIBBA13 3 end

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		-	т	_	-		т	Т	-т	<u> </u>	Т	П	Т	Т	Т	Т	Т	Ŧ	Т	丁		Т	Т		1		$\neg$
Single Exon Probes Expressed in Flacenta	Top Hit Descriptor	MRO-HT0559-200400-015-e08 HT0559 Homo saplens cDNA	Homo sapiens Ac-like transposable element (ALTE), mRNA	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds	MR3-HT0487-150200-113-g01 HT0487 Hojmo sapiens cDNA	qq07f02.x1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:1831835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN ; ;	xn27h03.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2694965 3'	Homo sapiens chromosome 21 segment HS21C083	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	hisogogari NCI_CGAP_GU1 Homo sapleris cDNA clone IMAGE:2970040 3' similar to contains MER18.rt MED-18 receitive element	with to repoure contains.  With the second contains L1.b3 L1  With the second contains L1.b3 L1	repotitivo alement;	Hano saplens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds	Hano sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds	AU132248 NT2RP3 Homo saplens cDNA clone NT2RP3004070 5' ~	AU132248 NT2RP3 Hamo sapiens cDNA clane NT2RP3004070 6	Homo sapiens atada telangiectasia (ATM) gene, complete cds	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0981	EST00008 Sozres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:184/869 6	EST00008 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1847869 5	Mus musculus WNT-2 gens, partial cds; pulative ankyrin-related protein and cystic fibrosis trensmembrane	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds	dn68e04.x1 Soares fetal_liver_spleen_1NFLS_S1 Hamo septens cDNA clone IMAGE:1849614.3' similer to go:m19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10	repetitive element;	qh66a04.x1 Soares_fetal_liver_cpleen_1NFI,S_S1 Homo septens cDNA clone IMAGE:1849614.3' similar to gc. M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10	repetitive element;
Exon Prope	Top Hit Database Source	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	IN	MALA TOT	ESITHOWAIN	EST_HUMAN	Ę	F	EST_HUMAN	EST_HUMAN	LN.	SWISSPROT	EST_HUMAN	EST_HUMAN		TN	INT		EST_HUMAN		EST_HUMAN
Singi	Top Hit Acesslan No.	2.0E-12 BE173035.1	11422229 NT	2.0E-12 AF196864.1	2.0E-12 BE165980.1	2.0E-12 Al334130.1	2.0E-12 AW242934.1	2.0E-12 AL163283.2	11418248 NT	7 7 20 200 111	1.0E-12 AW62/6/4.1	1.0E-12 AI871728.1	1.0E-12 AF000991.1	1.0E-12 AF000991.1	1.0E-12 AU132248.1	1.0E-12 AU132248.1	1.0E-12 U82828.1	Q9Y2G7	1.0E-12 BF642800.1	1.0E-12 BF642800.1		1.0E-12 AF229843.1	1.0E-12 AF196864.1		1.0E-12 AI248533.1		1.0E-12 AI248533.1
	Most Similar (Top) Hit BLAST E Value	2.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12	2.0E-12	0, 10,	1.05-12	1.0E-12	1.0E-12	1.0E-12	1.0E-12	1.0E-12	1.0E-12	1.0E-12 Q9Y2G7	1.0E-12	1.0E-12		1.0E-12	1.0E-12		1.0E-12		
	Expression Signal	1.33	2.19	1.88	8.32	0.76	1.53	1.34	1.46	,	2	1.78	1.04	1.04	40.43	40.43	1.6	1.62	0.59	0.59		0.63	2.53		10.78		10.78
	ORF SEQ ID NO:	34047	34395			37375		1	-  -		26385		28326			30139	١.		32804	32805		33208	33800		33840		33841
	Exon SEQ ID NO:	20574	L	ł	_		ı	25228	i i	l	13354	15185	1	1	1	1	ı	18342	ł	1		19821	ı	1	20382	<u> </u>	20382
	Probe SEQ ID NO:	7489	7838	9508	10191	10733	12129	12313	12516		125	2044	3138	3138	3978	3978	6088	6166	6282	6282		6662	7265		7300		7300

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Top Hill   Top Hil Acession   Database   Value   Database   Value   No.   Source   Value   No.   Source   Value   No.   Source   Value   No.   Source   Value   No.   Source   Value   No.   1.0E-12   AA782323.1   EST_HUMAN   1.0E-12   AA782323.1   EST_HUMAN   1.0E-12   AA782323.1   EST_HUMAN   1.0E-12   AA782323.1   EST_HUMAN   SoE-13   AB9953.1   EST_HUMAN   SoE-13   AB9953.1   EST_HUMAN   SoE-13   AB9953.1   EST_HUMAN   SoE-13   AB94398.1   EST_HUMAN   SoE-13   AB94398.1   EST_HUMAN   SoE-13   AB94398.1   EST_HUMAN   SoE-13   AB94398.1   EST_HUMAN   SoE-13   AB94398.1   EST_HUMAN   SoE-13   AB94398.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA435773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_HUMAN   SoE-13   AA983773.1   EST_H			-				
0.69 1.0E-12 U68059.1 NT 1.25 1.0E-12 AA782233.1 EST_HUMAN 1.24 1.0E-12 AA782233.1 EST_HUMAN 1.54 1.0E-12 AA782233.1 EST_HUMAN 1.59 1.0E-12 AA782288.2 NT 1.19 1.0E-12 AA782288.2 NT 1.19 1.0E-12 AA782288.2 NT 1.28 1.0E-13 AB722980.1 NT 2.81 8.0E-13 AB722980.1 NT 2.73 8.0E-13 B09053.1 EST_HUMAN 0.63 8.0E-13 U80017.1 NT 0.63 8.0E-13 U80017.1 NT 0.63 8.0E-13 AB84398.1 EST_HUMAN 0.63 8.0E-13 AB84398.1 EST_HUMAN 0.63 8.0E-13 AB84398.1 EST_HUMAN 0.63 8.0E-13 AB84398.1 EST_HUMAN 1.58 7.0E-13 Q10473 SWISSPROT 0.99 8.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-13 AA835773.1 EST_HUMAN 1.58 5.0E-		ORF SEO ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3529B   0.69   1.0E-12   U66059.1   NT     38536   2.32   1.0E-12   AA782323.1   EST_HUMAN     38536   2.32   1.0E-12   AA782323.1   EST_HUMAN     1.54   1.0E-12   AA78239.1   EST_HUMAN     1.59   1.0E-12   AA78299.1   EST_HUMAN     1.50   1.0E-12   AA78299.1   EST_HUMAN     2.82   1.0E-12   AA78299.1   NT     2.82   1.0E-13   AB029900.1   NT     2.83   1.21   8.0E-13   M99653.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94398.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94393.1   EST_HUMAN     3.4907   0.63   8.0E-13   AB94393.1   EST_HUMAN     3.4908   5.0E-13   AA435773.1   EST_HUMAN     3.4807   0.69   5.0E-13   AB94393.1   EST_HUMAN     3.4807   0.69   5.0E-13   AB94393.1   EST_HUMAN     3.4807   0.69   5.0E-13   AB94393.1   EST_HUMAN     3.4808   2.64   5.0E-13   AB94393.1   EST_HUMAN     3.4808   2.64   5.0E-13   AB94393.1   EST_HUMAN     3.4808   2.64   5.0E-13   AB94394.1   EST_HUMAN     3.4808   2.64   5.0E-13   AB94394.1   EST_HUMAN     3.4809   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.4809   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.4809   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.4809   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.4809   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.4809   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.5509   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.5509   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.5509   5.65   6.0E-13   AB94394.1   EST_HUMAN     3.5091   5.0E-13   AB94394.1   EST_HUMAN     3.5091   5.0E-13   AB94394.1   EST_HUMAN     3.5091   5.0E-13   AB94394.1   EST_HUMAN     3.5091   5.0E-13   AB94394.1   EST_HUMAN     3.5091   5.0E-13							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV27S1P, TCRBV2S1A1T, TCRBV13S3, TCRBV27S1P, TCRBV7S3A2T, TCRBV13S2A1CRBV5S2A2PT, TCRBV7S2A1N4T,
38521 1.25 1.0E-12 AA782323.1 EST_HUMAN 38835 2.32 1.0E-12 AW862164.1 EST_HUMAN 1.54 1.0E-12 AR78592.1 EST_HUMAN 1.19 1.0E-12 AR78598.1 EST_HUMAN 30223 1.21 8.0E-13 AB929900.1 NT 28957 6.03 8.0E-13 U29185.1 NT 28958 6.03 8.0E-13 U29185.1 NT 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.63 8.0E-13 AB94398.1 EST_HUMAN 34907 0.693 8.0E-13 AA435773.1 EST_HUMAN 34908 5.0E-13 AA935773.1 EST_HUMAN 34908 5.0E-13 BP778544.1 EST_HUMAN 4 8 A A ABST AB94398 3 SWISSPROT 4 8 A A ABST AB94398 3 SWISSPROT 5 A 5 A 5 A 5 A 5 A 5 A 5 A 5 A 5 A 5 A	ш			1.0E-12	U66059.1	۲N	TCRBV13S9/13S>
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1.93 1.0E-12 AL163289.2 NT 1.19 1.0E-12 P44839 SWISSPROT 2.82 1.0E-12 AF224669.1 NT 2.82 1.0E-13 AB22990.1 NT 2.83 8.0E-13 AB22990.1 NT 2.83 8.0E-13 L29185.1 NT 2.8450 0.63 8.0E-13 L29185.1 NT 2.8450 0.63 8.0E-13 L29185.1 NT 2.8450 0.63 8.0E-13 L29185.1 NT 2.8450 0.63 8.0E-13 L29185.1 NT 2.8450 0.63 8.0E-13 L29185.1 SWISSPROT 2.8450 0.63 8.0E-13 L29185.1 SWISSPROT 2.8450 0.63 8.0E-13 L29185.1 SWISSPROT 2.8450 0.63 8.0E-13 L29185.1 SWISSPROT 2.8450 0.65 8.0E-13 L29185.1 EST_HUMAN 3.1329 0.69 8.0E-13 L29185.1 EST_HUMAN 3.1329 0.69 8.0E-13 L29185.1 EST_HUMAN 3.1329 0.69 8.0E-13 L29185.1 EST_HUMAN 3.1329 0.99 8.0E-13 L29185.1 EST_HUMAN 3.1329 0.99 8.0E-13 L29185.1 SWISSPROT 3.156 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 EST_HUMAN 3.1570 0.99 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 SWISSPROT 3.1570 0.99 8.0E-13 L29185.1 EST_HUMAN 3.1570 0.99 8.0E-13 L29185.1 EST_HUMAN 3.1570 0.99 8.0E-13 L29185.1 EST_HUMAN 3.1570 0.99 8.0E-13 L29185.1 EST_HUMAN 3.1570 0.99 8.0E-13 L29185.1 EST_HUMAN 4.88 4.0E-13 L29185.1 EST_HUMAN 4.88 4.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 EST_HUMAN 5.0E-13 L29185.1 ES	ıΥ	-	1.54	1.0E-12		EST_HUMAN	wi33h08x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
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2.82 1.0E-12 AF224690.1 NT 30223 1.21 8.0E-13 ABQ28900.1 NT 28957 5.03 8.0E-13 U29185.1 NT 28958 6.03 8.0E-13 U29185.1 NT 34909 0.63 8.0E-13 U80017.1 NT 34909 0.63 8.0E-13 ABB4398.1 EST_HUMAN 34907 0.63 8.0E-13 ABB4398.1 EST_HUMAN 34907 0.63 8.0E-13 BE778223.1 EST_HUMAN 34907 0.63 8.0E-13 BE778223.1 EST_HUMAN 31329 0.93 8.0E-13 AL163207.2 NT 31329 0.93 8.0E-13 AL163207.2 NT 31329 0.93 8.0E-13 AL163207.2 NT 31329 0.93 8.0E-13 AN37838.1 EST_HUMAN 33572 0.99 5.0E-13 PO9983 SWISSPROT 37808 2.64 5.0E-13 PO9983 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO9383 SWISSPROT 37808 2.64 5.0E-13 PO7313 EST_HUMAN 37808 2.64 5.0E-13 PO7313 SWISSPROT 37808 2.64 5.0E-13 PO7313 SWISSPROT 37808 2.64 5.0E-13 PO7313 SWISSPROT	18		1.19	1.0E-12	P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR
30223   1.21   8.0E-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-13   MD-	1 20		2.82	1.0E-12	AF224669.1	F	Homo sapiens mannosidase, beta A, tysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
281 8.0E-13 N99653.1 EST HUMAN 28958 6.03 8.0E-13 U29185.1 NT 28958 6.03 8.0E-13 U29185.1 NT 28958 6.03 8.0E-13 U29185.1 NT 34907 0.63 8.0E-13 U89017.1 NT 34907 0.63 8.0E-13 L894388.1 EST_HUMAN 34907 0.63 8.0E-13 L894388.1 EST_HUMAN 0.77 7.0E-13 Q89165 SWISSPROT 0.77 7.0E-13 Q89165 SWISSPROT 1.53 7.0E-13 BE778223.1 EST_HUMAN 31329 0.83 6.0E-13 AL163207.2 NT 28430 5.65 6.0E-13 AL163207.2 NT 1.58 5.0E-13 R78338.1 EST_HUMAN 1.15 5.0E-13 R78338.1 EST_HUMAN 1.15 5.0E-13 R78338.1 EST_HUMAN 283572 0.99 5.0E-13 R78338.1 EST_HUMAN 28008 2.64 5.0E-13 P09983 SWISSPROT 28430 6.05 3.0E-13 P09983 SWISSPROT 28508 2.64 5.0E-13 P037864.1 EST_HUMAN 28508 2.64 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R78338.1 EST_HUMAN 28508 5.0E-13 R7	12			9.0E-13	AB029900.1	Ę	Homo saplens CST gene for cerebroside sulforransferase, exon 1, 2, 3, 4, 5
26957         5.03         8.0E-13 U29185.1         NT           26968         6.03         8.0E-13 U29185.1         NT           28136         2.73         8.0E-13 U80017.1         NT           34907         0.63         8.0E-13 AB84388.1         EST_HUMAN           34907         0.63         8.0E-13 AB84388.1         EST_HUMAN           0.77         7.0E-13 Q85165         SWISSPROT           0.77         7.0E-13 Q85165         SWISSPROT           1.53         7.0E-13 BE778223.1         EST_HUMAN           31329         0.83         6.0E-13 AL163207.2         NT           31329         0.83         6.0E-13 AL267928.1         EST_HUMAN           1.15         5.0E-13 R78338.1         EST_HUMAN           1.58         5.0E-13 R78338.1         EST_HUMAN           33572         0.99         5.0E-13 R78338.1         EST_HUMAN           37808         2.64         5.0E-13 R7835773.1         EST_HUMAN           37808         2.64         5.0E-13 R7835773.1         EST_HUMAN           37808         2.64         5.0E-13 R7835773.1         EST_HUMAN	12	L		9.0E-13	N69653.1	EST_HUMAN	za26b08.s1 Soaros fetal liver optoen 1NFLS, Homo capienc cDNA clone IMAGE:293651 3'
28936   6.03   8.0E-13   U29185.1   NT	ΙĐ	L		8.0E-13	U29185.1	F	Homo sapiens prion protein (PiP) gene, complete cds
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2.82 8.0E-13 U78027.1 NT 0.77 7.0E-13 Q965165 SWISSPROT 32 7.0E-13 BE778223.1 EST_HUMAN 1.53 7.0E-13 D10473 SWISSPROT 28430 5.65 6.0E-13 AL163207.2 NT 31329 0.89 6.0E-13 AL267228.1 EST_HUMAN 1.15 5.0E-13 R78338.1 EST_HUMAN 1.15 5.0E-13 R78338.1 EST_HUMAN 1.15 5.0E-13 R78338.1 EST_HUMAN 1.15 5.0E-13 P08983 SWISSPROT 33572 0.99 5.0E-13 P08983 SWISSPROT 37808 2.84 5.0E-13 P07313 SWISSPROT 4.88 4.0E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313 SWISSPROT 5.50E-13 P07313	Ιğ			8.0E-13	AI884398.1	EST_HUMAN	wm31h09x1 NCI_CGAP_Ut4 Homo sapien's cDNA olone IMAGE:2437601 3'
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A BB A DE-13 AW378814 1 FST HIJMAN	116				P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
	18				AW378614 1	FST HIMAN	PM2-HT0224-221099-001-e11 HT0224 Horio sapiens cDNA

Page 232 of 550 Table 4 Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2531	15656		1.61	4.0E-13	4.0E-13 AF003529.1	TN	Homo sapiens glypican 3 (GPC3) gene, partal cds and flanking repeat regions
4869	18002		1.06	4.0E-13	4.0E-13 AA454054.1	EST_HUMAN	zx48d07.r1 Soares_testis_NHT Homo sapions cDNA clone IMAGE:795469 5'
5704		32189		4.0E-13	4.0E-13 BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355				4.0E-13	4.0E-13 AB037750.1	N	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	l .			4.0E-13	4.0E-13 AA431528.1	EST_HUMAN	zw76g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA.
7898	I			4.0E-13	4.0E-13 N44291.1	EST HUMAN	yy33g05.r1 Soares metanocyte 2NbHM Horiro sepiens dDNA clone IMAGE:273080 5' similar to PIR:A32995 A32995 t complex sterility protein - mouse ; ,
9042		35683		4.0E-13	4.0E-13 AL043810.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434A0128 5'
9702	1			4.0E-13	4.0E-13 AA076907.1	EST_HUMAN	7804H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7804H11
	i .			100	A 1000001 A	MAMILL FOR	gn32d05.x1 NCi_CGAP_Kid6 Homo sepieris cDNA clone IMAGE:1899943 3' similar to contains Alu
10226	- 1	1		4.0E-13	4.0E-13 AIZB9831.1	EST HUMAN	repening element. 2728-10 st 30ares testis NHT Homo septens cDNA olono IMAGE:728614 3'
1430	24500	38167	1 1 1	4.0E-13	4.0E-13 AA435819.1	EST HUMAN	Z78g10.51 Soares_testis_NHT Homo septens cDNA clone IMAGE:728514 3'
2	l						Home sarians X-linked anhidrolite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
184	13408		4.35		3.0E-13 AF003528.1	NT	regions
88	1		1.81		3.0E-13 AA430310.1	EST_HUMAN	Zw68g08.r1 Soares_festis_NHT Homo sapians cDNA clone IMAGE:781406 6
1502		27737	98.0	3.0E-13	3.0E-13 AI904151.1	EST HUMAN	CM-BT043-090299-075 BT043 Hamo sapiens cDNA
2443	ı		1.53	3.0E-13	3.0E-13 AJ271738.1	NT	Hamo sapiens Xq pseudoautosomal region; segment 2/2
2548	1		2.28		3.0E-13 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2729	L	28957	3.69	L	3.0E-13 BF372982.1	<b>EST_HUMAN</b>	CM3-FT0100-140700-242-h08 FT0100 Homo saplens cDNA
3256	16430		2.44		3.0E-13 AA745844.1	EST HUMAN	ob18402.s1 NCI_CGAP_Kid5 Home sapiers cDNA clone IMAGE:1324035 3
3592	16756	29771	9.73		3.0E-13 P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3592	16756	29772	6.73		3.0E-13 P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGES I SUBUNII (VERSION 1)
	<u>.</u>					NAME OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERS	2088h10.r1 Stratagene lung carcinoma 937218 Homo saplens cDNA clone IMAGE:565315 5 similar to
2657	18851	32133	0.68		3.0E-13 AA134017.1	ES L'ACIMAIN	The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
5657	18851	32134	0.68		3.0E-13 AA134017.1	EST_HUMAN	contains THR.t2 THR repetitive element;
	1			l	2 05 13 01005630 1	NAMI IH TAR	wz88c02xf NCI_CGAP_Brr26 Homo sapions cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN. :
4110	5A7AL	32028	27.0				Use serious V28 serious and D House containing dual specificity phosphatasa 9 (DUSP9), ribosomal
							promo septents Azo region real Azo todos contenimis deal appendimento (CAMIKI), creatina transporter (CRTR), protein L18a (RPL18a), Ca2+/Calmodulin-dispendent protein kinase I (CAMIKI), creatina transporter (CRTR),
8067	21149	34669	7.1		3.0E-13 U52111.2	NT	CDM protein (CDM), adrenoleukodystrophy protein >

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptar
8268	21350	34865	0.5	8	.0E-13 AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Rareactive factor
8288	21350	34888	0.5	. "	.0E-13 AA352487.1	EST HUMAN	EST60487 Activated T-cells XX Homo sepians cDNA 5' end similar to similar to serine protease P100, Rarective factor
10401	ı	l		ြ	.0E-13 AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-910 DT0007 Hojno sapiens cDNA
10915	23998		3.1	3.0E-13	3.0E-13 Al084768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Honio saplens cDNA
11301	ı		3.41	3.0E-13	3.0E-13 BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-e03 BT0281 Homo sapiens cDNA
11898	24886		1.62	3.0E-13	1.0E-13 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21 C048
154	13379				2.0E-13 U52111.2	Ę	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dépendent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	26502	2.06		20E-13 U23839.1	TN	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1289	14455	27521	6.83		2.0E-13 AF239710.1	M	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16246			2.0E-13		TN	Hamo sepiens hypothetical protein PRO2130 (PRO2130), mRNA
3070		29267	0.61	2.0E-13	8924119 NT	IN	Homo saplens hypothetical protein PRO2130 (PRO2130), mRNA
3596	09/91	29776	1.68		2.0E-13 AF109907.1	IN	Homo sepiens S164 gene, partial ods; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	ļ.				2.0E-13 AL163278.2	LN LN	Homo saplens chromosome 21 segment HS21 C078
6250	l	32770				SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19506		85.0		2.0E-13 X79417.1	LN	S.scrofa rps12 mRNA for ribosomal protein 312
6954	•	33704			20E-13 X16912.1	TN	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7189						NT	Homo sapiens N-myristoy/transferase 1 (NN/T1), mRNA
7189			9.0	2.0E-13	10835072 NT	L	Homo sapiens N-myristoy/transferase 1 (NN/T1), mRNA
10675	23709	37317	241	2.0E-13	5031896 NT	TN	Homo septiens mab-21 (C. elegens)-like 1 (MAB21L1) mRNA
12388			22.49		2.0E-13 AW892155.1	EST_HUMAN	CM0-NN0001-100300-274-e11 NN0001 Ho;no sapiens cDNA
302	13518	28551	1.34	ı	.0E-13 S74129.1	TN	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086				1.0E-13 AJ007973.1	NT	Homo saplens LGMD2B gene
1367	14521	27596	1.4		.0E-13 X87344.1	IN	H. sepiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
							nw21g02.s1 NCI_CGAP_GCE0 Homo sapitans cDNA clone IWAGE:1241138 3' similar to contains THR.t3
2079					.0E-13 AA720574.1	EST_HUMAN	THR repetitive element ;
4715	17850	30833	1.32	Ì	1.0E-13 BF340987.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA done IMAGE:4185866 5

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						A	Ongle Court loves Chiesesea III lavelina
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8094	21178	34691	0.97	_	.0E-13 AA5778121	EST_HUMAN	nn24d01.s1 NCI_CGAP_Gas1 Homo saplens cDNA clone INAGE:1084801 3' similar to contains Alu repetitive element.contains element MER24 repetitive element;
8084			0.97	_	.0E-13 AA577812.1	EST_HUMAN	nn24d01.s1 NCI_CGAP_Gas1 Homo saplens cDNA clone INAGE;1084801 3' similar to contains Alu repetitive element;contains element MER24 repetitive element;
10295					.0E-13 O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10508	23543	37154	9.0	-	.0E-13 AF300701.1	본	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds
11661	24740	38431	9.74	_	.0E-13 BF108755.1	EST_HUMAN	745610.x1 Soares_NSF_F8_9W_OT_PA_> S1 Homo capiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12206	1		1.38		.0E-13 AV715377.1	EST_HUMAN	AV715377 DCB Homo sepiens cDNA clane DCBAIE03 5,
12920	25605		3.48		.0E-13 AJ271735.1	٦	Homo sapiens Xq pseudoautosomal region; segment 1/2
13077	l		1.85	_	.0E-13 X87579.1	۲	H.saptens CD4 gene
97.0	100			ľ	7 02776	LA LA MAANI	a[24c01.st Scares_basts_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
3	2005	20003	3.70	۱.	.UE-14 AA/01/39.1	NAWAIN TO LEGIS	I opourvo eienieni.
	i i				7 02777	146	ajZ4c01.s1 Soares_tests_NHT Homo septens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
448	13000	50084	1.84		9.0E-14 AA/81109.1	EST HOMAN	Information of the Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Con
2007	1				Ţ		1 Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Comp
2811		29036		0		Į.	Fromo septents i i i gene cutster for trenoli ractor, complete cos
3180	16355		7.5	6	.0E-14 AW513298.1	EST_HUMAN	xo54h05.x1 NCI_CGAP_Ut1 Homo saplens/cDNA clone IMAGE:2707833 3'
							aj24c01.s1 Soares_bests_NHT Homo saplens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
3310	13554		-	9.0E-14	9.0E-14 AA781159.1	EST_HUMAN	repetitive element;
3898	17057	30057	7.37		9.0E-14 D14547.1	IN	Human DNA, SINE repetitive elament
4879	18010	30994	2.23		9.0E-14 AJ002153.1	NT	Saguinus cedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17		8.0E-14 BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3213424 3'
4068	17222		3.64		8.0E-14 R76269.1	EST_HUMAN	y772e03.r1 Soares placenta Nb2HP Homo suplens cDNA clone IMAGE:1447963'
9647	21090	34605	38.93		8.0E-14 X89211.1	NT TA	H.sapiens DNA for endogenous retroviral like element
9760	22698			L	8.0E-14 AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:629970 3'
11717	24757				8.0E-14 BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo saplens cDNA
12611	25410	32048	2.43	6	.0E-14 AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328143.3'
	ľ						xf67e10.x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2
1658			4.76	Ĺ		EST_HUMAN	MER10 repetitive element;
9120	22199		0.73	_	.0E-14 AL163285.2	본	Homo sapiens chromosome 21 segment HS21C085
378	13585	26620	12.43	8	.0E-14 AF020503.1	Ţ	Homo sapiens FRA3B common fragile region, disdenosine triphosphate hydrolase (FHIT) gene, exon 5

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				_		-	_		_			1				-		_	_	_	_		_	_7		_		$\neg$
Single Excit Flobes Expressed in Flacetina	Top Hit Descripta	Homo sapiens FRA3B common fragile región, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	Hamo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)	xb03b05.x1 NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE:2675185 3' similar to contains L1.t2 L1 repetitive element;	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	S-ANTIGEN PROTEIN PRECURSOR	Hamo sapiens LGMD2B gene	zk67a06.r1 Scares_pregnant_uterus_NbHPU Homo saplens cDNA clone IMAGE:487838 5'	yy73c12.s1 Soares_multiple_sclerosts_ZNbHMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.t3 L1 repetitive element;	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING9, 9, 13 and 14 genes	TCAAD101470 Bediatric acute melorannis (arkemia call (FAR M1) Rador-HGSC project=TCAA Homo	sapiens oDNA clone TCAAP1470	wm08c03.x1 NCI_CGAP_Ut4 Homo saplens cDNA clone INAGE:2435332 3' similar to contains Alu	repetitive element	R.norvegleus mRNA for CIPG2 protein	(e91c12.x1 NCI_CGAP_Pr28 Homo sapient); cDNA clone IMAGE;2094070 3' similar to TR: 000519 000519 FATTY ACID AMIDE HYDROLASE. ;	te91c12.x1 NCI_CGAP_Pr28 Homo saplenti cDNA done IMAGE:2094070 3' similar to TR:000519 000519	FATTY ACID AMIDE HYDROLASE.;	EST185054 Brain IV Homo sapiens cDNA	Iyy07b10.r1 Scares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:270523 6	xp45ff2xf NCI_CGAP_HN11 Homo saplens cDNA clone IMAGE:2743343 3' similar to contains Alu	repetitive element.contains element MER9 repetitive element;	Hamo sapiens chromosame 21 segment HS21 C085	601435233F1 NIH_MGC_72 Home sapiens cDNA clone IMAGE:3920169 5	Hamo sepiens Xq pseudoautosomal region; segment 2/2	Hamo saplens Xq pseudoautosomal region; segment 2/2	Hamo saplens chromosome 21 segment HS21C103
e Exori Pione	Top Hit Database Source	TN	LN	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	LN	EST_HUMAN	EST HUMAN	L L		EST_HUMAN		EST HUMAN	L	EST_HUMAN		<b>EST_HUMAN</b>	EST_HUMAN	EST_HUMAN		EST_HUMAN	NT	EST_HUMAN	NT	NT	N
ignic .	Top Hit Acession Na.	6.0E-14 AF020503.1	6.0E-14 AF020503.1	Q63120	5.0E-14 AW073791.1	P08547	P04928	4.0E-14 AJ007973.1	4.0E-14 AA046502.1	4.0E-14 N48328.1	4.0E-14 XB7344.1		4:0E-14 BE242466.1		4.0E-14 AI886224.1	3.0E-14 X95469.1	3.0E-14 Al420786.1		3.0E-14 AI420786.1	3.0E-14 AA388311.1	3.0E-14 N42165.1		3.0E-14 AW265354.1	3.0E-14 AL163285.2	3.0E-14 BE891550.1	2.0E-14 AJ271736.1	2.0E-14 AJ271736.1	2.0E-14 AL163303.2
	Most Similar (Top) Hit BLAST E Value	6.0E-14	6.0E-14	5.0E-14 Q63120	5.0E-14	5.0E-14 P08547	4.0E-14 P04928	4.0E-14	4.0E-14	4.0E-14	4.0E-14		4:0E-14		4.0E-14	3.0E-14	3.0E-14		3.0E-14	3.0E-14	3.0E-14		3.0E-14	3.0E-14	3.0E-14	2.0E-14		ŀ
	Expression Signal	2.19	2.19	4.17	1.32	5.28	1.61	10.15	0.73	1.04	0.71		5.5		6.69	1.50	0.93		0.93	9.0	0.86		5.87	1.88	1.51	2.33	2.33	11.36
	ORF SEQ ID NO:	3662	36883	26842	31254			28174		30533	<u> </u>		38729			27204	33434					İ	31533		31853			26925
	Exan SEQ ID NO:	23066	23088	13818	18288	18844	16030	15069	17007	17549	)	1	25024	)	- 1	14145	20025	Į	20025	20308	22066					Ш	13598	
	Probe SEQ ID NO:	10027	10027	83	5168	5650	1147	1928	3847	4407	8145		12043		12986	972	6883		6873	7173	28887		11512	12894	13212	401	401	708

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	Top Hit Descriptor	RC5-BT0377-091299-031-D12 BT0377 Homo saplens cDNA	Homo saplens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	Hano sapiens chromosame 21 segment H\$210009	11.2-JT0072-240800-142-D07 UT0072 Hanja septens cDNA	ta78n01 x2 NCI_CGAP_HSC2 Homo saplens cDNA clone IMAGE:2050225 3' similar to contains L1.t3 L1 repetitive element:	Human beta clobin rection on chromosome 11	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA	ZINC-FINGER PROTEIN NEURO-D4	IL2-HT0397-071299-024-D04 HT0397 Honio saplens cDNA	IL2-HT0397-071299-024-D04 HT0397 Honio saplens cDNA	wr59g10.x1 NCI_CGAP_Uff Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive	dement	AV741648 CB Homo sapiens cDNA clone (CBFBBF04 5'	UI-H-BI1-edw-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo septens cDNA clone IMAGE:2718234 31	Homo sapiens putative G6 protein (GR6) gene, complete cds	Homo sapiens mabdold tumor deletion region protein 1 (RTDR1), mRNA	Homo saplens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (Geom) sone complete dels	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-11)	RC2-CT0432-310700-013-a09_1 CT0432 Homo saplens cDNA	RC2-CT0432-310700-013-a09_1 CT0432 Homo saplens cDNA	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'	xq39h10.x1 NCI_CGAP_Luz8 Homo saplens cDNA clone IMAGE::2753059 3'	Bos taurus xenobiotic/medium-chain fatty acid: CoA ligaso form XL-III mRNA, nuclear mRNA encoding	mitochondrial protein, complete cds	Homo sapians prominin (mouse)-like 1 (PROML1), mRNA	Homo sapians prominin (mouse)-like 1 (PROML1), mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
-	Top Hit Database Source	EST_HUMAN   RC		王	EST_HUMAN IL	_	I	Т	П	EST_HUMAN IL	EST_HUMAN IL	Г		EST_HUMAN A	EST_HUMAN U	NT TN		N	Ĭ	NT H	H 11			SWISSPROT HI	EST_HUMAN R	Г	Г	EST_HUMAN xx					
	Top Hit Acession	2.0E-14 AW372868.1	7657529 NT	2.0E-14 AL163209.2	Γ	2 0E 14 A1312351 1	ļ	-		91.1	2.0E-14 BE158761.1		2.0E-14 AI978795.1		2.0E-14 AW139800.1	2.0E-14 AF008191.1	1 7657529 NT	1.0E-14 AL163246.2	1.0E-14 AL163268.2	1.0E-14 AL163268.2		1.0E-14 L44140.1			1.0E-14 BF33527.1	1.0E-14 BF335227.1		1.0E-14 AW 27 58 52.1		1.0E-14 AF126145.1	11437150 NT	Ī	7427522 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-14	2.0E-14	2.0E-14	2.0E-14	2 OF 44	2 OF-44	20E-14	2.0E-14 P56163	2.0E-14	2.0E-14		2.0E-14	2.0E-14	2.0E-14	2.0E-14	2.0E-14	1.0E-14	1.0E-14	1.0E-14	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1.0E-14	1.0E-14	1.0E-14 P05227	1.0E-14	1.0E-14	1.0E-14	1.0E-14		1.0E-14	1.0E-14	1.0E-14	9.0E-15
	Expression Signal	1.04	0.89	1.63	76.0	ě	S: "	1.04	1.06	24.48	24.46		0.59	0.51	3.62	2.5	1.26	2.32	7.91	10.7		8.8 8.33	8.4	1.41	3.14	3.14	1.68	2.01		1.98	10.9	10.B	1.81
	ORF SEQ ID NO:			28835		00000			33987		L		39758	37273				27313				28512	L							32429			
ſ	SEQ ID	15588	15660				L	1	L		L		23159		L	L	16660	L		1_		16168	15607	L	ı	l_	L.	J	L	19116	26834		14760
	Probe SEO ID NO:	2481	2535	2593	5641	2730	2000	7023	7437	7678	7676		10121	10630	11019	12890	13163	1092	1438	1438		205	2480	3010	3238	3238	3992	4596		5930	6813	6813	1607

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Probe SEQ ID NO:	Exon SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
							Homo sapiens transcription factor IGHM er/hancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes,
2242	15375		1.38	9.0E-15	9.0E-15 AF196779.1	N	complete cds; and L-type calcium channel (i>
7665		34207		9.0E-15	9.0E-15 P21410	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8208				9.0E-15	3.0E-15 BE903559.1	EST_HUMAN	601877750F1 NIH_MGC_21 Hamo sapienis cDNA clare IMAGE:3980159 5'
13089	i		, 2.87	9.0E-15	3.0E-15 AL163247.2	TN	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	3.0E-15 BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo capiens cDNA clone IWAGE:3164023 5'
7331	20412	33874	1.13	7.0E-15	7.0E-15 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5
10650	23684		2.34	7.0E-15	.0E-15 AW241958.1	EST HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.t2 THR repetitive element;
12270			1 44	7 OF-15	0E-15 AA284465 1	EST HIMAN	257408.1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:701883 5' similar to go:L21934 STEROLO-ACYLTRANSFERASE (HUMAN) contains L1.t1 L1 repetitive element:
1018		27250	7,51	6.0E-15	3.0E-15 AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
5263	Ŀ		0.88	6.0E-15	-	EST HUMAN	CM4-NN1011-100300-110-d10 NN1011 Homo sapiens cDNA
6041	L	32546		8.0E-15		N	O.aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	3.0E-15 X73462.1	NT	O.anles mRNA for hair keratin cystelne-rich protein
11583	26231		1.54	6.0E-15	3.0E-15 AW 836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo saplens cDNA
423	13618	26858		5.0E-15	5.0E-15 AL183208.2	NT	Homo sapiens chranosame 21 segment HS21C008
2819	15933	29044	1.78	5.0E-15	5.0E-16 U91328.1	L	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium physphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-15	5.0E-15 P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE : ENDONUCLEASE)
8	13240	28240	2.33	4.0E-15	4.0E-15 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6804	19959		6.0	4.0E-15	4.0E-15 AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11318	21066		2.11	4.0E-15	4.0E-15 AJ130894.1	TN	Homo saplens mRNA for transcription factor
11316	l			4.0E-16	4.0E-16 AJ130894.1	LN	Homo sapiens mRNA for transcription factor
4333	17476		79.7	3.0E-15	3.0E-15 N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo saplens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5141	18264			3.0E-15	3.0E-15 AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141		31233	79.0	3.0E-15	3.0E-15 AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
ලෙදුය			1.11	3.0E-15	3.0E-15 Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430			3.13	3.0E-15	3.0E-15 M27685.1	NT	Mus musculus ultra high sulfur keratin gena, completa cds
7430	20507		3.13	3.0E-16	3.0E-16 M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds

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Pode   Earl   Pode   Earl   Moval Similar   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   Top Hi Acession   To		_		_		,		_	٠.,						_		_		_	-	_	_	_	_	
Expn NO:         CAPE SEQ Fignal         Expression Fignal         Most Similer Top Hit Acession Velue         Top Hit Acession Velue           22167         23.6         5.0         H. Top Hit Acession Velue         Top Hit Acession Velue         Top Hit Acession Velue           22167         27.4         8.11         3.0         1.6         AA807128.1           26081         26511         3.71         2.0         1.6         AA807128.1           13687         26622         3.28         2.0         1.6         AF223391.1           14712         3.74         2.0         1.6         AF223391.1           14763         29779         0.72         2.0         1.6         AF223391.1           16763         29779         0.72         2.0         1.6         AF223391.1           16763         29779         0.72         2.0         1.6         AF223391.1           16763         29779         0.72         2.0         1.6         AF223391.1           16763         29779         0.72         2.0         1.6         AF223391.1           20498         3.2639         1.11         2.0         1.6         AA706195.1           20498         3.5         2.0         <	Top Hit Descriptor	0c36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repetitive element;	Homo sapiens DNA, DLEC1 to ORCTL4 gane region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete ode)	Hamo sapiens Xq pseudoautosamal region; segment 1/2	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, alternatively spileed	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	יייייייייייייייייייייייייייייייייייייי	Homo sapiens hypothetical protein FLD20212 (FLD20212), mKNA	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	Po nich	wf07f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043   Q61043 NINEIN.;	601344253F1 NIH_MGC_B Homo saplens ¢DNA clone IMAGE:3677268 5'	601344253F1 NIH_MGC_B Homo saplens cDNA clone IMAGE:3677268 5	Home sapiens ASCL3 gene, OEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene	ZITT e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Hamo saplens cDNA clone IMAGE:460924 3'	za78d10.r1 Soares, fetal Jung, NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE:	Human DNA, SINE repetitive element	zi77g08.r1 Soares, testis, NHT Homo sepiens cDNA clone IMAGE:728414 5'	2777g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA	CM0-HT0244-201099-078-a12 HT0244 Hano saplens cDNA	Homo sapiens Xq pseudoautosamal region; segment 1/2	Homo sepiens calcium channel alpha1E sut unit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
Exon NO:         ORF SEQ Signal NO:         Expression Signal Signal Signal NO:         Most Similar Alaborate No:         Most Similar Public No:         Most Similar No:         Top Hit Acession No:           23.167         23.167         2.38         3.0E-15 Ab026898.1           24.112         37748         8.11         3.0E-15 Ab026898.1           13.687         26621         3.28         2.0E-15 AF223391.1           14712         20778         0.72         2.0E-15 AF223391.1           14783         29779         0.72         2.0E-15 AF223391.1           16783         29779         0.72         2.0E-15 AF223391.1           16783         29779         0.72         2.0E-15 AF223391.1           16783         29779         0.72         2.0E-15 AF223391.1           16783         23838         1.11         2.0E-15 AF223391.1           16783         32838         1.11         2.0E-15 AF223391.1           20626         24102         2.75         2.0E-15 AF223391.1           20627         2.76         2.0E-15 AF223391.1           20628         3.2839         1.11         2.0E-15 AF223391.1           20629         2.0E-15 AF3771735.1         2.0E-15 AF3771735.1           20749         3.2839	Top Hit Detabase Source	EST_HUMAN	LN FN	ĻΝ	Ĭ	Į.	<u> </u>	121	L	뉟	Ļ	2	EST_HUMAN	EST_HUMAN	EST_HUMAN	Į.	EST_HUMAN	EST HUMAN	L	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	N	IN
Exan NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	Top Hit Acession No.	AA807128.1	AB026898.1	AJ271735.1	AF223391.1	AF223391.1	7 7000001	AF223381.1	8923201	AF223391.1	A E000000 4	Ar 223331.1	AI806335.1	BE562352.1	BE562362.1	AJ400877.1	AA704195.1	W05084.1	D14547.1	AA397758.1	AA397758.1	١			
Exan NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	Most Similar (Top) Hit BLAST E Value	3.0E-15	3.0E-15	3.0E-15	2.0E-15	2.0E-15	0	2.05	2.0E-15	2.0E-15	7 00 0	C1-307	2.0E:15	2.0E-15	2.0E-16	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	2.0E-15	20E-15	2.0E-16	2.0E-15
SEQ ID ORF 24112 24112 26081 13687 13687 14712 16783 20348 20348 222188 222488 22289 22289 22289 22289 22289 22289 22289 22289 224152 24152 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 16788 1678	Expression Signal	2.38	8.11	92.8	3.71	3,28	000	9.60	0.89	0.72	0 73	0.72	2.76	1.11	1.11	1.58	2.73	5.05	2.86	0.91	0.91	1.18	1.18	3.69	3.89
$\frac{-\omega}{\omega}$					_	1														L				<u> </u>	
	Exan SEQ ID NO:	23167	24112	26081	13478	13587	1 207	200	14712	16763	18787	3	17880	19483	19483	20346	20498	20628	22186	22349	22340	22659	22659	24152	
		10129	11033	12820	88	379		9/6	1559	3589	2636	SSC	4745	8311	6311	7263	7421	7554	6	9273	9273	9804	8604	11077	13018

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					5		Chigge Lacil Triodes Laptices and Triodes Laborates
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13016	16763	97762	3.89	7	.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15948		3.09	_	.0E-15 Al689984.1	EST_HUMAN	626/05x1 NCI_CGAP_Lu24 Homo sepieris cDNA clone IMAGE:22707453' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE:
3077	16253		1.42	,	.0E-15 BE043584.1	<b>EST_HUMAN</b>	hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA done IMAGE:2999162 5
3211	16385	98E6Z	1.18	ļ	.0E-15 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4479	17619		0.61	1.0E-15	.0E-15 BE182698.1	EST_HUMAN	RC3-HT0849-100500-022-b05 HT0849 Homo sapiens oDNA
6502	19668	33032	1.72		.0E-15 T95763.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS. Homo saplens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element;
7149	20284		1.98		.0E-15 BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Hono sapiens cDNA
7184	20049	33460	0.79	[	.0E-15 P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8427	21508		66.0		.0E-15 AL163280.2	NT	Homo saplens chromosome 21 segment HS21C080
8615	21696		4.94	1.0E-16	.0E-16 AI200976.1	EST_HUMAN	qf68h06.x1 Soares_tectis_NHT Homo saptions cDNA clone IMAGE:1755227 31
8615	21695		4.94	1.0E-15		EST_HUMAN	qf88h08.x1 Soares_testis_NHT Homo sapitins cDNA clone IMAGE:1755227 3'
8238	22316			١	AL163207.2	NT	Homo saplens chromosome 21 segment HS21C007
9242	22319			· L	4507208 NT	NT	Homo saplens spernidine synthase (SRM) mRNA
9448	22564	36127	66.0	1	0E-15 Q38575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9832	22872	36455	0.94	_	0E-15 AA864653.1	EST HUMAN	ch37c03.s1 NCI_CGAP_Kid6 Homo sepiens cDNA clone IMAGE:1459972.3' similar to contains L1.t3 L1 repetitive element:
11057	24134			1		L LN	Homo saplens major histocompatibility locus class III region
							tr31c05.x1 NCI_CGAP_Ov23 Homo septens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive
13104	- 1			١	AI78394	4.1 EST_HUMAN	eement
4826	- 1	30744				L	Home sapiens cut (Uresophila)-like 1 (CCAA)T displacement protein) (CUTL1) mRNA
11241	24310		1.41		9.0E-16 F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Home sapiens cDNA clone c-23f05
11895	24880	38685	1.48		9.0E-16 AI244341.1	EST_HUMAN	q76a02.x1 NOL_CGAP_Kid3 Homo saplens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
11005	24090	28888	1.48		D OF-18 A1244341 1	TAT IMAN	q76a02.x1 NC_CGAP_Kid3 Homo saplens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element
5840	19000				4885120 NT	LZ	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7498	20571				088807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7496		34044	1.3	7	7.0E-16 O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
13043	25895		38.08		7.0E-16 T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#337210) Homo sapiens cDNA clone IMAGE:119062 5'

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Probe SEQ ID NO:	SEQ D	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	
2208	15342		9.12	8	.0E-16 AW972611.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo septens cDNA
1522	14875	27757	96.0		5.0E-18 AJ251154.1	뒫	Mus musculus affectory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
97.AE	15887		2.24	7.70 F	5 NE-16 144992175 1	NAMIN TOT	ot80c04.s1 Soares_total_fetus_Nb2HF8_gw Homo sepiens cDNA clone IMAGE:1623078.3' similar to contains element 1, repetitive element :
1180	24789			6.0E-16	5.0E-16 BF217368.1	EST HUMAN	601885734F1 NIH_MGC_57 Homo septents cDNA clone IMAGE-4104129 5'
13162	25749			L	11418127 NT	Z	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2312	15444		1.01	4.0E-16	AB001523.1	TN	Homo saplens gene for TMEM1 and PWP?, complete and partial cds
2463	16581	28708		4.0E-16	4.0E-16 AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo saplens cDNA
2453	15581	28709			4.0E-16 AW 797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Hamo sapiens cDNA
3546	16711		·	4	4.0E-16 Q16653	SWISSPROT	INVELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30391	8.68	4		EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo saplens cDNA
4280	17405			4	75.1	EST_HUMAN	PM4-BT0650-010400-002-509 BT0650 Hemo capiens cDNA
5257	18377	31343			4.0E-16 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20842	34448	42.68		4.0E-16 AL163284.2	TN	Homo sapiens chromosome 21 segment H321C084
9495	22552	36114	0.72	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12293	25218			4.0E-16 P08548		SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.66		4.0E-16 C05947.1	EST_HUMAN	C05947 Human pancreatic Islet Homo sapiens cDNA clone hbc5355
12392	25277	32078	3.23	4.0E-16	6912469 NT	FX	Homo sepiens Grb2-associated binder 2 (KIAA0571), mRNA
12682	25454		1.33		4.0E-16 R18591.1	EST_HUMAN	y/985/11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395			3.0E-18 AW022862.1	EST_HUMAN	d/45c01.yr Morton Fetal Cochlea Homo sablens cDNA clone IMAGE:2486376 5
136	13361				3.0E-16 AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
478	13873		1.58	L	3.0E-16 AL046445.1	<b>EST_HUMAN</b>	DKFZp434P037_r1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp434P037 5'
488	13882		2.33		3.0E-16 AF135448.1	TN	Homo sapiens TSX (TSX) pseudogene, exxin 5
1483	14536	27720	2.73		3.0E-16 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
1	1001		72.7		2 OE 10 D02200	TOGGGGIA	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP320]
3	1051	18787		L	20200	CALICATION	au78b08 v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5's Imilar to
4711	17848	30830	0.69		3.0E-16 AW160828.1	EST_HUMAN	SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5057	18185	31160			3.0E-16 AV661393.1	EST_HUMAN	AV661383 GLC Hamo squiens cDNA clane GLCGSA01 3'
5392	18594		0.99		3.0E-16 AA077225.1	EST_HUMAN	7810F02 Chromosome 7 Fetal Brain aDNA Library Homo sapiens oDNA alone 7810F02
5734	18927	32223	1.67	3	.0E-16 AF003529.1	TN	Homo sepiens glypican 3 (GPC3) gene, paitlal cds and flanking repeat regions
8858	21937	35473	4.25	ຶ	3.0E-16 Al002836.1	EST HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;

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				Mace Similar	Sing	e Exon Prope	Single Exon Probes Expressed in Placema
Praba SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Sumia (Top) Hit BLAST E Value	Top Hit Acessian Na.	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	3.0E-16 BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo saplens cDNA done IMAGE:4332032 5
10324			2.59	3.0E-16	3.0E-16 L78810.1	TN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	L	31557			3.0E-16 AL043268.2	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5
200	L		1.03		2.0E-16 AL163279.2	NT	Home sapiens chromosome 21 segment HS21 C079
2459	16586		96'0	l	2.0E-16 AA621761.1	EST_HUMAN	aroccio4.s1 Scares_testis_NHT Homo saplens cDNA clone IMAGE:1030855 31
2753	ı		1.14	2.0E-16	2.0E-16 J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4294	i	30424		2.0E-16	2.0E-16 X89211.1	TN	H. saplens DNA for endogenous retroviral like element
4803	1			2 0F-18	2 0F-16 Al208733 1	EST HUMAN	qg56f03.xf. Soares_testis_NHT Homo septens cDNA clone IMAGE:1839197.3' similar to contains MER29.t3 MER29 repetitive element:
5289	1			2.0E-16	2.0E-16 BE061178.1	EST HUMAN	RC3-BT0046-131199-003-H12 BT0046 Homo sepiens cDNA
888	1	L		2.0E-16	2.0E-16 Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7803	i			2.0E-18	2 0E-16 Al470723.1	EST HUMAN	the state of the contains element of the contains of the contains element the sapetitive element; the sapetitive element;
25.55	1	L		2.05-16	2.0E-16 AI732837.1	EST HUMAN	nz47108.x5 NCI_CGAP_Pr12 Homo saplens cDNA clone IMAGE:1280947 similar to TR:054849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:008905 ;contains MER7.t1 MER7 repetitive element;
8352	1	1		2.0E-18	2.0E-16 BE858028.1	EST_HUMAN	7f82h09,x1 NCi_CGAP_Pr28 Homo septens cDNA clone IMAGE:3303521 3'
8352	21433	L		2.0E-16	2.0E-16 BE858028.1	EST_HUMAN	7/82h09x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:3303521 3'
8724	1				2.0E-16 AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-a01 PT0034 Hoino sapiens cDNA
8724			-		2.0E-16 AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
280	١	1	2.2B	L	1.0E-16 AF200719.1	Į,	Homo sapiens piluitary tumor transforming gene protein (PTTG) gene, complete cds
383	1		"	_	1.0E-16 AA628592.1	EST_HUMAN	af39g11.s1 Soares_total_fetus_Nb2HFB_9W Homo septens cDNA clone IMAGE:1034084 3' similar to contains OFR to OFR repetitive element;
2028	ı				1.0E-16 BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 SN0148 Homo sapiens cDNA
6839	1	32335			1.0E-16 AF163864.1	TN	Homo saplens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	ì		18	l	1.0E-16 U45983.1	N	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
0.70	}	00000	Ì		1 05 16 0002770	TORDENING	MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7726	19002					LN L	Homo sapiens CCR8 chemokine receptor (GMKBR8) gene, complete cds
9483	1.				1.1	EST HUMAN	QV2-PT0012-040400-124-e05 PT0012 Horno sapiens cDNA
3832	1	29994			9.0E-17 AW900048.1	EST HUMAN	CM1-NN1003-200300-153-601 NN1003 Homo sepiens oDNA
6864	L	<u>.                                    </u>			9.0E-17 Al392964.1	EST_HUMAN	1922c11.x1 NCI_CGAP_CLL1 Homo sapieris cDNA clone IMAGE::2109524 3' sImilar to contains MER28.12 MER28 repetitive element;

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h81dD4x1 Sceres\_NFL\_T\_GBC\_S1 Homb sapiens cDNA abne IMAGE:2978695 3' similar to contains L1.t2 d20e04x1 NCI\_CGAP\_Kid8 Homo sapieni) oDNA clone IMAGE:2818622 3' similar to contains Alu repetitive za14b02.s1 Soares fetal liver spleen 1NFLS. Homo sapiens cDNA clone IMAGE:292491 3' sImilar to contains xg49g12.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane Hamo sepiona DNA, DLEC1 to ORCTL4 gene region, ecction 1/2 (DLEC1, ORCTL3, ORCTL4 genes, ov45e04.x1 Soares\_testis\_NHT Homo saplens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene RC1-HN0003-220300-021-b04 HN0003 Home sapiens cDNA yd26b04.r1 Soares felal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:109327 xd89c09.x1 Sogres\_NFL\_T\_GBC\_S1 Homb sepiens cDNA done IMAGE:2604784 3'
MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG L1 repetitive dement : MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67) yc06h08.r1 Stratagene Iung (#837210) Hamio saplens cDNA clone IMAGE:78838 5' Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds ImoBb04.x1 NCI\_CGAP\_Lu24 Homo sepiens cDNA clone IMAGE:3181999 3' ImoBb04.x1 NCI\_CGAP\_Lu24 Homo sepiens cDNA clone IMAGE:3181999 3' Mus musculus apolipoprotah B editing complex 2 (Apobec2), mRNA Homo sapiens putative MTAP (MTAP) mRtA, partial cds, alternatively spliced Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element QV3-BN0047-270700-283-e12 BN0047 Hojmo sepiens cDNA QV3-BN0047-270700-283-e12 BN0047 Hojmo sepiens CDNA Homo sepiens SEC14 (S. œrewisies)-like 2 (SEC14L2), mRNA Top Hit Descriptor QV0-OT0032-080300-155-401 OT0032 Homo seplens cDVA Homo seplens chromosome 21 segment H321C080 NR0-HT0559-080300-003-e04 HT0559 Homo saplens cDVA AV730759 HTF Homo sapiens cDNA clone HTFAQB07 6' element contains MER19.b1 MER19 repetitive element ; Homo sapiens chromosome 21 segment HS210047 PTR5.t3 PTR5 repetitive element repetitive element complete cds) EST\_HUMAN EST\_HUMAN EST\_HUMAN NT EST\_HUMAN HUMAN EST HUMAN **EST HUMAN** EST\_HUMAN EST HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN SWISSPROT EST\_HUMAN EST\_HUMAN EST\_HUMAN Top Hit Database Source EST 11417988|NT 눋 ż 6753097 Top Hit Acession 6.0E-17 AW662772.1 6.0E-17 P20138 5.0E-17 T64110.1 6.0E-17 T81043.1 3.0E-17 AB026898.1 3.0E-17 BF327012.1 3.0E-17 BF327012.1 3.0E-17 H717 3.0E-17 P35410 3.0E-17 BE326522.1 3.0E-17 BE326522.1 9.0E-17 AW 150257.1 6.0E-17 AW983880.1 AW129165.1 8.0E-17 AF200719.1 8.0E-17 AW880701.1 8.0E-17 AL163280.2 8.0E-17 BE172081.1 7.0E-17 AF229843.1 4.0E-17 AW129165.1 4.0E-17 AL163247.2 8.0E-17 AV730759.1 7.0E-17 AF216650.1 4.0E-17 Al073546.1 3.0E-17 AW119123. ğ 3.0E-17 N68451.1 3.0E-17 (Top) Hit BLAST E 7.0E-17 Most Similar Value 1.12 28. 5.19 0.72 2.35 4.09 2.08 1.17 0.78 2.58 5.62 1.32 3.1 7.91 2.37 1.81 2.51 1.91 Expression Signal ORF SEQ ID NO: 38270 36528 32973 34308 28428 35074 37235 33387 29897 32187 28463 25226 15300 22943 23626 SEQ ID 19810 13234 22704 24773 21544 23626 14840 19979 16437 21381 14209 17155 23534 13431 ë 434 8828 208 6443 12308 2165 Probe SEQ ID 3998 5701 5438 11783 3263 3732 8 10591 8289 10499 88 10591 1043 1487 9562 ë

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חוקם בייתון והספר ביים מחוקם	Top Hit Descriptor	AV720204 GLC Hamo saplens cDNA done GLCDIF08 5	qt83a08x1 NCI_CCAP_Eso2 Homo sapiens cDNA clone INAGE:1959922 3' similar to contains Alu	repetitive element;	qr63a06x1 NCI_CGAP_Eso2 Homo saplens cDNA clone IMAGE:1959922 3' simitar to contains Alu repetitive element,	2g81d04.s1 Scares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)	Mus musculus ultra high sulfur keratin gene, complete cds	Mue musculus ultra high culfur keratin gene, complete cds	Hamo sapiens MHC class 1 region	DKFZp762J0610_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'	Hamo saplens mRNA for KIAA1418 protein, partial cds	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin	600944690F1 NIH_MGC_17 Homo saptent cDNA clane IMAGE:2980615 67	Hano sapiens chromosame 21 segment HS21C047	Hamo saplens chromosome 21 segment HS21C047	Human CYP19 gene for arometase cytochrome P-450, promoter region (containing two cis-acting	transcriptional regulatory elements)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	we94b04.x1 Soares_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:2348719 3'	we94b04.x1 Soares_NFL_T_GBC_S1 Hamo sapiens cDNA clane IMAGE:2348719.3'	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo saplens chromosome 21 segment HS21C007	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B	Home septens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3		Noted / 1 Scares retailities spieen Tin LS home suppers contained and invade: 120000 5
	Top Hit Database Source	EST_HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	N TN	۲	۲N	EST_HUMAN	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	NT	N T		본	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	NT	SWISSPROT	IN	1	IN I	EST_HUMAN
5	Top Hit Acession No.	3.0E-17 AV720204.1		2.0E-17 AI270080.1	2.0E-17 A[270080.1	2.0E-17 AA722832.1	2.0E-17 Q28983	2.0E-17 Q28983	2.0E-17 P12036	2.0E-17 M27685.1	2.0E-17 M27685.1	2.0E-17 AF055066.1	2.0E-17 AL134881.1	2.0E-17 AB037839.1	2.0E-17 Q95156	2.0E-17 AA300640.1	20E-17 BE299888.1	2.0E-17 AL163247.2	20E-17 AL163247.2		2.0E-17 D13391.1	2.0E-17 P98063	2.0E-17 P98063	2.0E-17 AI798902.1	2.0E-17 AI798902.1	1.0E-17 P08183	.1.0E-17 AJ271736.1	1.0E-17 AL163207.2	1.0E-17 P02461	1.0E-17 U79410.1	4 05 47 45204880 4	AF224009.1	1.0E-17 R09942.1
	Most Similar (Top) Hit BLAST E Velue	3.0E-17		2.0E-17	20E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	20E-17	2.0E-17	20E-17		2.0E-17	2.0E-17	2.0E-17	2.0E-17	2.0E-17	1.0E-17	1.0E-17	1.0E-17	1.0E-17	1.0E-17	7	1DV.	1.05-17
	Expression Signal	1.23	İ	2.65	2.78	1.43	2.59	2.59	98.9	1.76	1.75	1.92	1.39	0.89	1.24	1.05	2.71	3.53	3.53		6.02	26.0	0.97	0.93	0.93	2.79	2.01	4.83	2.05	3.18		1.03	9.42
	ORF SEQ ID NO:			28805	28605		28765	28766	29191		31697			34568	34875		38715							37261						28669			
	Exan SEQ ID NO:	25751	L	13574	13574		i .	l	16172		1	Į.	l			21731	23111	ı	1					23652	23652	ı	14894	14956	L	15542		- 1	17401
	Probe SEQ ID NO:	13165		383	364	1012	2518	2618	2886	5482	5482	8394	6619	9008	8275	8651	10073	10108	10108		10468	10590	10590	10618	10618	769	1746	1807	2184	2412	100	/gg	4256

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Probe SEQ ID NO: 10210 110210 110210 110210 110210 110210 110226 12826 12826 3367 3367 3367 11389 11389 11389 11389 11389 11389 11389 11389 11389	Exan SEQ ID NO: 19946 19946 20322 23246 13570 13570 13570 13570 13570 13570 13570 13570 13570 13570 13570 13570 223671 223671 223671 223671 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 223672 22	ORF SEQ.  ID NO:  10 NO:  33344  33346  33410  33410  34146  26600  26600  26600  26600  26600  26600  28652  35161  35161  38124	Signal Signal 1.62 1.62 1.62 1.04 1.09 1.06 1.08 1.08 1.08 1.08 1.08 1.08 1.08 1.08	Most: Version 1	Ai185642.1 Ai185642.1 Ai185642.1 Ai185642.1 Ai185642.1 Ai185634 AW 986538 AW 986538 AW 316976. AW 316976. AW 316976. AW 316976. AW 316976. AW 316976. AM 316976. AM 316976. AM 316976. AI163210.2 AI163246.2 AI163246.2 AI163246.1 US7929.1	TOP HIT Database Source EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT EST HUMAN NT EST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Source Source EST HUMAN redshots XI Sceres_fetal Line_XINHL19W Home saplens cDNA clane INAGE:1743825 3*  EST_HUMAN redshots XI Sceres_fetal Line_XINHL19W Home saplens cDNA clane INAGE:1743825 3*  EST_HUMAN redshots XI Sceres_fetal Line_XINHL19W Home saplens cDNA clane INAGE:1743825 3*  EST_HUMAN REASHORAT-LISE_EURPARE)  EST_HUMAN REASHORAT-LISE_EURPARE)  I EST_HUMAN REASHORAT-LISE_EURPARE)  SWISSPROT MY COLORAP PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  EST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  RENDSOMAL PROTIENT L4 (HUMAN);  RENDSOMAL PROTIENT L4 (HUMAN);  RENDSOMAL PROTIENT L4 (HUMAN);  RENDSOMAL PROTIENT L4 (HUMAN);  RENDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REDSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT L4 (HUMAN);  REST_HUMAN REGSOMAL PROTIENT
1171 4433 5387	1 111	1 111		1 11	AI28021 AF0879	T_HUMAN	qm86g11.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo capients cDNA clone IMAGE:1893668 3' clmiar to containto Alu repotitive element; Mus musculus gasdermin (Gsdm), mRNA Human endegenous retrovirus HERV-P-147D
8917	П				5.0E-18 BE143312.1	T_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11223	24292	37832	3.43	5.0E-18	10242378 NT	N L	Homo sapiens lymphocyte activation-essociated protein (LOC51088), mRNA
11223	L		3.43	5.0E-18	10242378	LN L	Hamo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12675	L		6.29	5.0E-18	AW867182.1	EST HUMAN	MR1-SN0035-060400-001-g11 SN0035 Hcmo sapiens cDNA
13063	L		28.86	5.0E-18		EST_HUMAN	AV650547 GLC Homo saplens cDNA clone GLCCGA023'
	L						ho36h04.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
127	13355	26388	0.91	4.0E-18	4.0E-18 BE044076.1	EST_HUMAN	MER29 repetitive element ;
427		78596	18.0	4 0F-18	4 0E-18 BE044078 1	EST HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiena cDNA clone IMAGE:3039511 3' simitar to contains MER29.b3 MER29 repetitive element:
	l						rq24f11.s1 NCI_CGAP_Co10 Homo sapleirs oDNA clone IMAGE:1144845.3' stmilar to gb:M26328
1754	]	27988	S	١			KERATIN, IMPELICYTOSKELETAL 18 (HUMAN);
1938	15081		1.05	4.0E-18	4.0E-18 AI738592.1	EST_HUMAN	wi33h08.x1 NC_CGAP_Co16 Homo seprens cDNA clone IMAGE;2392095 3
2274	16407	28536	1.26	4.0E-18	4.0E-18 Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,8-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2274	15407	28537	1.26	4.0E-18	4.0E-18 Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINY.TRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE; (I-BRANCHING ENZYME) (IGNT)
3892				4.0E-18	6.1	EST HUMAN	er83b08.x1 Barstead colon HPLRB7 Homo saplens cDNA done IMAGE:2173139 3' similar to contains Alu repetitive element,
67. A.73	ı	L		4.0E-18		EST HUMAN	OL23e06.X1 Soures NPL T GBC S1 Homo sapiens cDNA clone IMAGE:1627138 3*
2				4.0E-18		EST HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1627138 3'
	i i	l		0, 10,		144611 11 140	mod4a08.s1 NCI_CGAP_Ain1 Homo septents cDNA clone IMAGE:1286998 similar to contains L1.t2 L1
R702	7117		0.02	4.0E-10	4.0E-10 AA7.40011.1	NICIMICIL 103	repound outliers,
11254	24323	37964	7.59	4.0E-18	4.0E-18 AA371807.1	EST_HUMAN	EST 83633 Prizitary giano, subtracted (projecurygrown normone) II Homo exprens curva a end similar to EST containing O family repeat
877	87071	27414	. 84	3.0E-18	3 0F-18 AA814188 1	FST HUMAN	ob23h11.s1 NCI_CGAP_Kid5 Homo sepiers cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. :
953	1_			3.0E-18	Γ	EST HUMAN	CM0-BT0680-210300-288-507 BT0690 Homo saplens cDNA
4060	L			3.0E-18		F	Homo sapians chromosame 21 segmant HS21C047
8969	L			3.0E-18	3.0E-18 BE001671.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
11167	24238	37869	1.99	3.0E-18	3.0E-18 BF218650.1	EST_HUMAN	601884858F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103862 5
12832	匚		4.56	3.0E-18	3.0E-18 AW022015.1	EST_HUMAN	df31h12.y1 Marton Fetal Cochlea Homo saplens cDNA clane IMAGE:2485128 5'
261	13480	26512	4.2	2.0E-18	2.0E-18 AW836820.1	EST_HUMAN	QV1_T0038-150200-070-e07_LT0038 Homo sepiens cDNA
1178					2.0E-18 BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clore IMAGE:3355044 5'
3183	16368	28374	0.94		2.0E-18 Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
569	13752	26780	5.1	9.0E-19	9.0E-19 AA281961.1	EST_HUMAN	zt11406.r1 NCI_CGAP_GCB1 Homo sepieris cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
183		ł	3.91	9.0E-19	0.0E-10 AA281961.1	EST HUMAN	zt11406.r1 NCI_CGAP_GCB1 Homo sapieris cDNA clone iMAGE:712811 6' similar to contains MER19.t2 MER19 repetitive element ;
8032	1_					Π	HSC23F051 normalized infant brain cDNA Homo septens cDNA clone c-23f05
8888	1	35501	2.57				Homo sapiens chromosome 21 segment HS21C003
9888	ı						Homo sepiens chromosome 21 segment HS21C003
11392	Ш			6	.0E-19 AB032969.1	NT	Homo sepiens mRNA for KIAA1143 protein, partial cds
12171	13752	26780	19.34		9.0E-19 AA281961.1		zt11d06.r1 NCI_CGAP_GCB1 Hame saplens cDNA clone IMAGE:712811 5' stmilar to contains MEK19.tz MER19 repetitive element ;
1073	14239		1.58		8.0E-19 AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
8342	<u> </u>	34948		<b>"</b>	.0E-19 BE158936.1	EST_HUMAN	MRO-HT0404-210200-001-906 HT0404 Homo sapiens cDNA
2319	15461	28583	1.74	7.0E-19	4758139 NT	LΝ	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide θ (RNA helicase, 54kD) (DDX6) mRNA
6585		L			7.0E-19 AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452	L				.0E-19 P26444	SWISSPROT	BETA CRYSTALLIN A2
10216		36841	0.54	_	.0E-19 Al344951.1	EST_HUMAN	tb01c08,x1 NCI_CGAP_Lu26 Homo saplents cDNA clone IMAGE:2052302 3
12316	1		1.72		.0E-19 AA705684.1	EST HUMAN	zi60b01.s1 Soares fetal liver spieen 1NFLS_S1 Homo saplens cDNA clone IMAGE:4351453
3879	1		1.16	ľ	3.0E-19 AW852930.1	EST_HUMAN	PMo-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4685	17722		1.56	ľ	3.0E-19 P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.58		3.0E-19 P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	•		1.2	ľ	.0E-19 AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
02.03		20,400	647	<u> </u>	5 DE-10 C00103	CWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN
6346		l			5.0E-19 AW663302.1	EST HUMAN	hh77b08.y1 NCI_CGAP_GU1 Homo sapien; cDNA clone IMAGE:2968787 6'
10639	L	1			5.0E-19 A.J297699.1	본	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
	L	ı					x87b02.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2664171 3' similar to contains
11829	24818	38509	8.14		5.0E-19 AW183725.1	EST_HUMAN	element MSR1 repetitive element ;
	1	ŀ					Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13SA2T, TCRBV4S3A1N1T, TCRBV5SS2,
							TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1,
13083	3 25895	10	1.34		5.0E-19 U65060.1	ᅜ	TCRBV23S1A2T, TCRBV12>
288	L			,	4.0E-19 AB007970.1	NT	Home sepiens mRNA, chromosome 1 specific transcript KIA40501
2747	ľ	28975	1.15		4.0E-19 BF697362.1	EST_HUMAN	502130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5

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Chigin LACIT TODGS LAPIGOSOS III TOGGING	Top Hit Descriptor	Homo sepiens mannosidase, beta A, tysoscinal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	BETA-2 ADRENERGIC RECEPTOR	BETA-2 ADRENERGIC RECEPTOR	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 8)	AV708136 ADC Hamo expiens cDNA clone ADCAMA11 5	Hamo sepiens NPD008 protein (NPD008) niRNA, complete ads	Horno sapiens similar to aldo-kato reductas¢ family 1, member B11 (aldose reductase-like) (H. sapiens) (LOG63222), mRNA	M.musculus mRNA for TPCR33 protein	Homo sapiens phorbolin I protein (PBI) mRNA, complete cds	Hamo sapiens chromesame 21 cogment HS21C001	costect. NCL CGAP_Kid5 Homo sepiens cDNA clone IMAGE:1915888 3' similar to TR:Q68386 Q69386 POJ JFNV GFNF	ANIZAGED LTE Homo equience CONA close HTFAZCOR S'	COLOGO TITL DUTING SEQUENCE COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO COLOGO CO	Mus musculus Keraun-associated protein 9-1 (Number 1), month	2234c09.r1 Sogres retina N2b4HR Homo séplens cDNA clone IMAGE:360880 5	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2	601804125F1 NIH_MGC_21 Homo sapiens cDNA done IMAGE:3638310 5	yo78g07.r1 Soares adult brein NZb4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element :	Human gene for Ah-receptor, exon 7-9	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	a49br12.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:1393631 3' similar to conteins MER37.t2 MFR37 repositive element:	wmothor of NCI COAP 112 Home seniors CDNA clone IMAGE:2443287 3' similar to TR:016530 016530	PMS3 MRNA;	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds	nh22d03.s1 NCI_CGAP_Pr1 Homo capiens oDNA done IMAGE:953093 cimilar to contains L1.t1 L1	repetitive element;	Oryctologus cuniculus Na+/gucose cotransporter-related protein mRNA, complete cds	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds	Homo saplens pituitary tumor transforming gene protein (PTTG) gene, complete cds
10000	Top Hit Database Source	<u>로</u>	SWISSPROT BI	SWISSPROT B		SWISSPROT L	EST_HUMAN A	NT H		NT	I L	H	POT WIND	Τ	HOMAN		EST HUMAN Z	SWISSPROT O	EST_HUMAN G	NAMIN TOU	T		PS NAMIN TOTAL	Т		NT	т	T_HUMAN	NT		Y Y
Signio	Top Hit Acession No.	4.0E-19 AF224669.1					3.0E-19 AV708136.1	3.0E-19 AF223467.1	11432214 NT	3.0E-19 X89685.1	7.	2.0E-19 AL163201.2	2 05 40 41344783 4		2.0E-19 AV /31382.1	7657286 NT	2.0E-19 AA012854.1		1.0E-19 BE408611.1	1 OE-10 H30705 1		4758977	1 0E 10 0 0 08 24 0 87 1	100000	1.0E-19 AI890866.1			1.0E-19 AA595527.1	1.0E-19 U08813.1	1.0E-19 U08813.1	1.0E-19 AF200719.1
	Most Similar (Top) Hit BLAST E Vælue	4.0E-19	3.0E-19 Q28997	3.0E-19 Q28997	3.0E-19 043900	3.0E-19 O43900	3.0E-19	3.0E-19	3.0E-19	3.0E-19	3.0E-19	2.0E-19	200	200-10	2.0E-19	2.0E-19	2.0E-19	2.0E-19 Q95155	1.05-19	4 OF 40	1.0E-19	1.0E-19	1 00 40	1.05	1.0E-19	1.0E-19		1.0E-19	1.0E-19	1.0E-19	1.0E-19
	Expression Signal	1,2	1.02	1.02	0.85	0.85	1.42	0.69	1.88	1.09	16.36	20.08	767	5 3	0.81	0.63	10.24	0.84	1.86	7	2.4	6.72	4	-	6.73	2.6		•0.63	1.05		0.75
	ORF SEQ ID NO:	31725	L	L		30527	30688			34614		28865					35146			20/06			Cosec	1	31631				34355	Ц	
	SEQ ID NO:	18710	ı	17113	17643	i	ĺ	18596	20615	1		1	1	ł	- 1		21606	23151	ı	16987	1	L	ı	Н	18652	L		26213	20862	H	Ш
	Probe SEQ ID NO:	5512	3955	3855	84	4400	4569	5394	7543	8658	12583	2627	901	900	6179	7493	8526	10113	494	86	2782	2808	9400	§	5452	9188		6337	7808	7806	7977

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Top Hit Descriptor	Rabbit phosphorylase kinase beta subunit mRNA, complete cds	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:123243 6 similar to contains OFR repetitive element;	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	RC0-ST0174-191099-031-b05 ST0174 Homo saplens cDNA	y/31e09.r1 Scares melanccyte 2NbHM Horno saplens cDNA clone IMAGE:272872 5	60/279682F1 NIH_MGC_39 Homo sapienis cDNA clone IMAGE:3811493 5	Mus musculus keratin-associated protein 9:1 (Krtap9-1), mRNA	Mus musculus keratin-associated protein 9,1 (Krtap9-1), mRNA	qg86(09,x1 Soares_NFL_T_GBC_S1 Homb sapiens cDNA clone IMAGE:1842089 3'	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1842089 3'	PM4-AN0098-050900-003-a04 AN0098 Homo saplens cDNA	DKFZp547D092_r1 547 (synonym: hfbr1) Homo saplens cDNA clone DKFZp547D092 5'	n146c04.s1 NCI_CGAP_Pr4 Homo septens cDNA clone IMAGE:1043718 similar to contains MER29.b2	MER29 repetitive element;	ri46c04.s1 NCI_CGAP_Pr4 Homo saplensicDNA clone IMAGE:1043718 similar to contains MER29.b2	MER29 repetitive element;	Homo sapiens ribosomal protein L13a (RPL13A), mRNA	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IWAGE:3916231 5'	AV725123 HTC Homo saplens cDNA clone HTCBTA01 5'	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250	2h78d08.s1 Soares fotal liver spleen_INFLS_S1 Homo sepiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;	zh78d08.s1 Soares fetal liver spleen 1NFLS S1 Homo saplens cDNA clone IMAGE:418191 3' cimilar to	ocntains MER30.11 MER30 repetitive element;	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	Mus musculus MMAN-g mRNA, complete cds	Mus musculus MMAN-g mRNA, complete cds	HYPOTHETICAL PROTEIN DJ845024.1	Homo sapiens chromosome 21 segment HS21C047	HISTONE H2B C (H2B/C)	1左64g03.x1 NCI_CGAP_Ov35 Homo saplens cDNA clone IMAGE:2293396 3'	AVI PTOMS DOCUMENT OF ANY DEPOSIT COMMA
Top Hit Database Source	NT	EST HUMAN OF	Г	EST_HUMAN RO	EST_HUMAN 1973	EST HUMAN 60				EST_HUMAN   qg	EST_HUMAN PN	Г	PIP	EST_HUMAN  ME	Г	EST_HUMAN ME		SWISSPROT AL			EST_HUMAN AF	EST HUMAN 00	Г	EST_HUMAN   000	П	П	NT IN	SWISSPROT HY	NT He	SWISSPROT HI	EST_HUMAN 126	FOT HIMAN ON
Top Hit Acession No.	1.0E-19 M64657.1			1.6	1.0E-19 N44631.1	1.0E-19 BE616028.1	7857286 NT	7657286 NT	8.0E-20 AI221371.1	8.0E-20 AI221371.1	7.0E-20 BF326455.1			7.0E-20 AA557657.1		7.0E-20 AA557857.1	6912633 NT		34.1	5.0E-20 AV725123.1	5.0E-20 AF075301.1			6.0E-20 W90525.1	-				4.0E-20 AL163247.2	Γ	4.0E-20 AI874352.1	
Most Similar (Top) Hit BLAST E Velue	1.0E-19	1.0E-19 T99920.1	1.0E-19	1.0E-19	1.0E-19	1.0E-19	8.0E-20	8.0E-20	8.0E-20	8.0E-20	7.0E-20	7.0E-20		7.0E-20		7.0E-20	7.0E-20	6.0E-20 P39188	6.0E-20	5.0E-20	5.0E-20	S 0F-20		6.0E-20	5.0E-20	5.0E-20	6.0E-20	5.0E-20 OG0809	4.0E-20	4.0E-20 Q99880	4.0E-20	A 05.20
Expression Signal	19.	2.72	0.69	25.12	1.59	1.87	2.4	2.4	1.48	1.46	0.71	5.66		8.83		8.83	2.89	3.64	4.58	1.8	1.42	90		6.96	0.78	138	1.28	1.13	96.0	1.13	5.61	4 42
ORF SEC ID NO:	35261			37032	37042	37888					L		<u> </u>	35305		35306		28822			33799	34733		34734					27889			37357
Exon SEQ ID NO:	21724			<u>」</u>	L		L	19939	l	ı	<u></u>			21773		21773	Ι.	l	1_		20347	21213	L	21213	L		1	1	١.		l.,	L
Probe SEQ ID NO:	8644	8939	0588	10380	10400	11184	6784	6784	7687	7687	88	718		8693		8693	12014	3645	4387	4718	7264	8131		8131	8285	9035	9035	984	1649	6765	8110	10717

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Top Hit Descriptor	Human BXP21 gene	OLFACTORY RECEPTOR-LIKE PROTEIN 114	zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to	contains L1.t3 L1 repetitive element :	Human DNA, SINE repetitive element	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE);	ENDONOGLEADE)	601514180F1 NIM_MGC_/11 Home septiens conte invacet.co. 1022 0	x24e10.x1 NCI_CGAP_U¼ Homo sapiens dDNA done IMAGE::2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5; :	ng69h09.s1 NCI_CGAP_Lip2 Homo capians oDNA done IMAGE:040097 similar to TR:G1224068 01224066 ORF2: FUNCTION UNKNOW'N. ;	ng69h09.s1 NCI_CGAP_LIp2 Homo sapiens cDNA done IMAGE:940097 similar to TR:G1224068	G1224068 ORF2: FUNCTION UNKNOWN.;	xx24e10.x1 NCI_CGAP_U4 Homo sapleris cDNA clone IMAGE:2781098 3° similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5: :	ZONADHESIN PRECIPSOR	ZONIADIECIN DEFOI IDCOD	CONSUMEDING THE CONSUMER AND AND AND AND AND AND AND AND AND AND	Homo sapens maraie denyalogerase 1, 140 (saubie) (m.D.1.) Illustra	EST180326 Liver III Homo seplens cDNA 5 end	Homo sapiens RGH1 gene, retrovrus-like element	Homo sapiens RGH1 gene, retrovirus-lika element	CHR220310 Chromosome 22 exon Homo sapians oDNA clone C22_381 5	zt/1406.rt NCI_CGAP_GC31 Homo saplens cDNA clone IMAGE:712811 5' similar to contains MER19.t2	MEK19 repetitive etement;	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155.3' sImilar to contains L1.t2 L1	epenive ecinent,	AF049567 Human activated dendritic cell mKNA Homo saptens culvA cione GAU3	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	nc60g08.r1 NOL CGAP_Pr1 Homo sepieris cDNA clone IMAGE:746694 similar to contains L1.t3 L1	repentive element;
Top Hit Detebese Source	NT	SWISSPROT		EST HUMAN		EST_HUMAN		Т	EST_HUMAN	EST_HUMAN	EST HUMAN	П	EST_HUMAN	EST HIMAN	Т	T.	ISSPROI		T_HUMAN			EST_HUMAN		EST_HUMAN		1	T HUMAN	NT	LN		EST_HUMAN
Top Hit Acession No.				~		<u>.</u>			3.0E-20 BE888422.1	2.0E-20 AW303868.1			.0E-20 AA516335.1	2 OF 20 AW303868 1				4538	Ţ.	2.0E-20 D10083.1	2.0E-20 D10083.1	.0E-20 H55371.1		.0E-20 AA281961.1		.0E-20 BF115158.1	.0E-20 AF049567.1	11418491 NT	0E-20 AE223384 4		.0E-20 AA420453.1
Most Similar (Top) Hit BLAST E Value	3.0E-20 U03888.1	3.0E-20 P23273		3.0E-20	3.0E-20 D14547.1	3.0E-20		3.0E-20 P11369	3.0E-20[E	2.0E-20 /	2.0E-20/		2.0E-20	200	200000000000000000000000000000000000000	Z-20.7	2.0E-20 Q28983	2.0E-20	2.0E-20	2.0E-20	2.0E-20	2.0E-20		1.0E-20		1.0E-20	1.0E-20	1.0E-20	4 DE 20	22	1.0E-20
Expression Signal	1.22	1.29		1.08	269	0.47		1.59	6.09	5.65	249		2.49	00 11	40.0	ó	5.15	0.0	76.0	2.65	2.65	2.17		6.61			0.74	2.08			2.91
ORF SEQ ID NO:	28468	30455	L	30864		37168			32109		27355		27356		1		31164			36030	l		Ì	28327					l		
SEQ ID	15341	ı	i i	17882	22214	23562		23984	25239	14030	14300		14300	7,000	1	- 1	1			22468	l_	26878		15995				22439	<u> </u>	1_	26323
Probe SEQ ID NO:	2207	4325		4747	9135	10527		10900	12331	853	1135		1135		9		2061	6256	6088	839-1	9391	12743		2020		4560	7034	9364	74047	Ì	12461

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Single Exon Probes Expressed in Placeria	Top Hit Descriptor	Rattus nonegicus mRNA for rTIM, complete cols	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, end sodium phosphate transporter (NPT3) gene, complete cds	Home sapiens chromosome 21 segment/HS21C002	zq15d06.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3	Home suplans chromosome 21 segment HS21 0001	Hamo sapiens LGMD2B gene	Homo sapiens dNT-2 gene (cr milochoncital 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5	Homo sapiens dNT-2 gene for milochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5	AV661044 GLC Hamo saptions cDNA clane GLCGOA10 3	601844465F1 NIH_MGC_54 Homo saptiens cDNA clone IMAGE:4064945 6	RC1-0T0083-100800-019-608 OT0083 Homo saplens cDNA	ICM/1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA	Hamo sapiens chromosame 21 segment HS21 0013	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA	Hamo sepiens mRNA for KIAA0397 protein, partial cds	Homo saplens mRNA for KIAA0397 protein, pertial cds	RC4-BT0311-141199-011-h06 BT0311 Homo saplens cDNA	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	ts30f03.x1 NOL_CGAP_Pan1 Homo septiens oDNA clone IMAGE:2230109 3' cimilær to TR:Q99854 Q99854 HYPOTHETICAL 51.1 KD PROTEIN;	2997a12.r1 Scares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'	2897a12.r1 Soares_fetal_heart_NbHH19W Homo septens cDNA done IMAGE:366910 6	zc28h02.rt Scares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323867 5	Homo saplens hyperion gene, exans 1-50	QV0-HT0103-091199-050-g11 HT0103 Homo sapieno oDNA	AU 136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'	ht09g01.x1 NCI_CGAP_KId13 Homo sepiens cDNA done IMAGE:3146256 3' similar to contains MER29.b3 MER29.b3 MER29 repetitive element;	B01680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5
e Exon Prope	Top Hit Database Source	NT	LN.	TN	EST_HUMAN	FN	NT	ΙΝ	Ĕ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	NT	NT	EST_HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Singi	Top Hit Acession No.	4.0E-21 AB019576.1	4.0E-21  U91328.1	4.0E-21 AL163202.2	3.0E-21 AA218891.1	3.0E-21 AL163201.2	3.0E-21 AJ007973.1	3.0E-21 AJ277557.1	3.0E-21 AJ277557.1	3.0E-21 AV681044.1	3.0E-21 BF184739.1	3.0E-21 BF361093.1	3.0E-21 AW897760.1	3.0E-21 AL163213.2	2.0E-21 BE163247.1	2.0E-21 AB007857.2	2.0E-21 AB007857.2	2.0E-21 BE084410.1	Q28983	Q28983	2.0E-21 AI624582.1	2.0E-21 AA027211.1	2.0E-21 AA027211.1	2.0E-21 W44463.1	2.0E-21 AJ010770.1	2.0E-21 BE141785.1	2.0E-21 AU138779.1	2.0E-21 BE350127.1	2.0E-21 BE973829.1
	Most Similar (Тф) Hit BLAST E Value	4.0E-21	4.0E-21	4.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.05-21	3.0E-21	3.05-21	3.0E-21	3.0E-21	3.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21 Q28983	2.0E-21 Q28983	2.05-21	2.0E-21	2.0E-21			١.	2.0E-21	2.0E-21	2.0E-21
	Expression Signal	2.61	0.82	0.61	1.1	1.51	6.41	0.92	0.92	6.0	2.74	7.52	0.92	3.58	24.6	0.61	0.61	3.03	2.59	2.59	1.66	0.8	0.8	0.74	0.58	8.13	3.27	2.04	2.88
	ORF SEQ ID NO:	33568	36614					31878	31879			33483		31665		27189		L	28837	28938									38335
	Exen SEQ ID NO:	20147	23022		L_	1	l	18810	18810	i	1	Ι.	1	26099		14131	14131	14400	_		]	1_	1.	L	┺	1	L	ı	24652
	Probe SEQ ID NO:	7011	6983	10010	1884	2348	3149	5616	5816	5856	6308	7215	9894	12879	150	858	898	1241	2703	2703	5604	98	5694	9167	8467	8558	9023	11313	11699

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	Top Hit Descriptor	601680836F1 NIH_MGC_83 Homo septens cDNA clane IMAGE:3951008 5'	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds	nA6004.s1 NCL CGAP Pr4 Homo eaplens cDNA clone IMACE:1043718 similar to contains MER29.b2	WER29 repetitive element ;	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3*	DKFZp43410830_r1 434 (synonym: htes3) Hamo septens cDNA clone DKFZp43410830 5'	gg47e05.x1 Scaras_testis_NHT Homo scipiens cDNA clone IMAGE:1838338 3' similar to gb:M64241 QM PROTEIN (HUMAN);	Homo sepiens chramosome 21 segment HS21C003	Homo sapiens chronosome 21 segment HS210003	Homo saplens SET domain and martner transposase fusion gene (SETMAR) mRNA	Homo sapiens chromosome Xp22 410-8	ES4603.X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT:	Homo sapiens chromosome 21 segment HS21C001	Homo saplens chromosome 21 segment HS21C001	AV761874 MDS Homo caplens cDNA clone MDSCCG05 5'	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'	CM0-HT0179-281099-076-h05 HT0179 Homo saplens cDNA	zk87e06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5	Homo sepiens chromosome 21 segment HS21C046	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)	Homo sapiens gene for activin receptor type IIB, complete cds	Homo sapians HSPC220 mRNA, complete cds	EST00738 Fetal brain, Stratagene (саt#936208) Ното sapiens cDNA clone HFBCF07	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812.3'	Ното sapiens chromosome 21 segment HS21С103	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	naa27b06.x1 NOL_CGAP_Pr28 Homo sapiens oDNA olone IMAGE:3255898 3' similar to contains Alu	repetitive element;	Homo sapiens Xq pseudoautosomal region; segment 1/2	Hamo sapiens chromosome 21 segment HS21C002	601862813F1 NIH_MGC_57 Homo sapiens CDNA clone IMAGE:4095434 5
-	Top Hit Database Source	EST_HUMAN 60	되	돌	EST_HUMAN ME	EST_HUMAN ar	П	EST HUMAN PF	¥	보 보		Ĭ	HIMAN	Τ	Ĭ	EST HUMAN A	EST_HUMAN A	HUMAN	EST_HUMAN  zk		ISSPROT			T_HUMAN	Ĭ	EST HUMAN W		Ī	au	T_HUMAN	I I		EST_HUMAN 60
18	Top Hit Acession No.				1.0E-21 AA557657.1		1.0E-21 AL079752.1				5730038 NT	1.0E-21 AF046133.1		9.0E-22 AL 163201.2	Γ			E-22 BE144748.1	E-22 AA0465021	6.2	E-22 Q61838	E-22 AB008681.1	1	E-22 M78590.1	E-22 AF009660.1	E-22 AW029123.1	E-22 AL163303.2	E-22 U60822.1					DE-22 BF218030.1
	Most Similar (Top) Hit BLAST E Value	2.0E-21	2.0E-21		1.0E-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	0 0E.22	9.0E-22	9.0E-22	9.0E-22	9.0E-22	8.0E-22	8.0E-22	7.0E-22	7.0E-22	7.0E-22	7.0E-22	7.0E-22	7.0E-22	6.0E-22	5.0E-22	6.0E-22		5.0E-22	4.0E-22	4.0E-22	4.0E-22
	Expression Signal	2.88	6.44		1.89	4.93	2.73	4.7	0.47	0.47	1.31	1.67	ar c	2.02	2.02	3.1	1.39	7.93	3.36	3.78	3.27	16'0	1.24	2.77	2.05	1.25	3.27	2.98		1.63	77.0	2.81	1.97
	ORF SEQ ID NO:	38336			27509			33885					}_		35421	L				26898		31241			36418		33192						37677
	SEO ID NO:	24852	ı	ı	14440	14587	1	20422	l	ı	ı	1		1	ı	1	24992	14144	21182	13867	1_	L	21987	22111	22842	ı	ı	l	ı		16887	28224	24042
	Probe SEG ID NO:	11589	12572		1284	1434	6816	7342	10448	10448	10812	13014	100	2808 808	8803	11031	12007	971	8080	682	4398	5150	8888	9032	9802	8436	6646	10525		12833	3726	8608	10961

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		 ₽	TOMAN		2										illar to									-		R29.b2
Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C009	m14h10.r1 NCI_CGAP_CG14 Homo saplens cDNA ctore IMAGE:2156611 3' simitar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN);contains L1.t1 L1 repetitive element;	wi60b04.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2429639 3' similor to SW:RL21_HUMAN P48778 60S RIBOSOMAL PROTEIN L21.;	Human chromosomal protein HMG1 related gene	qb28c07.x1 Soares_pregnant_uterus_NtiHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.t2 MER12 repetitive element;	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE : ENDONUCLEASE)	QV0-HT0368-090200-099-f12 HT0368 Homo sepiens cDNA	RC5-BT0707-150300-021-H10 BT0707 Homo saplens cDNA	R.rattus RY2G5 mRNA for a potential ligand-binding protein	R.rettus RY2G5 mRNA for a potential ligand-binding protein	yx73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR	Homo saplens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA	zc20f01.r1 Sogres_senescent_fibroblasts_NbHSF Homo sepiens cDNA clone IMAGE:322873 5' sImiliar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA	q78h06.x1 Scares_NhHMPu_S1 Homo taplens cDNA clone IMAGE:1878299 3' similar to contains MER29 t3 MER29 repetitive element:	m04h11.s1 NCI_CGAP_Pr22 Homo sepiens cDNA clone IMAGE:1219269 3'	mo4h11.s1 NCI_CGAP_Pr22 Hamo sapiens cDNA clone IMAGE:1219269 3'	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA done IMAGE:2874655 3'	Homo eaplens chromosome 21 segment HS21C080	PM4-SN0020-010400-009-h02 SN0020 Homo saplens cDNA	Human familial Alzheimer's disease (STM2) gene, complete cds	Human DNA, SINE repetitive element	MR0-BT0659-220200-002-h07 BT0659 Homo sepiens oDNA	cz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similær to contains MER29.b2 MER29 repetitive element ;
Top Hit Database Source	NT.	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	N	IN	EST_HUMAN	SWISSPROT	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	FST HIMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	ΝΤ	NT	EST HUMAN	EST_HUMAN
Top Hit Acession No.	.0E-22 AL163209.2	.0E-22 A 469879.1	3.0E-22 AI859038.1	214718.1	3.0E-22 Al090125.1	71369	3.0E-22 BE156813.1	3.0E-22 BE089841.1	(60660.1	(60660.1	124942.1	24916	8394043 NT	2.0E-22 AW817794.1	2.0E-22 W39456.1	2.0E-22 BF092116.1	0 OE. 22 A1278522 4	2.0E-22 AA715315.1	2.0E-22 AA715315.1	2.0E-22 AW 418960.1	2.0E-22 AL163280.2	1.0E-22 AW865517.1	1.0E-22 U60871.1	1.0E-22 D14547.1	1.0E-22 BE084667.1	1.0E-22 Al366435.1
Most Similar (Top) Hit BLAST E Value	4.0E-22	3.0E-22/	3.0E-22	3.0E-22 D14718.1	3.0E-22	3.0E-22 P11369	3.0E-22	3.0E-22	3.0E-22 X60660.1	3.0E-22 X60860.1	20E-22 N24942.1	2.0E-22 P24916	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2 OE. 20			2.0E-22	2.0E-22	1 0E-22	1.0E-22	1.0E-22	1.0E-22	1.0E-22
Expression Signal	3.85	28,	1.83	1.66	3.18	8.0	1.1	1.88	1.14	41.1	4.04	1.72	3.98	1.41	1.47	3.58	47.	0.85	0.85	1.52	2.33	2.05	2.38	1.53	1.09	1.05
ORF SEQ ID NO:			28873	L	31038	34573		35042	35172				29684				_	L	36831	1	31954				34478	37432
Exen SEQ ID NO:	26672	14154	1	1	18062	21061	1	1	Į.		Į.	ı	16674	L	L	١	<u> </u>			1	25856	1	ı	16664	20971	23809
Probe SEQ ID NO:	13021	8	2838	3763	4922	8011	8425	8430	8555	8555	2008	2590	3507	4341	5973	808	2007	10001	10001	12058	12139	1927	2651	3497	7820	10776

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the comment of the comment of the comment of the comment of the comment of the comment of the	\$ <sup>Cm</sup>	Top) Hit Top Hit Acessian No. Value No. 1.0E-22 Al365435.1 ES 9.0E-23 AM/8022801.1 ES 8.0E-23 AF108349.1 NT 6.0E-23 AF124669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF224669.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF179818.1 NT 6.0E-23 AF280107.1 NT 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV8877827.1 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV887777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0E-23 AV87777 ES 6.0	T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	Top Hit Descriptor  MER29 repetitive element :  ILL2-UMO076-201-CIL1 Hamo sapiens cDNA cione IMAGE:2020881 3' stirrilar to contains MER29.b2  MER29 repetitive element :  ILL2-UM0076-2070400-061-F1 UM0076 Hamo sapiens cDNA  Gallas gallus Dach2 protein (Dach2) mRNA, complete cds  AN647246 GLC Hamo sapiens cDNA clene GLCAWUZOY 3  Homo sapiens Not56 (D. melanogaster)-Il/ke protein (NOT681) mRNA  Fattus norvegicus RIM18 (Rim18) mRNA, complete cds  Homo sapiens mannosidase, beta A, lyescomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3  (UBE2D3) genes, complete cds  Homo sapiens mannosidase, beta A, lyescomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3  (UBE2D3) genes, complete cds  Homo sapiens mannosidase, beta A, lyescomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3  (UBE2D3) genes, complete cds  Homo sapiens chromosome Xq28 malandyma antigen family A2a (WAGEA2A), melanoma antigen family A12  (MAGEA1), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin  (CALT), NAD(DH) delydzogarase-ills pizaten (NSDHL), and LLP  Forigo pygmaeus offactbry receptor (PPY116) gene, partial cds  Forigo pygmaeus offactbry receptor (PPY116) gene, partial cds  Homo sapiens chromosome Z1 segment HSZ10027  Homo sapiens chromosome Z1 segment HSZ10027  Human endogenous retroine et S10 polypeptide (Mage S100)  Human endogenous retroine et S40 polypeptide (Mage S100)  Human endogenous retroine et S40 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)  Human endogenous retroine P450 polypeptide (Mage S100)  Human endogenous retroine P450 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)  Homo sapiens cychrome P450 polypeptide (Mage S100)
1 !	13868 26899			AJ289880 1	N.	Homo sapiens KIAA0651 gene (partial), X13 gone and LZ1rL1 gene
		3.46		2.0E-23 M55270.1	NT	Human matrix Gia protein (MGP) gene, complete cds
2856 159	15970 29079	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
ı	ļ	-	2 OF-23	P22405	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

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Top Hit Descriptor	qs73ff1.x1 NCI_CGAP_Pr28 Homo saplans cDNA clone IMAGE:1943757 3' simillar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	yr16a02.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:205418 5'	yr16a02.r1 Soares fetal liver spieen 1NFLS Homo saplens cDNA clone IMAGE:205418 5'	Homo sepiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; oytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds,	Homo sapiens chromosome 21 segment HS21C103	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1	Homo sapiens T cell receptor beta locus, ¡TCRBV7S3A2 to TCRBV12S2 region	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000948 5'	Homo sapiens chromosome 21 cegment HS21C052	Homo saplens chromosome 21 segment HS21C010	801238455F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3608653 5	zw82c06.r1 Sogres_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2 PTR5 repetitive element ;	601301762F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3636254 5	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'	QV0-NN1020-170400-195-a11 NN1020 Homo septens cDNA	ab75a08.s1 Stratogene fetal retina 937.202. Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN .	OLFACTORY RECEPTOR-LIKE PROTEIN 13	OLFACTORY RECEPTOR-LIKE PROTEIN 13	Homo saplens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA	DKFZp434A2311_r1 434 (synonym: htes3) Homo saplens cDNA clane DKFZp434A2311 6'	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2813405 3' similar to contains Alu	Oppulve Section (Control of Trains Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control o	Agobo Tuodata MKNA 101   esus-Specific Trount ( 1.57.1), compare cus	Homo sapiens chromosome 21 segment HS21 0049	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gane, exons 7-49, and partial cds, alternatively spliced
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	Н	LX		LN	LN	T HUMAN	TN	IN	EST_HUMAN	EST HUMAN	HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	Г	SWISSPROT		EST_HUMAN	EST_HUMAN		LICINAIN	Z	NT	Z	L
Top Hit Acession No.	0E-23 Al201458.1	0E-23 BE165980.1			AF280107.1	1,163303.2	2.0E-23 M32658.1	\F009660.1	4U133931.1	0E-23 AL163252.2	0E-23 AL163210.2	0E-23 BE378471.1	AA448097.1	.0E-23 BE409843.1	0E-23 BE409643.1	.0E-23 AW901816.1	9.0E-24 AA663213.1	8.0E-24 P23269	P23269	11422027 NT	AW937954.1	.0E-24 AL039498.1		7.0E-24 AW 303317.1	AB001421.1	6.0E-24 AL163249.2	AJ229043.1	5.0E-24 AF223391.1
Most Similar (Top) Hit BLAST E Value	2.0E-23	2.0E-23	2.0E-23 H59931.1	2.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23 /	2.0E-23	1.0E-23	1.0E-23	1.0E-23	1.05-23	1.0E-23	1.0E-23	1.0E-23	9.0E-24	8.0E-24	8.0E-24	8.0E-24	7.0E-24	7.0E-24	101	7.0E-24	6.0E-24	6.0E-24	5.0E-24	5.0E-24
Expression Signal	1.3	3.63	4.43	4.43	6,28	0.95	8.7	3.68	2.3	1.57	5.42	3.27	4.61	2.19	2.19	1.35	1.87	1.12	1.12	0.95	0.94	16.79		1.61	2.21	12.8	62'6	1.27
ORF SEQ ID NO:			30246			35685				30769			35169	L	١		l _	30888								27100	30241	34493
Exen SEO ID NO:	16824	1	ı	1	21140	22/23	ı	1	ſ	i	ı	<u></u>	21632	L	1_	26074	Ĺ	ı	17906	ı	L	ı	i i	- 1		14038	17234	ìì
Probe SEQ ID NO:	3457	3810	4086	4085	8057	9044	12265	12844	12983	4650	4888	6861	9554	10909	1000	13082	999	4777	4771	6578	3976	5281		10878	724	861	4078	7935

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Top Hit Descriptor	RCO-GN0090-250900-022-h09 GN0090 Homo sapiens cDNA	nn31k05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clane IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;	RC3-ST0197-130100-014-f06 ST0197 Homo sapiens cDNA	801078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484498 51	Homo sapiens mRNA for KIAA1093 protein, partial cds	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV14S1, TCRBV14S1, TCRBV14S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1, TCRBV16S1, TCRBV14S1, TCRBV14S1, TCRBV14S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV3S2>	hh88c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967850 3' similar to contains MER29.b2 MER29 repetitive element ;	EST374149 MAGE resequences, MAGG Homo saplens cDNA	Homo saplens chromosome 21 segment HS21C052	601810449F1 NIH_MGC_46 Homo saplens cDNA clone IMAGE:4053398 5'	zp11f09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:509161 5'	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA	Hano sapiens chromosame 21 segment H321 C009	Mus musculus morac-interacting afron kinase (Crik) mikiva, complete das	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone Mir ip 12-3n is	LIKEZDYOLLI (17 Tr. 161 (Symonym. nemyz) nomo saprens conva cume divizzy o tentra de contente	Yezbue, T. Soares rata liver spiedn in FL.3 nome sapidite curva crate invace. 2.12.12.2.3 5 similar to contains MER28 repetitive element;	ti77a09.x1 NCI_CGAP_Ktd11 Homo septens cDNA clone IMAGE:2138008 3'	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'	Human O family dispersed repeat element	Homo sapiens CGI-127 protein (LOC51646), mRNA	QV0-ST0294-100400-185-c10 ST0294 Homo seplens cDNA	Mus musculus mRNA for HGT keratin, pertial cds	Homo sapiens PTEN (PTEN) gene, exon 2
Top Hit Database Source	EST_HUMAN	EST_HUMAN	_	EST_HUMAN	ΤN	ΤN	Ż	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	1	HUMAN	NT NT	N	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	INT	EST_HUMAN	NT	N
Top Hit Acession No.	4.0E-24 BF389469.1	0E-24 AA594178.1		l		0E-24 U66081.1	0E-24 U66061.1	0E-24 AW614871.1	3.0E-24 AW962076.1	4L163252.2	3F127762.1	4A167539.1	2.0E-24 AW898189.1	4L163209.2	AF086824.1	AJ003536.1	AL119158.1	H69214.1	2.0E-24 AI521759.1	AI521759.1	M28877.1	7706340 NT	.0E-24 AW820194.1	.0E-24 D86423.1	.0E-24 AF143313.1
Most Similar (Top) Hit BLAST E Value	4.0E-24	4.0E-24	4.0E-24	4.0E-24	4.0E-24	3.0E-24	3.0E-24	3.05-24	3.0E-24	3.0E-24	3.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24		1	2.0E-24		1.0E-24	1.0E-24	1.0E-24	1.0E-24
Expression Signal	6.0	2.77	0.71	2.06	4.02	0.73	0.73	200	1.24	3.79	1.34	2.55	0.82	0.63	0.0	0.58	3.81	0	1.08	1.06	21.43	4.81	1,65	0.72	1.93
ORF SEQ ID NO:		32559				33551	33552			36188	32034	L					35559		36698	L		27972		29278	
Exon SEQ ID NO:	17514	İ	L	24514	1	20134	20134		1	[	1	1					22017	22056		1	l	L	15855		17528
Probe SEQ ID NO:	4371	8052	888	1454	12669	9227	9227	84.0	8873	9885	12756	2422	3899	7515	7643	7648	8838	7708	10058	10058	12580	1731	2738	3085	4385

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					similar to		ilar to contains			AGE-B1							ing repeat				E:548943 6'		ne families	1.5				
Single Exon Probes Expressed in Pracellia	Top Hit Descriptor	PM1-HT0454-080100-002-h09 HT0454 Homo saplens cDNA	Homo sapiens HSPC059 protein (HSPC059), mRNA	Homo sapiens HSPC059 prolein (HSPC059), mRNA	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sepiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element:	nn54h11.s1 NOL CGAP Kid6 Hamo seplens cDNA clone IMAGE:1087749 3'	ZIBGQ04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTRs.t3 PTR5 repetitive element;	R.rattus RY2G5 mRNA for a potential ligend-binding protein	R.rattus RY2G5 mRNA for a potential ligend-binding protein	Homo seplens MAGE-B2 (NAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds	Human DNA, SINE repetitive element	Human DNA, SINE repetitive element	Hamo saplens chromosome 21 segment HS21C018	QV-8T087-301298-008 BT087 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C085	Human DNA, SINE repetitive element	Homo sapiens X-linked enhidrolito ectodermal dyspiasia protein gene (EDA), exon 2 and flanking repeat regions	H.saplens DNA for endogenous retroviral like element	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2908368 3'	Hamo sapiens chromosome 21 segment HS210002	zn30d08.r1 Stratagene neuroepithelium NTZRAMI 937234 Homo sapiens cDNA clone IMAGE;548943 6' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	EST368629 MAGE resequences, MAGC Homo sapiens cDNA	Homo seplens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	zq52h04.r1 Stratagene neurcepithellum (#937231) Homo sapiens cDNA clone IMAGE:645271 5	Home sapiens chromesome 21 segment HS210002	Home saplens chromesame 21 eagment 4/S21 Cob2	Homo saplens chromosome 21 segment HS21C010	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA done IMAGE:2319519 3' strillar to WP:F49C12.11 CE03371;
EXOII LIODE	Top Hit Database Source	EST HUMAN	F	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	Į.	N L	F	NT	EST_HUMAN	TN	NT	TN	NT	EST_HUMAN	IN	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	IN	TN	TN	EST_HUMAN
olugie	Top Hit Acession No.	.0E-25 BE162737.1	B923786 NT	8923786 NT	.0E-25 AA189080.1	.0E-25 AA582690.1			.0E-25 X80660.1	.0E-25 U93163.1	.0E-25 D14547.1	.0E-25 D14547.1	9.0E-28 AL163218.2	9.0E-28 Al905368.1	9.0E-26 AL163285.2	1.0E-28 D14547.1	.0E-26 AF003528.1	7.0E-26 X89211.1	7.0E-26 AW340163.1	.0E-26 AL163202.2	.0E-26 AA115895.1	7.0E-26 AW954559.1	3.0E-28 AF029308.1	3.0E-26 AA206131.1	3.0E-26 AL163202.2	5.0E-26 AL163202.2	3.0E-26 AL163210.2	5.0E-26 AI708235.1
	Most Similar (Top) Hit BLAST E Value	1.0E-25	1.0E-26	1.0E-25	1.0E-25	1.0E-25 /	1.0E-25	1.0E-25 X60660.1	1.0E-25	1.0E-26	1.0E-25	1.0E-25	9.0E-28	9.0E-28	9.0E-28	8.0E-28	7.0E-28	7.0E-26	7.0E-26	7.0E-26	7.0E-28	7.05-26	8.0E-28	8.0E-26	6.0E-26			5.0E-26
	Expression Signal	2.71	1.16	1.16	0.95	2.95	3.56	1.32	1.32	3.11	1.62	1.62	1.94	2.35	6.33	1.51	5.61	1.68	1.92	0.84	6.83	5.49	3.83	69.0	0.62	0.62	2.15	0.89
	ORF SEQ ID NO:	١		31384		33686	Ì	36388	36389		L	١					27840		30407		_				37400			27426
	SEQ ID NO:	18112		1	1	ì	1	1	1	1	ı	1	1	L.	L	1	L	ı	1	ı	1	L	<u> </u>	L	ł _	<u> </u>	L	LШ
	Probe SEQ ID NO:	4983	5298	5238	6697	6936	8038	9748	9746	11212	12280	12280	2553	11252	12140	5811	1608	4089	4275	5755	11966	12901	2300	3427	10753	10753	11979	1204

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acescion No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	9.0E-27 BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo saplens cDNA
0503	27760		5 02	. 9.0E-27	9.0E-27 U93163.1	Ż	Homo sepiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
							naa03c07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' sImilar to contains OFR.t1
12143	25118	-	6.6	9.0E-27	9.0E-27 BF445556.1	EST_HUMAN	OFR repetitive element;
;				100		POD POD	wyd9c04.xf NCI_CGAP_Lu19 Home sepjens cDNA clone IMAGE:2406160 3' similar to contains THR.b2 THR rendition element
F	13248	7074B	77.4	8.0E-2/	T	NOMOL IS	transpound of management HS21C027
571	13763		4.57	8.0E-27	8.0E-27 AL163227.2	Z	Tano sepiens anomosome z riseginent fraz Louzi
4 84	14891	27678	23.84	8.0E-27	8.0E-27 AW162737.1	EST_HUMAN	eda/nub.x1 Schneider Bala Drain Court france Sapiens CDNA Come Invace. 21 Sozza 3 Similia. IO 40: NO 30: TUBULIN ALPHA-1 CHAIN (HUMAN);
1448		27870		8.0F-27		EST HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo saplens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2236	ŀ	28499		8.0E-27	Γ	EST HUMAN	PM2-SN0018-220300-002-e07 SN0018 Homo capiens cDNA
							ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
3254	16428	29448	1.8	8.0E-27 P12238	P12236	SWISSPROT	NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3434	16602	28621	0.75	8.0E-27	8.0E-27 AF181897.1	NT	Homo sepiens WRN (WRN) gene, complete cds
5812		32308	1.07	8.0E-27	8.0E-27 AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
7117	1		2.65	8.0E-27	8.0E-27 BE926560.1	EST HUMAN	MR4-BT03398-260800-204-d06 BT0398 Homo saplens cDNA
7402	20057	33487	67 6		8 0F-27 N84970 1	EST HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo saplens cDNA clone J1751 6' similer to REPETITIVE ELEMENT L1
8410	ı	36048			B.0E-27 AW857579.1	EST HUMAN	CM1-CT0315-091299-063-407 CT0315 Homo saplans cDNA
9410		36049		8.0E-27	8.0E-27 AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo saplens cDNA
5		<u>.                                    </u>	1.77	7.0E-27	7.0E-27 Z70864.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19		7.0E-27 AW629172.1	EST_HUMAN	hi51h12.x1 Soares_NFL_T_GBC_S1 Horno septens cDNA clone IMAGE:2976879 3' similar to TR:076040 O76040 ORF2: FUNCTION UNKNOWN;
8908	ı		76.0		7.0E-27 D86984.1	NT	Human mRNA for KIAA0231 gene, partial cds
10988	24087		3.7	7.0E-27	7.0E-27 AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
10984		37679	3.21	6.0E-27	8.0E-27 M26697.1	TN	Human nucleolar protein (B23) mRNA, complete cds
							Homo sepiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
12094		38781	1,55		6.0E-27/U93163.1	L	(MAGE-B1) ganes, complete cds
7964	5,004		0.73		5.0E-27 AL163303.2	N.	Homo saplens chromosome 21 segment (1921C103
10442	23477			6.0E-27	6.0E-27 BF666614.1	EST_HUMAN	602/2149/F1 NIH MGC 56 Homo saplens cDNA clone IMAGE:42/852/ 5
10442		37082		┈┃	BF6661	EST_HUMAN	602121491F1 NIH_MGC_E6 Homo sapiens CDNA clane IMAGE:42/832/ 3
6883	20035		1.65	4.0E-27	9910569NT	N	Mus musculus sperm tall associated protein (Stap), mrnA

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מווקום ראסוון וסייסי באיניסיסים ווון ימיסיוים	. Top Hit Descriptor	Homo caplens chromosome 21 segment HS21C009	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	QVQ-OT0033-070300-152-b10 OT0033 Hamo sapiens cDNA	H. sapiens DNA for endogenous retroviral like element	Homo sapiens chromosome 21 segment HS21C079	R.rettus RYA3 mRNA for a potential ligarid-binding protein	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA	7844C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7844C08	601458531F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3882086 5	Homo sapiens alpha NAC mRNA, complote cds	nko1b10.e1 NCI_CGAP_P111 Homo capiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	hi51h12.x1 Sogres_NFL_T_GBC_S1 Hoino sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040 ORF2: FUNCTION UNKNOWN.;	Homo sepiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	Homo sepiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	y39e01.r1 Soares placenta Nb2HP Homo sapiens cDNA done IMAGE:150840 6' similar to SP:HMGC_MOUSE Q02591 HOMEOBCX PROTEIN;	wi28g07.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2426288 31	hh08h05.81 NCI_CGAP_Thy1 Homo sepiens cDNA done IMAGE:843737 similar to contains L1.t3 L1 repetitive element;	R.rattus RYA3 mRNA for a potential ligand-binding protein	EST00738 Fetal brain, Stratagene (cat#336206) Home saplens cDNA clone HFBCF07	EST00738 Fetal brain, Strategene (cat#938206) Homo sapiens cDNA clone HFBCF07	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5	ndo1510.51 NCI_CGAP_P111 Homo septens cDNA clone IMAGE:1000699 similær to gb::M17865 605 ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	Homo saplens putative MTAP (MTAP) miRNA, partial cds, alternatively oplicod	Homo saplens chromosome 21 segment HS21C040	Home sapiene DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Home contacts Retinantiative POL Journal (RPF-1) mRNA	
באסווו וסיים	Top Hit Database Source	LN	Ę	EST_HUMAN	TN	LN	ΙN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	TN	NT.	EST HUMAN	EST HUMAN	EST HUMAN	N N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	IN	N FN	Ę	1	IN C
A CHING	Top Hit Acession No.	4.0E-27 AL163209.2	4.0E-27 AF078779.1	4.0E-27 AW880859.1	(89211.1	4.0E-27 AL163279.2	(60658.1	3.0E-27 BE071924.1	3.0E-27 AA077705.1	3.0E-27 BF035327.1	2.0E-27 AF054187.1	2.0E-27 AA565345.1	2.0E-27 AW629172.1	2.0E-27 AF111167.2	2.0E-27 AF111167.2	102655.1	2.0E-27 Al866347.1	2 0F-27 AA551527 1	X60658.1	2.0E-27 M78590.1	2.0E-27 M78590.1	2.0E-27 AU121885.1	2.0E-27 AA565345.1	2.0E-27 AF216650.1	1.0E-27 AL163248.2	1 OF-27 AB026898 1	111	2000000
	Most Similar (Top) Hit BLAST E Value	4.0E-27	4.0E-27	4.0E-27	4.0E-27 X89211.1	4.0E-27	3.0E-27 X60658.1	3.0E-27	3.0E-27	3.0E-27	20E-27	20E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27 H02655.1	2.0E-27	2.05-27	2.0E-27 X60658.1	2.0E-27	2.0E-27	2.0E-27	2.05-27	2.0E-27	1.0E-27	1.05.27	יפרים	1.05-27
	Expression Signal	0.98	1.31	0.61	2.62	1.17	7.1	1.55	6.81	3.49	9.28	24.24	13.34	1.45	1.45	0.79	117	3,0	0.83	1.45	1.45	3.61	6.43	29.	234	70 7	18.	6.51
	ORF SEQ ID NO:			36577							26286			29489	29490	ì			36625					38791				33222
	Exan SEQ ID NO:	21207	ı	1		l.	L		1	ŀ	13280				1	İ	١	Щ.		L	L	<u> </u>		L	上		1	19833
	Probe SEQ (D NO:	8125	8172	8945	11903	13213	2030	4386	5462	999	42	1944	3178	3286	3000	8814	8282	0.469	9000	10241	10241	11197	Į.	12107	6449		1027	6874

PCT/US01/00663

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WO 01/57272

					•		
Probe SEQ ID	Exan SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Database	Top Hit Descriptor
_	Ö		Signal	SLASTE Value	g Ž	Source	
7010	20146	33566	1.65	1.0E-27	.0E-27 F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
7010	l		1.65	1.0E-27	.0E-27 F30158.1	EST_HUMAN_	HSPD20481 HM3 Homo sepiens cDNA clone s4000095C10
8803	ı	35430	1.16	1.0E-27	.0E-27 AB007923.1	TN	Homo sapiens mRNA for KIAA0454 protein, partial cds
9188	1		1.69	1.0E-27	.0E-27 BE079780.1	<b>EST_HUMAN</b>	RC6-BT0627-140200-011-E06 BT0627 Homo saplens cDNA
8923	22963	38551	2.65	1.0E-27		INT	Human mRNA for KIAA0260 gene, partial cds
12005	24990		3.05	1.0E-27	.0E-27 AF111093.1	, IN	Bos taurus latrophilin 3 spitce variant bbah mRNA, complete cds
144			2.26	ļ	9 0F-28 BE348399 1	EST HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313;
32	1	28567	2.17		9.0E-28 AU126260.1	EST HUMAN	AU126260 NT2RP1 Homo saplens cDNA clone NT2RP1000443 51
10601	23636			9.0E-28	Γ	EST_HUMAN	zp18g12.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:609862 3'
12224	26173		3.04	9.0E-28	9.0E-28 BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo saplens cDNA
	1						au83h08.x1 Sohncider fotal brain 00004 Homo capiens cDNA clone IMAGE:2782011 3' similar to
12565	26003		13.39		8.0E-28 AW157571.1	EST_HUMAN	1H:060302 060302 KIAA0656 PKO I EIN.; contains otement MEK.22 reportive element;
1208	14370		11.5	4	.0E-28 AU142750.1	EST_HUMAN	AU142750 Y79AA1 Homo septens cDNA clone Y79AA1000824 5'
11483	24522	38192	1.65	7.0E-28	11417856 NT	IN	Homo saplens gamma-glutemyltransferase-like activity 1 (GGTLA1), mRNA
12181	25141		5.04	7.0E-28	.0E-28 AV735348.1	EST_HUMAN	AV735348 CB Hamo sapiens cDNA clans CBFAKA12 5"
9119	22198		1.28	9	OE-28 AF016052.1	IN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
							ea60e03.rt NCI_CGAP_GCB1 Homo septions cDNA clone IMAGE:825340 5' similar to contains Alu
12866	25577		5.92	Θ	.0E-28 AA504582.1	EST_HUMAN	repetitive element,contains element PTR6 repetitive element;
							wo18c07.x1 NCI_CGAP_Pan1 Homo saptens cDNA clone IMAGE:2455692 3' similær to contains THR.b1
328	13542		2.75	į	5.0E-28 AI921003.1	EST_HUMAN	THR repetitive element;
4116	17270	30269	38.94		5.0E-28 R79762.1	EST_HUMAN	WB9110.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:146443 5
2689	16808	28926	1.46		4.0E-28 AW 195066.1	EST_HUMAN	xn33c09.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2895504 3' similar to SW:GG85_HUMAN Q08379 GOLGIN-95.;
3177					4.0E-28 BE409100.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo seplens cDNA clone IMAGE:3635305 5
7483	1			4	0E-28 Al198941.1	EST HUMAN	qf66ff0.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
	1.			l		<u> </u>	Uses sessions absonces a dissiliability the Treat recentive hate least transitioner name families
1165	- 1		4.1B			N.	
11255	24324		14.89	4	I.0E-28 AB038241.1	NT	Felis oatus GAPUH mixina tor giyosratae iyoonaya banasa, contraete cus
44979	20660	34030	78.7		4 0E-28 A1108041 1	FST HUMAN	iqf86f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:iM19503 LINE-1   REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12822	1	1			DE-28 AW854244 1	EST HUMAN	RC3-CT0254-240400-210-112 CT0254 Homo saplens cDNA
707	1.		,:		4141000000	FOT LIMANI	IDCO. CTT0370.0704.004. L04. CTT0370 Home series CDNA
12773	26069		1.02	1	.UE-28 AW 802330.1	NAMOR 163	

Page 264 of 550 Table 4 Single Exon Probes Expressed in Placenta

			T	7					1				 ā	T	T	1		<u> </u>	T	1			7	٦		0		Ī	Ī	Ī	٦
Top Hit Descriptor	Homo sapiens metalloproteasse-like, distntegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete ods	Homo sepiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	MR3-HT0713-280500-013-f09 HT0713 Homo sepiens cDNA	Homo sapiens MHC class 1 region	wj96f07xf NCI_CGAP_Lym12 Homo sapisens cDNA clone IMAGE:2410865 3' similær to contains Alu repefitive element:contains element HGR repetitive element ;	RC2-BT0642-210200-013-f03 BT0642 Homo caplens cDNA	Hamo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein related protein 2 (LRP2), mRNA	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41	qo35b06.x1 NCI_CGAP_Lu5 Homo capiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;	Hamo sapiens chromosome 21 segment HS21C009	hr 76c03.x1 NCI_CGAP_KId11 Homo sepiens cDNA done IMAGE:3134404 3' similar to contains LOR1.b1	LOR1 repetitive element ;	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5	Sus scrofa domestica submadilary apomucin mRNA, completa cds	EST384394 MAGE resequences, MAGL Homo sapiens cDNA	Homo saplens mannosidase, beta A, Iysosomai (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBE2D3) genes, complete cds	y/79c09.r1 Soares Infant brain 1NIB Homp sepiens cDNA clone IMAGE:44300 5	Human gene for Ahreceptor, exon 7-9	QV1-BT0821-120900-360-b03 BT0821 Homo capiens cDNA	Human zinc finger protein ZNF131 mRNA, partial cds	Homo saplens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA	EST179615 HCC cell line (matastasis to liver in mouse) Il Homo sapiens cDNA 5' end similar to similar to	retroviral LTR	Homo sapiens gamma-glutamytransferasie-like activity 1 (GGTLA1), mRNA	Homo sapiens gamma-glutamytransferasi-like activity 1 (GGTLA1), mRNA	251c01.r1 Soares retina N2b4HR Homo saplens cDNA clone IMAGE:380448 5	Homo sapiens chromosome 21 segment HS21CD47
Top Hit Database Source	NT		EST_HUMAN	卢	EST HIMAN	EST HUMAN	1	LN	EST_HUMAN	NT	EST HUMAN	LN.		EST HUMAN	EST_HUMAN	뉟	EST_HUMAN		NT	EST HUMAN	NT	EST_HUMAN	NT	N.	NT.		EST_HUMAN	TN	NT	EST_HUMAN	TN
Top Hit Acesslan No.	E-28 AF166382.1			3.0E-28 U63688.1			30460	11430460 NT				2.0E-28 AL163209.2	Γ	2.0E-28 BF224402.1			2.0E-28 AW972305.1		ſ			.0E-28 BF333236.1		11429885 NT	8922793 NT		.0E-28 AA308744.1	4758431 NT	4758431 NT		.0E-28 AL163247.2
Most Similar (Top) Hit BLAST E Value	3.0E-28 A	3.0E-28	3.0E-28	3.0E-28	4 RC-30 8	3.0E-28	3.0E-28	3.0E-28	2.0E-28	2.0E-28	2.0E-28	2.0E-28		2.0E-28	2.0E-28	2.0E-28	2.0E-28		2.0E-28	2.0E-28 H06376.1	1.05-28	1.0E-28	1.0E-28	1.0E-28	1.0E-28		_	1.0E-28	1.0E-28	-	[
Exprecsion Signal	2.29	0.94	2.28	2.08	   	3.29	122	1.22	12.79	9.24	2.16	0.81		1.48	8	0.83	2.23		2.52	1.74	2.85	3.91	0.95	1.95	3.03		4.75	5.91	L	7.68	4.56
ORF SEQ ID NO:			35647				31993			27411				32968		34837			38603		27744						36099				
SEQ ID	14468	18349	22108	1		1		ı		14353		1	1	19604	18827		<u> </u>	1_	24900	25424	L	L	L	L	L	L	22535		L	25145	1
Probe SEQ ID NO:	1312	5227	9027	11176	4.000	12803	12865	12865	9	1191	2546	3448		6437	6460	8234	9783		11913	12631	1508	2294	4691	8044	8208		9478	10080	10080	12186	13013

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	hi76g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978286 31	HYPOTHETICAL GENE 50 PROTEIN	EST378521 MAGE resequences, MAGI Homo sapiens cDNA	Rettus norvegicus mRNA for 45 kDa secietory protein, pertial	wp69b01.x1 NCI_CGAP_Brn25 Homo sepiens cDNA ctone IMAGE::2466985 3' stirtilar to 1R:015475   015475 UNNAMED HERV-H_PROTEIN ;contains LTR7.b1 LTR7 repetitive element;	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA	802184092F1 NIH MGC 42 Homo sapiens cDNA clone IMAGE:4300079 6'	Hamo septens chromosame 21 segment HS210003	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA	601451827F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3855726 5'	cn15c02.x1 Normal Human Trabocular Bono Collo Homo capient cDNA clone NHTBC_cn15c02 random	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2330170 3' sImilar to contains	MER29.t2 MER29 repetitive element;	wd36g08x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element;	Human 90 kD heat shock protein gene, complete cds	Homo sapiens PTS gene for 6-pyruvöyltefrahydropterin synthase, complete cds	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA	601162657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5	Human gene for Ah-receptor, exon 7-9	xv17f03.x1 Soares_NFL_T_GBC_S1 Horno sapiens cDNA clone IMAGE::2813406 3' similar to contains Alu repetitive element,contains MER19.t2 MER19 repetitive element;	Homo sapiens chromosome 21 segment HS21C048	ht0901.x1 NCI_CGAP_Kid13 Homo saplens cDNA done IMAGE:3146256 3' similar to contains MER29.b3 MER29.b3 MER29.b3	262b01.r1 Soares testis NHT Homo septiens cDNA clone IMAGE:726889 5' similar to TR:G1335769	G1335769 GAG-POL POLYPROTEIN. ;	Human HsLIM15 mRNA for HsLim15, complete cds	Human HsLIM15 mRNA for HsLIm15, complete cds	Homo sapiens envelope protein RIC-6 (env) gene, complete cds	Homo saplens envelope protein KIC-8 (env) gene, complete cas
Top Hit Database Source	EST_HUMAN	SWISSPROT	EST_HUMAN	LΝ	EST HIMAN	EST HIMAN	FST HUMAN	LN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	       	EST_HUMAN	EST_HUMAN	Ż	TN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	LN LN	EST HUMAN		EST_HUMAN	NT	NT	L	۲
Top Hit Acession No.	.0E-29 AW663987.1	3.0E-29 Q00130	7.0E-29 AW968447.1	7.0E-29 AJ132352.1	3 0E-20 A 1938748 1	A DE 20 REGADARA 1	3 0F-29 RE568097 1	3 0F-29 AI 163203 2	5.0E-29 AW887541.1	5.0E-29 BE612449.1	4.0E-29 AI752367.1	4.0E-29 BE164930.1		4.0E-29 AI678101.1	4.0E-29 AI678101.1	4 0F-29 J04988 1	3.0E-29 AB042297.1	3.0E-29 BF333238.1	3.0E-29 BE314018.1	3.0E-29 D38044.1	3.0E-29 AW303317.1	3.0E-29 AL 163248.2	3 0E-29 BE350127 1		3.0E-29 AA403053.1	3.0E-29 D63882.1	3.0E-29 D63882.1	2.0E-29 AF084869.1	2.0E-29 AF084869.1
Most Similar (Top) Hit BLAST E Value	9.0E-29	8.0E-29	7.0E-29	7.0E-29	8.05-20	A OF 20	8.0F-29	5 OF -29	5.0E-29	5.0E-29	4.0E-29	4.0E-29		4.0E-29	4.0E-29	4 0F-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29	3.0E-29		3.0E-29	3.0E-29	3.0E-29	2.0E-29	2.0E-29
Expression Signal:	1.8	72.57	1.98	9.03	ç	9.33	2 4	2 39	8.35	1.49	2.28	7.08		0.64	0.84	3.50	1.31		0.83		12		8	200	2.28	1.36	1.82		96:0
ORF SEQ ID NO:	31543		27870			/1007								34870	34871				]_		36119				38278				26728
Econ SEQ ID NO:	28122	L	L	l	<u>.</u>	13/9/	1	- 1	1		l	ı	1	21354	21354	L			1	L_		L	1	10363	24602	L			13699
Probe SEQ ID NO:	13135	12752	1632	13197	8	300	12480	1442	8020	12795	3304	6433		8272	8272	8044	4536	4855	6053	8931	9500	9731	79707	5	11546	12385	13092	505	502

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											_		_	_			··			<u> </u>	<u> </u>					_			*****	
	Top Hit Descriptor	w65d10.x1 NCI_CGAP_Ut1 Hamo septiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN);	wr65d10.X1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2492563 3' similar to TR:015546 016546 HERV-E ENVELOPE GLYCOPROTEIN ;	H.espiens mRNA for laminin-5, alpha3b chain	H, sapiens mRNA for laminin-5, alpha3b chain	Homo saplens chromosome 21 segment HS21C068	0s71e04.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.t2 L1 repetitive element;	wf27g07.x1 Scares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2356860 3' sImilar to contains	element MER6 repetitive element;	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo capienc cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;	601442208F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3846648 5	Homo sapiens DNA-binding protein (LOC56242), mRNA	Homo sapiens DNA-binding protein (LOC58242), mRNA	Homo sapiens chromosome 21 segment HS210048	Hamo saplens chromosome 21 segment HS210048	Homo sapiens chronosome 21 segment HS210048	Homo saplens chromosome 21 segment HS21C048	Homo sapiens splicing factor similar to drad (SPF31), mRNA	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA	R. rattus RYA3 mRNA for a potential ligand-binding protein	nr20c07;s1 NCI_CGAP_GCB1 Homo sapiens cDNA cione IMAGE:1288332 3' similar to contains MEK4.b1 MER4 repetitive element :	Homo sapiens zincliron regulated transporter-like (ZIRTL), mRNA	HSC23F051 normalized Infant brain cDNA Homo sapiens cDNA clone c-23f05	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat	PT2.1_13_B11.r tumor2 Homo sapiens clDNA 3'	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA	Human mRNA for integrin alpha subunit, complete cds	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds
#H GOL	Database Source	EST_HUMAN	EST_HUMAN	LN LN	ΝT	ΙΝΤ	FST HUMAN	r L	EST_HUMAN	EST HUMAN	EST HUMAN	NT	N	TN	N	ΤN	TN	LN1	EST_HUMAN	NT	FST HUMAN	LN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST HUMAN	EST_HUMAN	N
	Top Hit Acessian No.	2.0E-29 Al983604.1	2.0E-29 Al963604.1	2.0E-29 X84900.1	2.0E-29 X84900.1	20E-29 AL163268.2	2 OF -20 A1082459 1		2.0E-29 AI806418.1	2.0E-29 Al806418.1	2.0E-29 BE867157.1	10567821 NT	10567821 NT	2.0E-29 AL163248.2	2.0E-29 AL163248.2	2.0E-29 AL163248.2	2.0E-29 AL163248.2	11425108 NT	1.0E-29 AW 983880.1	1.0E-29 X60658.1	0 0E-30 04781215 1	11422746INT	8.0E-30 F08688.1	8.0E-30 AA383873.1	8.0E-30 AI557072.1	7.0E-30 BE091133.1	6.0E-30 D25303.1	6.0E-30 BE008028.1	6.0E-30 BE008026.1	6.0E-30 AF177227.1
<del> </del>	(Top) Hit BLAST E Vatue	2.0E-29	2.0E-29	2.0E-29	2.0E-29	20E-29	2 OE-20		2.0E-29	2.05-29	20E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	1.0E-29	1.0E-29	0.5-30	9 OF-30	8.0E-30	8.0E-30	8.0E-30	7.0E-30	6.0E-30	6.0E-30		
	Expression Signal	7.8	7.8	2.31	2.31	2.55	87.0		1.49	1.28	1.16	0.61	0.61	2.78	2.76	3.65	3.65	1.67	8.27	2.81	2 63	4.55	10.5	228	2.79	1.07	1.67	3.15		97.0
	ORF SEQ ID NO:	27794							32835	<u> </u>			L	ŀ	ì		l		35611	37503				35078		Ļ	28058			
	SEO D NO:	14718	1	1_	14831	17537	1	ļ	19481		24246	21856	21858	1	1	23479	L		L	L	40070	$\perp$	1	L	L	1_		L		_
1	SEQ ID NO:	1563	1563	1782	1782	4394	50.48	3	6309	7732	8464	8777	E E	9708	9708	10444	1949 1449	11767	8992	10850	0740	12268	8449	8465	8882	1646	1814	3259	4881	10760

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	lne)	SE:2116276 3' similar to contains Alu									INA clone IMAGE: 1938920 3' similar to	exone 1-6	plete cds	plete cds	GE:3146256 3' similar to contains MER29.b3			A CANADA	A clone 0-23105			9 003	ONA Gone IMAGE:2/22558 3	IE:3028438 5	35:3029438 5	NA clane GEN-570C01 5	GE:3284662 3' similar to SW:DHSA_HUMAN LAVOPROTEIN SUBUNIT PRECURSOR;	GE:3284662 3' similar to SW:DHSA_HUMAN LAVOPROTEIN SUBUNIT PRECURSOR;		
Top Hit Descriptor	Human lambda-immunoglobulin constant region complex (germline)	tegogos x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu propelling cloment:	reparation in	Human aconitate hydratase (ACOZ) gane, exon /	Homo capiens chromosome 21 segment HS21C078	Homo sepiens chromosome 21 segment HS21C010	Homo saplens chromosome 21 segment I-IS21C010	QV3-DT0043-090200-080-c06 DT0043 Homo saplens cDNA	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA	CM1-ST0181-091199-035-108 ST0181 Homo sapiens cDNA	qq93c05.x1 Soares_fotal_fetus_Nb2HF8I.9w Homo sapiens cDNA,clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive eleiment;	Homo sapiens telomerase reverse transcriptase (TERT) geno, exone 1-6	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	ht09g01.x1 NCI_CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MEK29.b3	MER29 repetitive element;	TRANSCRIPTION FACTOR AP-2	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA	HSC23F051 normalized infant brain cDNA Homo saplens cDNA clone c-23f05	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cUNA	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	Hamo sapiens Y-linked zinc finger protein (ZFY) gene, complete cas	UI-H-BI1-efo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA done IMAGE:2/225006 3	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5	C18339 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-5/0001 5	7e37c12.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P931040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR:	EST383857 MAGE resentiences, MAGI Homo sepiens cDNA	
Top Hit Database Source	TN.	MANUEL FOR	ESI HUMAIN	LN	N	LΝ	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	TN		EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	FOT UNANA	ביאוסום ו פש
Top Hit Acession No.	.0E-30 X51755.1	, 000000	5.0E-30.Al399992.1	5.0E-30 U87931.1	5.0E-30 AL163278.2	5.0E-30 AL163210.2	3.0E-30 AL163210.2	1.0E-30 AW837471.1	.0E-30 AW837471.1	.0E-30 AW812488.1	3.0E-30 A1338551.1	3.0E-30 AF128893.1	3.0E-30 AF078779.1	.0E-30 AF078779.1		3.0E-30 BE350127.1	P34056	2.0E-30 AW857315.1	2.0E-30 F08688.1	2.0E-30 BE175877.1	2.0E-30 BE765232.1	2.0E-30 AF114156.1	2.0E-30 AW 206581.1	2.0E-30 BE298945.1	2.0E-30 BE298946.1	2.0E-30 C18939.1	2.0E-30 BE670617.1	2 OF.30 RF670617.1	7 00274074	2.0E-30 AW9/1508.1
Most Similar (Top) Hit BLAST E Value	8.0E-30)	1	5.0E-30.7	5.0E-30	5.0E-30 /	5.0E-30	6.0E-30	4.0E-30	4.0E-30	4.0E-30	3.0E-30	ľ		ြိ		3.0E-30	3.0E-30 P34056	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30			2.0E-30	2.0E-30	2.05-30	2.05-30		
Expression Signal	1.75		43.22	5.79	2.12	2.78	2.76	2.38	2.38	1.56	4.56	1.15	0.53	0.45		0.74	1.52	1.42	2.53	5.5		6.83	1.95		2.02		17.1	121		3.78
ORF SEQ ID NO:			30274			38148	38149		28471			30013				37294	38211			27745		29179			31019		35452	CA / 3 C		36828
SEC ID	18485		17275	25928	24198	ŧ		L	ı	1	l	ì	1	1	l	23683	24541	L	L	L	15895	18162	17048		18030	L	21916	240	1	23238
Probe SEQ ID NO:	13161		4121	5353	11126	11423	11423	2210	2210	9106	1175	3863	8738	8883		10649	11482	692	1108	1509	2779	2986	3889	490	480	8734	9836	000	0000	10201

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Top Hit Descriptor	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similær to contains THR.b3 THR repetitive element;	C18939 Human placenta cDNA (TFujiwara) Homo saplens cDNA clone GEN-570C01 6	hd30b04.X1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element;	Hamo sapiens chromosome 21 segment HS21C003	ac77b08,s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'	602022560F1 NCI_CGAP_Brn87 Homo saplens cDNA clone IMAGE:4157991 5'	EST188888 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end	601809932F1 NIH_MGC_18 Homo eapiens cDNA clone IMAGE:4040694 51	MR0-BT0249-091289-101-g01 BT0249 Homo saplens cDNA	EST11698 Uterus Homo sepiens cDNA (f) end	CHR220532 Chromosome 22 exon Homo saplens cDNA clone C22_728 5'	yc65e08.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:86570 5'	yc65e06.r1 Stratagene liver (#937224) Homo saplens cDNA clone IMAGE:85570 5'	789b08.r1 Soares Infant brain 1NIB Horrio sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);	y/89b08.r1 Soares infant brain 1NIB Homo capiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-	RELATED PROTEIN RAB-2 (HUMAN);	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'	Rattus norvegicus putative four repeat lon channel mRNA, complete cds	Mus musculus syndecan 4 (Sdc4), mRNA	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA	Hamo sapiens chromosome 21 segment HS21C008	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 6' end	hw05a11 x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:3182012 3'	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012.3'	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds	601304125F1 NIH_MGC_21 Homo sapkins aDNA dane IMAGE:3638310 5	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapians MHC class 1 region
Yop Hit Database Source	EST_HUMAN	EST_HUMAN (		IN.	EST_HUMAN	EST_HUMAN (	EST_HUMAN	EST_HUMAN (			Г	EST HUMAN	EST_HUMAN				EST_HUMAN	INT			INT TN			П	Ι	TN	EST_HUMAN	ΙN	
Top Hit Acesslan No.	2.0E-30 AW 470791.1	.0E-30 C18939.1	97.1			.0E-30 BF347728.1	.0E-30 AA315045.1	.0E-30 BF183230.1	.0E-30 BE061586.1	.0E-30 AA299211.1		173025.1	.0E-31 T73025.1	.0E-31 R18214.1			I.0E-31 Z38293.1	9.0E-31 AF078779.1	6765441 NT	TN 6823389 NT	8.0E-31 AL163208.2	7.0E-31 AA372637.1	7.0E-31 BE326517.1	.0E-31 BE326517.1	.0E-31 AF208541.1	.0E-31 AF208541.1	.0E-31 BE408611.1	.0E-31 AF223391.1	3.0E-31 AF055068.1
Most Similar (Top) Hit BLAST E Vatue	2.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	-	Γ		1.0E-30	1.0E-30	9.0E-31 T73025.1	8.0E-31	9.0E-31		9.0E-31	9.0E-31	0.0E-31	9.0E-31	8.0E-31	8.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31	7.0E-31	6.0E-31	6.0E-31
Expression Signal	6.31	10.87	1.62	5.16	11.56	2.15	0.91	1.96	0.49	1.57	5.31	0.8	0.8	0.88		0.88	1.99	0.65	1.29	2.52	7.93	1.59	2.1	2.1	1.02	1.02	1.03	3.42	1.39
ORF SEQ ID NO:	36924		_			28782						30020				35136				L	L		28982						
Exan SEQ ID NO:	2322	L	<u> </u>	Ĺ	L	16658			l		L			i	1	21600	21904		<u> </u>	<u>L</u>	15811	L	15850	L		ı	ı	ł	1 1
Probe SEQ ID NO:	10287	762	551	734	2288	2533	3120	7801	8176	12786	12937	3862	3862	8518		8519	8825	8827	13183	1102	2484	729	2733	2733	8586	8595	9468	3769	8347

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Top Hit Descriptor	ht08g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;	AU119105 HEMBA1 Homo sapiens oDNA clone HEMBA1005050 5'	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'	Homo sapiens type I DNA topalsomerase gene, exon 8	Homo sapiens type I DNA topoisomerase gene, exon 8	7ko6f04.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone INAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT : conteins L1.t1 repetitive element ;	Hamo sapiens Xq pseudoautosomal region; segment 1/2	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP	ACETYLGALACTOSAMINYLTRANSFERASE) (UDF-GALNACFOLTPEPTIDE, NF- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNACFT1)	Hamo sapiens chromosome 21 segment HS21C080	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Rettus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens gene for ectivin receptor type IIB, complete cds	Homo saplens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA	Homo sapiens NADH dehydrogenase (utilquinone) 1 beta subcomplex, 8 (19kD, ASHI) (NDUFB8) mRNA	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA	Homo sapiens chromosome 21 segment HS210006	Horse mRNA for fertiin L-chain, complete cds	ZL06d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)	601458531F1 NIH_MGC_68 Homo septens cDNA clane IMAGE:3862086 5	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA	tg 44g05.X1 Soares_NFL_T_GBC_S1 Homo capiens cDNA clone IMAGE:21116723	DKFZp76191513_r1 761 (synonym: haniy2) Homo sepiens cDNA clone DKFZp761G1613 6'	ea88f11.s1 Stratagene fetal retina 937202 Homo sepiens cDNA clone IMAGE:838413 3' similer to contains THR:t2 THR repetitive element ;	UI-H-BI3-ekb-f-09-0-UI s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
Top Hit Database Source	EST_HUMAN	EST_HUMAN				TN		L		SWISSPROT	Γ		TN	NT	NT	NT	Ė	L	NT	NT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acessian No.	DE-31 BE350127.1	6.0E-31 AU119105.1			5.0E-31 M60694.1					0E-31 Q10473	30.2	5730038 NT	.0E-31 AF084464.1	11430273 NT	.0E-31 AB008681.1	6005871 NT	4826863 NT	11420329 NT	3.0E-31 AL163206.2	D14523.1	AA421242.1	P11174	3.0E-31 BF035327.1	AW838171.1	2.0E-31 Al393388.1	AL119245.1	AA458824.1	2.0E-31 AW444498.1
Most Similar (Top) Hit BLAST E Value	6.0E-31		ł	6.0E-31	5.0E-31	5.0E-31	5.0E-31	4.0E-31		4.0E-31		4.0E-31	4.0E-31	4.0E-31	4.0E-31	3.0E-31	3.0E-31	3.0E-31	3.0E-31	3.0E-31	3.0€-31	3.0E-31	3.0E-31	2.0E-31		2.0E-31		Ш
Expression Signal	0.76	1.43	3.7	2.54	3.39	3.39	1.29	3.02		1.14	2.09	1.57	0.48	1.55	2	1.75	8.04		1.61	2.59	0.65	2.03	3.47		1.05	222	4.63	
ORF SEQ ID NO:	35148	37689				26451				27878			37402			28897	34041	L		36397		L	L					31563
Exon SEQ (D NO:	21607		L	25947	1_	L			l	14794			l	L	25609	15782	20569	L	L	L	L		ᆫ	L	15420	15545	l	1 1
Probe SEQ ID NO:	8526	10976	12327	12459	197	197	8640	89		1642	1861	2849	10784	12787	12924	2660	7494	7883	8355	9779	10822	10867	.11421	1967	2288	2416	2511	5389

WO 01/57272 PCT/US01/00663

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					2		
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hit Descriptor
5829	19020	32326	3.43	2.0E-31	2.0E-31 BE350127.1	EST_HUMAN	ht09g01 x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
9277	22363		1.53	20E-31	2.0E-31 AA877784.1	EST_HUMAN	IND6704.81 NOL_CGAP_CO10 Hamo septens cDNA clone IMAGE:1161055 3' similer to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9408	22482	36046	3.46	2.0E-31	7661535 NT	NT	Homo sapiens B9 protein (B9), mRNA
10110	1		1-1	2.0E-31	2.0E-31 AV710948.1	EST_HUMAN	AV710848 Cu Homo sapiens cDNA done CuAALB07 6
10110	Į.	1	1.1	2.0E-31	2.0E-31 AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAAL B07 5
10280		36914	2.75	2.0E-31	2.0E-31 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5
10280	23315	36915	2.75	2.0E-31	2.0E-31 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838310 5'
12430	ı		3.49	2.0E-31	2.0E-31 AF148512.1	NT	Homo saplens hexokinase II gene, promoter region
12578	26202		2.59	2.0E-31	2.0E-31 AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
	ا			Lo	7	<u>!</u>	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
-	١	ĺ	18.81	1.05.51	1.0E-31 USS163.1	i.	(WACE, D.) gailes, complete to
1698			2.68	1.0E-31	1.0E-31 095371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1698	14848	27933	2.98	1.0E-31	1.0E-31 095371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1696	L		2.68	1.0E-31	1.0E-31 095371	SWISSPROT	OLFACTORY RECEPTOR 2C1
5407	L	31581	3.97	1.0E-31	1.0E-31 AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-e08_1 ST0220 Homo seplens cDNA
6281	L	ļ	2.57	1.0E-31	1.0E-31 AF048727.1	Į.	Homo sapiens minisatellite ceb1 repeat region
	<u> </u>	1					Bos taurus xenobiotic/medium-chain fatt/ acid.CoA ligase form XL-III mRNA, nuclear mRNA encoding
7441	_			1.0E-31	1.0E-31 AF126145.1	L L	mitochondrial protein, complete cds
9008	21055	34567	1.35	1.0E-31	1.0E-31 BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935233 5
40474	3LV CU	0802.6	ציי		1 0E-34   103161 1	Ę	Homo sepiens MAGE-82 (MAGE-82), MAGE-83 (MAGE-83), MAGE-84 (MAGE-84), and MAGE-81 (MAGE-81) cenes, complete cds
[	L	l					d21h03.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595
11158	24227	37857	2.35		1.0E-31 AI086434.1	EST_HUMAN	Q16595 FRATAXIN.;
8778	L	33327	2.19		9.0E-32 AV723976.1	EST_HUMAN	AV723976 HTB Hamo sapiens cDNA clane HTBAAG01 6
7530	1				9.0E-32 L31770.1	N	Bos taurus vacuolar H+-ATPase subunit mRNA, complete cds
7768	ı				11430822 NT	Ā	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2139	1	28397		8.0E-32	8.0E-32 AI056770.1	EST_HUMAN	oz 16a09.x1 Soares_fetal_liver_splean_1NFLS_S1 Homo saplens cDNA clone IMAGE:1875384 3'
5599	l	l	0.77	8.0E-32	8.0E-32 AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
90767	20020		000		Z 0E-92 V17383 1	F2	Human chromosome 22 immunoglobulin V(K)I gene, part. With 5 breakpoint between orphon and preinhouring non-amplified rection
12400	- 1		2007	ĺ.	DE00010 1	1444 TO 1	COMERCEDICAL MILE MAN continue a DMA drane 1140.CE - 2013.087 G
7523	20596		1.32		6.0E-32 BE888016.1	ESI_HUMAN	TOTAL 1930FT INIT WIND A THE TOTAL COURS INVEST: 30 1300 C

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ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal Value	2.5 6.0E-32 AA864653.1 EST_HUMAN	27282 10.42 6.0E-32 AF116827.1 NT	1.64 4.0E-32 AL163246.2 NT	34326 3.4 4.0E-32 11432574 NT	34327 3.4 4.0E-32 11432574 NT	0.93 4.0E-32 BE064410.1 EST_HUMAN	26699 2.64 3.0E-32 Y17293.1 INT	27721 15.82 3.0E-32 AV731500.1 EST_HUMAN	28168 0.75 3.0E-32 5174574 NT		29169 0.76 3.0E-32 51/45/4(N	38221 3.1 3.0E-32/AV758634.1 ESI_HUMAN	38222 3.1 3.0E-32 AV758634.1 EST_HUMAN	37868 3.43 3.0E-32 AA777621.1 EST HUMAN	7.95 3.0E-32 BE279086.1 EST_HUMAN	29168 4.86 3.0E.32 6174574 NT	29169 4.95 3.0E-32 5174574 NT	6.47 3.0E-32 BE279086.1 EST_HUMAN	32907 0.89 2.0E-32 M35418.1 NT	33166 5.55 2.0E-32 Z38133.1 NT	33157 5.65 2.0E-32 Z38133.1 NT	35085 3.34 2.0E-32 AA114294.1 EST_HUMAN	35086 3.34 2.0E-32 AA114294.1 EST_HUMAN	31923 1.28 2.0E-32/AV736449.1 EST_HUMAN	31924 1.28 2.0E-32 AV736449.1   EST_HUMAN	1.0E-32 BE743289.1 EST_HUMAN	33476 6.64 1.0E-32 11439789 NT	35413 4,56
ORF SEQ ID NO:				١	1	l																						1 1
S Exon SEQ ID NO:	26181	L	L	İ	1	1	1	L		1	- 1	- 1	94 22649	76237	L		43 16149	ı	82 19551	6608 19768	1	8473 21554	1	L	L	L	L	
Probe SEQ ID NO:	12869	1059	ő		7779	8554	4	1484	2073		2973	9594	9594	44.166	12433	12843	12843	130	6382	89	8	8	8	13154	Ę	3163		87

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Top Hit Descriptor	hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 088539 WW DOMAIN BINDING PROTEIN 11.;	Homo sapiens calcium channel alpha1E: subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spiloed	602021164F1 NCL_CGAP_Bm67 Hamp sepiens cDNA done IMAGE:4156670 5	Homo sepiens chromosome 21 segment HS21C080	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA	to12b09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element:	AV730056 HTF Homo septens cDNA clone HTFAVEO6 5'	EST383398 MAGE resequences, MAGI. Homo sepiens cDNA	Human HLRP mRNA for leukocyte common antigen-related peptido (protein-tyrosine phosphate) (EC	3,1,3,48)	602021164F1 NCI_CGAP_Bm67 Homo saplens cDNA done IMAGE:4156870 5	EST383657 MAGE resequences, MAGI. Homo saplens cDNA	no16h01.s1 NCL_CGAP_Phe1 Homo seplens cDNA dane IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element ;	Homo sapiens chromosome 21 segment HS21 C085	HSPD21201 HM3 Homo sepiens cDNA clane 64000107H06	HSPD21201 HM3 Hamo sepiens cDNA clone s4000107H06	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA	Mus musculus SRY-box containing gene 6 (Sox6), mRNA	Mus musculus SRY-bax containing gene 6 (Sax6), mRNA	QV1-FT0169-100700-271-aC2 FT0169 Homo sapiens cDNA	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC6A7), mRNA	Homo sapiens spermidine synthase (SRM) mRNA	Homo sapiens spermidine synthase (SRM) mRNA	Homo sapiens chromosome 21 segment HS21C085	Homo sepiens mRNA for KIAA0699 protein, partial cds	xq33f11.x1 NCI_CGAP_Lu28 Homo septens cDNA clone IMAGE:2782461 3	2433f11x1 NCI_CGAP_Lu28 Homo sapiens cUNA clone IMAGE:2/32491 3
Top Hill Database Source	hw EST_HUMAN W	T LN	T HUMAN				to'	T	Г	Τ	NT 3.		EST_HUMAN E	EST HUMAN re	Г	EST_HUMAN H	EST_HUMAN H					EST_HUMAN Q						П	EST_HUMAN X
Top Hit Acession No.	0E-33 BE327112.1		Ī		5031736 NT	5031736 NT	0E.33 AISB0115 1	7.0E-33 AV730056.1	0F-33 AW971307 1		0E-33 X54890.1		7.0E-33 AW971568.1	7.0E-33 AA601416.1	AL163285.2	F30631.1	6.0E-33 F30631.1	J04038.1	11429198 NT	6755609 NT	8.0E-33 6785609 NT	BF373515.1	11141884 NT	4507208 NT	4507208 NT	5.0E-33 AL163285.2	AB014599.1	5.0E-33 AW 264679.1	AW 264679.1
Most Similar (Top) Hit BLAST E Value	9.0E-33	0 00 33	9.0E-33	9.0E-33	7.0E-33	7.0E-33	7.05-33	7.0E-33	7.0F-33		7.0E-33	7.0E-33	7.0E-33	7.05-33	8.0E-33	6.0E-33	6.0E-33	6.0E-33	6.0E-33	8.0E-33	6.0E-33	5.0E-33	5.0E-33	6.0E-33	5.0E-33	5.0E-33	5.0E-33	5.0E-33	5.0E-33
Expression Signal	8.4	2.57	1.84	4.55	2.73	2.73	3 04	7.85	15	2	0.87	1.88	1.59	9.74	0.93	0.91	16.0	1.86	3.12	2.03	2.03	1.9	1.32	1.63	1.63	2.92	99'0		0.82
ORF SEQ ID NO:			35607		26320							37777	38258	32082		32717			35517		36840			28190					37098
SEQ ID	16735	l		1			45962	П		1	22226	24142		1	1	L	L	<u>L</u>	ı		23250	1	15074	15090	L	<u> </u>	17319	1 1	23489
Probe SEQ ID NO:	3570	į	8089	11038	28	62		27.14	32.4	3	9147	11067	11526	12413	3830	6192	6192	8778	8833	10214	10214	1818	1831	1947	1947	2346	4169	10454	10454

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Тор Hit Descriptor	Homo sapiens ubiquitin protein ligase E3A (human papilioma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo saplens chromosome 21 segment HS21C007	Homo sapiens RAB1, member RAS chicogene family (RAB1) mRNA	ab51b11.r1 Stratagene lung carcinoma 937219 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;	Homo sapiens chromosome 21 segment HS21C010	UFH-BI2-ahlc-03-0-UI.s1 NCI_CGAP_ISub4 Homo sapiens cDNA clone IMAGE:2727149 3'	271a08.r1 Stratagene colon (#937204)/Homo sapiens cDNA done IMAGE:610038 6' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA	Homo sapiens polymerase (DNA diroctid), alpha (POLA), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	MER29 repetitive element;	AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'	ak32b12.s1 Soares_tests_NHT Homo septens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE. ;,	db67g03.x1 Soares_fetal_heart_NbHH19W Homo saptens cDNA clone IMAGE:1705204.3' similar to contains OFR.t1 OFR repetitive element:	qb67g03.x1 Soares_fetal_heart_NbHH;6W Homo sapiens cDNA clone IMAGE:1705204 3' similar to	contains OFR.tt OFR repetitive element;	MRO-HT0405-160300-202-d08 HT0405 Homo saplens cDNA	ab51g11.r.1 Stratagene lung carcinoma 937218 Homo sepiens cDNA clone IMAGE:844388 5' similar to	gB:X00/34 cas1 10BULIN BELA-5 CHAIN (HOWAIN)	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), miXNA	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA	ql96d01.x1 Soares_NhHMPu_S1 Home sapiens cDNA clone IMAGE:1880161 3'	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1075973 3' similar to gb:M28336 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);	Homo sapiens X-linked anhidrotito ectoclermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
Top Hit Database Source	FZ	Z	Ę	EST_HUMAN	Ε	EST_HUMAN	EST_HUMAN	Z	ΕŽ	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN		EST HUMAN	INT	LN.	EST_HUMAN	EST HUMAN		Ā	N-
Top Hit Acession No.	11433063 NT	4.0E-33 AL163207.2	4758987 NT	0E-33 AA626621.1	.0E-33 AL163210.2	4.0E-33 AW 293349.1	.0E-33 AA063053.1	FN 4685888	FN 4685888	3 0E-33 BE350127.1		3.0E-33 BE350127.1	3.0E-33 AV647851.1	.0E-33 AA861510.1	2.0E-33 AI160189.1		2.0E-33 Ai160189.1	2.0E-33 BE159039.1		AA626683.1	11421332 NT	2.0E-33 11421332 NT	.0E-33 AI277492.1	0E-33 A1052258.1		.0E-33 AF003528.1	.0E-33 M13975.1
Most Similar (Top) Hit BLAST E Value	5.0E-33	4.0E-33	4.0E-33	4.0E-33	4.0E-33	4.0E-33	4.0E-33	4.0E-33	4.0E-33	3.05-33		3.0E-33	3.0E-33	3.0E-33	2.0E-33		2.0E-33	2.0E-33	L					,			
Expression Signal	1.45	2.25	3.37	1.16	4.78	2.38	24.75	0.79	0.79	5.62		5.83	1.16	. 0.87	1.67		5.53	4.53		۳	1.6	1.6	1.39	2.15			0.86
ORF SEQ ID NO:			28454			30722			L					37298							31294	31295					34113
Exan SEQ ID NO:	25165	١.	1		L.		18717	L	L			14278	16084	1	1	1	13256	17877	l	- 1	18325	18325	ŀ	77802	L		20637
Probe SEQ ID NO:	12212	1162	2184	2491	2610	4806	5519	6522	6522	4443		1114	2522	10655	ŧ		107	4539		5100	5204	5204	6553	830.1		9	7585

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Table 4

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PLEXIN 4 PRECURSOR (TRANSMEMORANCE PROTEIN SEX)	SWISSPROT	2.0E-34 P51805	Г	8.64		24492	11431
MER29.12 MER29 repetitive element:	EST_HUMAN	2.0E-34 AI678101.1		0.75	35775	2 22230	9152
wa39J00X1 Oceres VFL T GRC S1 Homo sepiens cDNA clone IMAGE:2330170 3' similar to contains	EST_HUMAN	2.0E-34 AI678101.1		0.75	35774	2 22230	9152
601438531F1 NIFT_MGC_so nome septems colves clear allocations IMAGE:2330170 3' similar to contains	EST_HUMAN	3.0E-34 BF035327.1	3.0E-34	2.96		24481	11420
Human ig germine H-chain U-region genes, paruai cus	3	3.0E-34 M37277.1		0.66	32890	19531	6361
601874850F1 NIH_MGC_54 Homo sapiens CUNA cione IMAGE: 4102213 3	EST HUMAN	4.0E-34 BF209778.1	4.0E-34		П	П	9238
elG5c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE: 140/9003	EST_HUMAN	4.0E-34 AA861773.1	4.0E-34		П	┪	6981
Homo sapiens splicing factor 3a, subunit 3, BUKU (ST3A3), MRNA	8 NT	5803166 NT	4.0E-34	6.0		┪	3241
tt94c06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone INAGE.2249194 3	EST_HUMAN	4.0E-34 AI804667.1	4.0E-34	2.09	28309	П	205
Homo sapiens chromosome 21 segment Hozi Cure	NT	5.0E-34 AL163209.2	5.0E-34	1.83		П	11632
Homo sepiens mRNA for KIAA 1435 protein, partial cos	NT	5.0E-34 AB037856.1	5.0E-34	2.02	П	П	10890
Rattus norvegicus putative four repeat ion channel mixiva, complete cus	NT	5.0E-34 AF078779.1	5.0E-34	1.17	35693	┑	9067
Human splicing factor SRp55-1 (SRp-55) mRNA, complete cas	NT	5.0E-34 U30883.1	5.0E-34	5.24	31257		5173
Homo sapiens Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newbr (LOC31/29), ill Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-binding protein Newse-bin	NT	7706500 NT	5.0E-34	3.16		15072	1929
	NT	U03686.1	6.0E-34	2.22	32099	25216	12290
PM0-BN0086-100300-001-c00 BN0065 Homo sapiens CUNA	EST HUMAN	6.0E-34 AW998611.1	6.0E-34	1.58		╗	5247
Human G2 protein mRNA, partial cds	ZT	6.0E-34 U10991.1	6.0E-34	1.74		╗	- &
Human G2 protein mRNA, partial cds	NT	6.0E-34 U10991.1	6.0E-34	1.74	26711	╗	8
y14c10.r1 Scares placenta Nb2HP Homo sapiens cDNA cione IMAGE:146722 o	EST_HUMAN	7.0E-34 H12866.1	7.0E-34	3.85		П	12482
yd15e05./1 Soares fetal fivor spicen 1NFLS Homo captene cUNA cione IMAGE: 108320 5	EST_HUMAN	7.0E-34 T70845.1	7.0E-34	0.54		П	10204
yd15e05.rd Soarec fotal liver spieen 1NFLS Homo sapiens cUNA clone IMAGE: 108320 5	EST_HUMAN	7.0E-34 T70845.1	7.0E-34	2.5			1476
MR4-BT0399-200100-001-h03 BT0399 Homo sapiens CUNA	EST_HUMAN	8.0E-34 BE069882.1	8.0E-34	0.67		╗	7974
QV2-BT0258-071299-019-g07 BT0258 Homo sapiens cDNA	EST_HUMAN	8.0E-34 BE:062570.1	8.0E-34	1.93	30739	17767	4620
Homo septens hypothetical protein FLJ10900 (FLJ10900), mKNA		8922751 NT	8.0⊑-34	96.0	28501	٦	2240
Homo sapiens Xq pseudoautosomal region; segment 1/2	NT	9.0E-34 AJ271735.1	9.0E-34	4.77	1	П	13179
AV727809 HTC Homo sapiens cDNA clone H I CCNC12 5	EST_HUMAN	1.0E-33 AV727808.1	1.0E-33	2.19	31979	٦	12980
	NT	1.0E-33 AF003528.1	1.0E-33	5.7		13247	12929
Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	⅃					Т	16,00
RC5-NN1055-260400-021-G03 NN1055 Homo saplens cDNA	EST HUMAN	1.0E-33 AW904491.1	1.0E-33	1 25		Т	12768
Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cde	_	1.0E-33 U60822.1	1.0E-33	2.44	38652	Т	11962
QV3-BN0047-230200-102-b03 BN0047 Homo sepiens cDNA	EST_HUMAN	1.0E-33 AW996818.1	1.0E-33	1.56	38340	Т	11602
Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	NT	1.0E-33 U60822.1	1.0Ε-33	1.4		26229	10227
		₹ 	BLASTE Value	Signal	ō NO:	NO:	NO SEC
Top Hit Descriptor	Top Hit	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Ewan	Probe

7L7LS/I0 OM

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Table 4

Single Exon Probes Expressed in Placenta

I AMPRIMITATIVE THE CALL AND ASSESSMENT PROPERTY.	N	0.UE-30 AB-232.1	0.05-33	0.07	30524	21985	8906
- 13		0000921	T		I	Τ	8081
Home serious trate frontional demain (PTPRF interaction) (TRIO) mRNA	ES! HUMAN	AV/29/1			Ī	Г	4164
Thomas septens zing linger protest ago (Zivi Avo), ilivian	q	6005975 N		4.83		15166	2025
enbandas, teas with Home septens convenient towards a	EST_HUMAN	AA75711		1.06		14598	1445
Homo eapiene phosphatoyinositol glycan, class t. (Piot.), mixiva	NT	11425417 NT	7.0E-35	1.61	33164	19773	6613
	EST_HUMAN	8.0E-36 BF569282.1	8.0E-36	5.89		25283	12404
	EST_HUMAN	8:0E-35 BE378480.1	8:0E-35	1.53	37645	24011	10929
	EST_HUMAN	8.0E-35 BF,183195.1	8.0E-35	2.61	31097	18118	4989
	EST HUMAN	8.0E-35 BF 589937.1	8.0E-35	3.63	28020	14926	1776
nga33a08x1 NCI_CGAP_Kid11 Homo septents curva cione invasce:32200134 3 similar to TR-075012 DIACYLGLYCEROL KINASE IOTA.;	EST_HUMAN	8.0E-35 BF 589937.1	8.0E-35	3.63	28019	14925	1776
Homo sapiens promblen (PHB) mixing	NT	6031190	8.0E-35	7.21		13453	232
hh77b06.91 NCL_CGAP_GUT Homo sapiens cuiva ciune limage: 2ecoror o	EST_HUMAN	AW 6633	9.0E-35	1.3	29800	16896	3735
	NT	1.0E-34 ALH63210.2	1.0E-34	5.84		25660	12950
CG31611.s1 NC  CGAP_GC31 Homo eaplans cUNA cichia IMAGE:1331310-3 simulat co go:x00243 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);	EST_HUMAN	1.0E-34 AA807097.1	1.0≣-34	2.44		26125	12680
Homo sapiens nucleobindin 2 (NUCB2), mkina	NT	11439599 NT	1.0E-34	2.92	38202	24532	11473
601470592F1 NIH_MGC_57 Homo sapiens cUNA cione IMAGE:36/34/6 3	EST HUMAN	1.0E-34 BE781780.1	1.0Ε-34	1.51	38187	24518	11459
	EST_HUMAN	1.0E-34 BE781790.1	1.0E-34	1.61		24518	11459
	EST_HUMAN	1.0E-34 AL036635.1	1.0E-34	8.07		22038	9898
OLFACTORY RECEPTOR-LIKE PROTEIN F5	SWISSPROT	P23266	1.0E-34 P23266	0.54		22592	9527
601484430F1 NIH_MGC_69 Homo saplens cDNA clone IMAGE:3888999 5	EST_HUMAN	1.0E-34 BE:874052.1	1.0Ε-34	2.26		19440	6286
	EST_HUMAN	1.0E-34 BE874052.1	1.0E-34	2.26	32787	19440	6266
RC2-BT0506-240400-016-h08 BT0506 Homo sepiens cDNA	EST_HUMAN	1.0E-34 BE071414.1	1.0E-34	8.26		17739	4802
Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds	NT	.0E-34 AV009397.1	1.0E-34	0.79		17331	4181
Hamo sepiens WNT3 precursor (WNT3) mRNA, complete cds	T	.0E-34 AY009397.1	1.0E-34	0.79	30323	17331	4181
Homo sepiens X-linked anhidrotto ectodermal dysplasia protein gene (EUA), exon z and tianking repeating regions	NT	1.0E-34 AF003528.1	1.0E-34	2.51	29927	522891	3764
AU136024 PLACE1 Homo sapiens cDNA clone PLACE1003383 5	EST_HUMAN	1.0E-34 AU136024.1	1.0E-34	7.18			1738
ADP,ATP CARRIER PROTEIN, LIVER ISOFORM 12 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)	SWISSPROT	P12236	1.0E-34 P12236	10.13	27767	14687	1534
PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)	SWISSPROT	P51805	2.0E-34 P51805	8.54	38157	24492	11431
	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Velue	Expression : Signal	ORF SEQ	SEQ ID	Probe SEQ ID NO:
		9.19					

7/2/5/10 OM

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Table 4

Single Exon Probes Expressed in Placenta

W/03a05.x1 NCI_CGAP_GC8 Homo sapiens cDNA clane IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;	EST_HUMAN	3.0E-35 AVV003063.1		1.6	3 . 37022	23413	10378
Homo sapiens calcium channel aiphai E subunii (CACIMA IE) gene, exons i mo, and percer out, and neurory spliced	NT	3.0E-35 AF223391.1		1.45		22738	9689
	EST_HUMAN	3.0E-35 BF/433100.1		23.43	31635	18856	5456
(1/2589 X NC) CGAP LU24 nono sepiens cuna cione invase: 350301 3 similar lo 17. 45421 (1902H7 F-BOX PROTEIN FBL2;	EST_HUMAN	3.0E-35 BF433100.1		23.43	31634	18656	5456
Homo sapiens phospholipid scramblase 1 gene, complete cas	ZT	3.0E-35 AF224492.1		2.64	ŭ	15539	2408
601125260F1 NIH_MGC_8 Homo sapiens CUNA Gone INVAGE 3345063 5	EST_HUMAN	3.0E-35 BE268182.1		33.92	27843	14763	1610
Homo saplens Y-linked zinc finger protein (2FY) gene, complete cas	NT	4.0E-35 AF114156.1		2.5	38786		12098
DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens CUNA Clone UKFZp434L148 3	EST_HUMAN	4.0E-35 ALI046596.1		8.0.8	35332		8715
MER29 repetitive element;	EST_HUMAN	4.0E-35 BE350127.1	4.0E-35	1.67		20437	7358
PTR5 repetitive element;	EST_HUMAN	4.0E-35 H91193.1	4.0E-35	11.21	28114	15008	1862
yu98a07.rl Scares fetal liver spicen 1NFLS Homo sepiens cDNA clone IMAGE:241236 5 similar to contains							
601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5	EST_HUMAN	4.0E-35 BE257807.1	4.0E-35	20.46	27703	14619	1465
zh84f12.rd Soares_febal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428013 つ	EST_HUMAN	5.0E-35 AA001786.1		2.54		╗	11451
qg38c05.x1 Soares_testis_WHT Homo sapiens cDNA cicre MAGE:183/1445 3 similar to SW Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249;	EST_HUMAN	5.0E-35 Al 208765.1	5.0E-36	2.17	35016	21486	8405
qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA cicno MANGE:183/1445 3 similar to SW:Y249_HUMAN Q82539 HYPOTHETICAL PROTEIN KIAA0249.;	EST_HUMAN	5.0E-35 Al 208765.1	5.0E-35	2.17	35015	21486	8405
601431984F1 NIH MGC / Z Homo sapiens CUNA Cidne Invision 1972 1971	EST HUMAN	5.0E-35 BE890992.1	5.0E-35	4.25		21459	8378
cds; metann pseudogene and glucocereniosidass pseudogenia, and unoninosponiania (111122) yenra, paramicols	Z	6.0E-35 AI-023268.1	6.0E-35	1.72	30653	17667	4529
Homo saplens clk2 kinase (CLK2), propin1, cote1, gliucocerebrosidase (GBA), and metaxin genes, complete					$\neg$	_ [	
Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA	NT	6912639	5.0E-35	2.87		Т	3074
Homo saplens mRNA for KIAA0406 protein, partial cds	TN	5.0E-35 AB007866.2	5.0≅-35	0.99		П	2844
H. sepiens immunoglobulin keppa light chain variable region L14	NT	5.0E-35 X63392.1	5.0E-35	2.25		$\Box$	1746
Homo sapiens carbamy phosphate synthetese I mRNA, complete cds	N	5.0E-35 AF154830.1	5.0⊑-35	0.61		13373	14
Homo saplens mRNA for KIAA1365 protein, partial cds	NT	6.0E-35 AB037786.1	6.0⊑-35	2.97		23145	10107
Human mRNA for KIAA0388 gene, partial cds	3	6.0E-35 AB002364.1	6.0E-35	0.61	٦	22907	9867
H. sepiens mRNA for novel T-cell activation protein	TN	6.0E-35 X94232.1	6.0E-35	0.57	35525	21985	8908
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
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Placenta	

2826	2607	932	771	771	47	47	13056	12931	12342	12342	12157	12157	11036	7253	7283	5700	4792	4019	4010	3847	3386	3386	2748	2292	1215	111	Probe SEQ ID
15940	15730	14107	13952	13952	13286	13280	16005	25814	25247	25247	16556	16556	24115	20336	20336	18894	17927	17176	17176	16810	16556	16556	15865	15424	14376	16005	Exon SEQ ID NO:
29050	2884/		27001			26295	26372		32112	32111	29571		37749		33785	32186		30185	30184		29571	28570	28976	28558	27436	26372	ORF SEQ
1.34	1.08		35.82				1.74	7.22	1.33	1.33	1.22	1.22	2.93		9.0	1.93	3.01	0.85	0.85	0.77	1.08	1.08	. 1.13	4.56	1.89	1.25	Expression Signal
	1.05-30			Γ				Ţ			2.0€-35	П														•	Most Similar (Top) Hit BLAST E Value
1.0E-35 BE350127.1	7,00001141	167947.1	1.0E-35 AVV 3894 /3.1	1.0E-35 AW389473.1	1.0E-35 AA631949.1	1.0E-36 AA631949.1	2.0E-35 N88965.1	2.0E-35 AL163210.2	2.0E-35 BE904978.1	2.0E-35 BE904978.1	6912459 NT	-	2.0E-35 X59417.1	2.0E-35 BE832636.1	2.0E-35 BE832636.1	2.0E-35 BF332417.1	2.0E-35 H49239.1	20E-35 BE247575.1	2.0E-35 BE247575.1	20E-35/AB020/02.1	6912459 NI		A\V6650	2.0E-35 AB018413.1	2.0E-35 T11909.1	2.0E-35 N88985.1	Top Hit Acessian No.
EST_HUMAN	1	EST_HUMAN	EST_FICKIAN	EG LINAN	EST HUMAN	EST HUMAN	EST_HUMAN	2	EST_HUMAN	EST HUMAN	1	NT	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	2	2	Z	EST_HUMAN	3	EST_HUMAN	EST_HUMAN	Top Hit Database Source
	hingand at NCI CGAP Kild13 Homo septens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	SP-A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN;  Homo spaines hopothelical protein (LOCS1233), mRNA	habaant rt Spares falal liver spieen 1NFI S Homo saplens cDNA clone IMAGE:115752 5' similar to	11.2 ST0162-131000-008-11-2 ST0162 Homp sepiens cDNA	11 2 STO162-131000-008-412 ST0162 Homo sapiens cDNA	For the Designation of the Specific of NA library Homo sapiens cDNA clone CR12-1	REPETITIVE ELEMENT	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to	2		Homo sapiens Groz-associated private a (NACOS) I J. III MACE Associated S.	Homo sapiens Groz-essociated pinder Z (NIANOST) FIBNA	H. sapiens PROS-27 MRVA	CM2-M10125-280700-297-GUZ M10120 Horno sepiens CZMA	CM2-M 10125-280700-297-G0Z M 10120 Floring Superior CM2-M	QV0-B10701-210400-199-504 B10701 Homo sapiens colve	M18812.ri Soares Jerai Iver spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spiedni Iver Spi	CDNA clone TCBAP4328		TCRAPPE4328 Pediatric pre-B cell acute lymphoblastic leukernia Baylor-HGSC project=TCBA Homo sapiens	Home seniens mRNA for KIAA0895 protein, partial cds	nono sapiens Groz-associated binder 2 (Kindans71) mRNA	SW:TR12_HUMAN_Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;	Homo sapiens mknva for Gaba, complete cos	A9/11 Heart Homo septens GUINA Ciune Ae/1	REPETITIVE ELEMENT	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

	143	TOE-SOLD COCCOUNT		27.30	32040	23388	1/25/0
- 1	1	7.00-30 000072.			Γ	Т	/832
	3	1 00073 1	T		T	Т	
Human carcinoembryonic entigen gene family member 12 (CGM12) gene, excens L and L/N	NT	7.0E-36 U06672.1			٦	Т	7837
ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MIGHT 1) (MIGHT 1)	SWISSPROT	7.0E-36 Q27409		1.09	2 31361		5273
	SWISSPROT	7.0E-36 C27409		1.00	31360	18392	6273
Homo septens C-terminal binding protein a (C) and ) mixture	NT	4557498 NT		5.25		16363	3188
CM1-C10315-091288-063-007 C10315 nomo septens curva	EST HUMAN	AW8575			29192	16173	2997
EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR	EST_HUMAN	8.0E-36 AA348480.1		0.78	36070	22504	9430
B. DOWS BESC MIXINA TOF SCHOOL IN	Z	8.0E-36 X78479.1		0.67	32650	18310	6131
OUTOBEOGRAPH INTERNATION SEPTEMBER CONTRA CHOICE WAS OF LABORS OF A	EST_HUMAN	1.0E-35 EE792832.1	Γ		Γ	26539	12806
Homo sapiens casen kness i, eparen (Volky IC), mixiky	ONT	11418110 NT		1.26		Γ	12405
Homo sepiens fibulin 1 (FBLN1), mKNA	4 NT			6.35		П	12188
promina-7.001.r bytumor Homo sepiens cuiva o	EST_HUMAN	1.0E-35 AI525119.1	1.0E-35	2.04		25043	12062
Homo saplens mRNA for KIAA1057 protein, partial cas		1.0E-36 AB028980.1	1.0E-36	1.49	38744	25036	12055
Homo sapiens mikiNA for KIAA1057 protein, partial cas	NT	1.0E-35 AB028980.1	1.0E-35	1.49	38743	26036	12055
031341 BETA-GALACTOSIDASE ;	EST_HUMAN	1.0E-35 BF589594.1	1.0E-35	0.72	37463	23838	10805
naming of NOI COAP PD8 Homo septens cDNA clone IMAGE:3254051 3' similar to TR:031341					Ī	Т	1000
nas06d06.x1 NCI_CGAP_Pr28 Homo sapiens cUNA clone IMAGE:3254051 3 similar to 11x:031341   031341 BETA-GALACTOSIDASE ;	EST HUMAN	1.0E-35 BF589594.1	1.0E-35	0.72	37462	REBEC	10805
AU158595 PLACE3 Homo saplens cDNA clone PLACE3000382 3	EST_HUMAN	1.0E-35 AU158595.1	1.0E-35	2.46	36384		9742
	EST_HUMAN	1.0E-35 AU158595.1	1.0E-35	2.46	36383		9742
Homo sapiens KIAA0645 gene product (KIAA0645), mKNA	2 NT	11418002 NT	1.0E-35	0.91			7819
Homo sapiens mRNA for KIAA12/9 protein, partial cds	NT	1.0E-35 AB033105.1	1.0E-35	66.0	34196		7652
MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cUNA	EST_HUMAN	1.0E-35 AW 808665.1	1.0€-35	0.74	31476		7135
MR1-ST0111-111199-011-d07 S10111 Homo sapiens cDNA	EST_HUMAN	1.0E-35 AW 808665.1	1.0E-35	0.74	31475	18561	7135
Homo saplens chromatin assembly factor 1, subunit B (p60) (CHAP1B), mKNA	Ι.	11526236 NT	1.0E-35	1.48	31896		5627
Mus musculus activin receptor interacting protein 1 (AripT-pending), mixiva	5 NT	7656905 NT	1.0E-35	4.82	30662	17680	4542
Mus musculus activin receptor interacting protein 1 (Artp1-pending), mk/NA	5NT	7656905 N1	1.0E-35	4.82			4542
AV650422 GLC Homo sapiens cDNA clone GLCCE+06 3	EST_HUMAN	1.0E-35 AV650422.1	1.0E-35		29419		3232
AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3	EST_HUMAN	1.0E-35 AV650422.1	1.0Ε-35	1.67	29418		3232
Homo sapiens transcription elongation factor B (Sill), polypoptide 1-like (1000 IL) mixing	ONT ONT	6006030 NT	1.0E-35	1.87	29397	16386	3212
MER29 repetitive element;	EST_HUMAN	1.0E-35 BE350127.1	1.0E-35	1.34	29051	15940	2826
ht09g01 x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3							
Top Hit Descriptor		Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	SEQ ID
	T }}		Most Similar			,	2
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Table 4

Single	
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in Placenta	

170010 September 11 april 28 September 200	N'	3.0E-36 AF099810.1		2.93	26934	13896	714
AV /53628 IF Homo sapiens curva cione i Figacino i o	HUMAN	4.0E-36 AV753629.1			Γ	25951	12520
Homo septems nuclear factor of ecuivated 1-cells, cytoplastific 4 (N. O. O.4), in N. O.		11420516 NT	4.0⋶-36	1.91		25328	12476
ZUGSC10.71 Soares_testis_NH1 Homo septiens cUN/\ crone (MANGE: 7402a0 3	HUMAN	4.0E-36 AA400370.1	4.0E-36	3.13	37941	24304	11235
Homo capiens DNA for amyloid procursor protein, complete cas	L	4.0E-36 D87675.1	4.0E-36	1.45	35370	21831	8752
Homo sapiens DNA for amyloid precursor protein, complete cos		4.0E-36 C87675.1	4.0E-36	1.45			8752
Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29		4.0E-36 M33320.1	4.0E-36	1.78	34388	20886	7831
Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mk/NA		11497041 NT	4.0E-36	2.49	32704		6180
y/19f05_r1 Soares placenta Nb2HP Homo sapiens cUNA clone IMAGE. 138/13 0	EST_HUMAN	4.0E-36 F64023.1	4.0E-36	0.96			5833
Homo saplens chromosome 21 segment HS21C004	1_	4.0E-36 AL163204.2	4.0E-36	0.69			4877
601282286F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3504T68 5	EST_HUMAN 6	4.0E-36 BE389299.1	4.0E-36	1.1	29623		3435
601282266F1 NIH_MGC_44 Homo sapiens cUNA Gone IMAGE:3004100 3	EST_HUMAN	4.0E-36 BE389299.1	4.0E-36	1.1	29822	16603	3435
2820020.5prime NIH_MGC_7 Homo sapiens cDNA cicro IMAGE:2820020 5	乚	4.0E-36 AW247772.1	4.0Ε-36	4.14		П	2297
601298574F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:3628385 5	EST_HUMAN C	4.0E-36 BE382574.1	4.0Ε-36	1.36	27913	• ]	1677
PM3-BN0176-100400-001-g04 BN0176 Hamo sepiens CUNA	EST_HUMAN F	4.0E-36 BE010038.1	4.0E-36	1.57	27473		1252
Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	NT	417862	5.0분-36	2.36			12458
Homo sapiens Xq pseudoautosomal region; segment 1/2	NT	5.0E-36 AJ271735.1	5.0E-36	6.11		_	12166
Homo sapiens N-ethylmateimide-sensitive factor (NSF), mRNA		11079227 NT	5.0E-36	0.59		П	7966
Homo sapiens APIS-like 1 (APISL1), mRNA		5729729 NT	5.0E-36	1.31	31029		4909
Homo saplens API5-like 1 (API5L1), mRNA		5729729 NT	5.0E-36	1.31	٦	П	4909
Homo sapiens chromosome 21 segment HS21C009	27		5.0E-36	3.24		7	3700
601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE: 3607289 5	EST_HUMAN 6	BE388436.1	5.0E-36	21.08		╗	2809
	NT	5.0E-36 AJ271735.1	5.0E-36/	15.16		╗	4
MER9 repetitive element;	EST_HUMAN N	6.0E-36 Al380469.1	6.0€-36	3.49	38521	24830	11841
tt85c09x1 NCI_CGAP_CLL1 Homo saptens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2						Т	
C16927 Clontech human aorta polyA+ mRNA (#6572) Homo saptens cDNA clone GEN-535C11 5	HUMAN		6.0E-36 C16927.1	083	Ţ	Т	10436
Homo saplens syncytin precursor, mRNA, complete cds			6.0E-36/	4.62		╗	8853
ho8h02.x1 NCI_CGAP_Co14 Homo septens cUNA done IMAGE:303002/13 SITTILET G SW:IMAA_HUMAN P62292 IMPORTIN ALPHA-2 SUBUNIT :	EST_HUMAN F	6.0E-36 AW 780143.1	6.0E-36/	3.03	33792	20341	7258
th93b06x1 Scares_NSF_F8_9W_0T_PA_P_S1 Homo suplens cUNA cione IMAGE::120189 3 simular to gb:m11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);	EST_HUMAN G	6.0E-36 AI435169.1	6.0E-36	7.17	31624	18646	5 <b>44</b> 6
UI-H-BW1-env-c-12-0-UI.st NCI_CGAP_Sub7 Homo septens culva clone IMAGE:30833423	EST_HUMAN C		6.0E-36 E	0.59	29894	16890	3729
Homo septens TCL6 gens, exon 12	L	6.0E-36 AB035346.1	6.0E-36 /	5.59			2490
Homo sapiens ninjurin 2 (NINJ2), mRNA		7706622 NT	6.0E-36	1.92	28315	16201	2060
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Vatue	Expression Signal	ORF SEQ	Expn NO:	Probe SEQ JD NO:

Single Exon Probes Expressed in Placenta Page 280 of 550 Table 4

10534	10320	9229	8373	8373	8243	8243	8147	8147	6820	6519	6519	6312	6020	5847	3425	2275	2212	2212	908	9749	9749	25.80	6706	5970	5603	5074	┑	1	4624	2373	Probe NO:
23569	23355	22307	21454	21454	21325	21328	21229	21229	19973	19684	19684	19484	19203	19037	16594	15408	15346	15346	14083	22687	22687	22643	19864	19156	18798	8303	16412	24420	17761	15504	SEQ ID
3/1/6	36984	35850	34978	34977	34842	34841	34748	34747	33381	33056	33055		32523	32344		28538	28475	28474	27148	36259	36258	36242	33254	32471	31848	31174	29427	38086	30743	28630	ORF SEQ
0.04	3,83	3.33	0.68	0.68	0.76	0.78	4.06	4.06	0.72	1.9	1.9	4.27	1.23	0.64	3.33	1.83	1.71	1.71	1.74	0.74	0.74	0.94	13.94	3.75	2.68	10.78	2.6	1.84	7.5	1.19	Expression Signal
		T	Τ										1.0E-36			. 1.0E-36	1.0E-36												3.0E-36	3.0E-36	(Top) Hit BLAST E Value
OE-SOLAW OSSOCO. I	AMORESCE A	1.UE-36 AV/ 103638.1	1.0E-36 AU141666.1	1.0E-36 AU141688.1	1.0E-36 AA420467.1	1.0E-36 AA420467.1	1.0E-36 AA148034.1	1.0E-36 AA148034.1	1.0E-36 AL!120542.1	1.0E-36 R25012.1	1.0E-36 R25012.1	1.0E-36 Al367714.1	4827064 NT	1.0E-36 AL044446.1	1.0E-36 AF156962.1	1.0E-36 BF673761.1	1.0E-36 BE:146523.1	1.0E-36 BE146523.1	BE409310.1	.	4507848 NT	2.0E-36 BF512794.1	2.0E-36 T69629.1	2.0E-36 T08756.1	2.0E-36 AF-267747.1	2.0E-36 AW 880376.1	2.0E-38 BE259267.1	3.0E-36 BF035327.1	TN 65118101	7662401 NT	Top Hit Acession No.
EG! JOWNIA	EST DIMAN	EST DUMAN	EST TOMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	l.	EST HUMAN	EST HUMAN	EST HUMAN	Y	EST HUMAN	EST HUMAN	EST_HUMAN	NT	NT	Top Hit Database Source
	RC3-CT0270-047-00-07-17-10 CT0279 Homo sapiens cDNA	OV3-NN1023-D10800-1910-01010 Septions CDNA	CONTROL TO COMP REPRESENTATIONS CONTROL TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONT	AU 14 1000 ITH INC I HOME SECTION COME THYROTONION 5	ncougue.rt No. COAF_FO Home sapiens CDIA Clone TUVDO (2015)	no60e08.r1 NCI_CGAP_PTI Homo sapiens cuiva cione invage: 745e70	2051a12.r1 Stratagene endothelial cell 837223 Homo sapiens culvia cicrie inviacie: 394390 0		DKFZp761A228_r1 761 (synonym; hamy2) Homo septens cDNA done DKFZp761A229 5	yg36g10,r1 Soares Intent brain 1NIB Homo sapiens cuNA clone IMAGE:34028 5 similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN :	yg38g10.rl Scares infant brain 1 NIB Homo sapiens cUNA done IMA/GE:34525 5 SITTIET TO SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;	repetitive element;	Homo sapiens zinc tinger protein 147 (estrogen-responsive linger protein) (Zivr 147) rinxivx	DKFZp434G022_r1 434 (synonym; https3) Homo saplens cDNA clone DKFzp434G022 5	Homo sapiens human endogenous retrovirus W proC6-19 protease (pro) gene, pertial cds	602138493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5	RC1+T0217-131199-021-h07 HT0217 Homo saplens cDNA	RC1+HT0217-131189-021-h07 HT0217 Homo sapiens cDNA	601300838F1 NIH_MGC_21 Homo eaplens oDNA clone IMAGE:3635480 5	Homo capiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquítin specific protease 13 (Isopeptidese T-3) (USP13) mRNA	UI-H-BW1-emu-e-11-o-UI:s1 NCI_CGAP_Sub7 Homo sapiens cDNA cione IMAGE:3071132 3	yc44a07.r1 Stratagene liver (#937224) Homo saptens cDNA clone IMAGE:83508 5'	EST06648 Infant Brain, Bento Scares Homo sepiens cDNA clone HIBBJ28 5' end	Mus musculus p47-phox gene, complete cds	QV0-OT0030-240300-174-h04 OT0030 Homo septens cDNA	601106343F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3342706 5'	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	Mus musculus junctophilin 1 (Jp1-pending), mRNA	Horno sepiens KIAA0952 protein (KIAA0952), mRNA	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

nomo sapiens NOD i provin (NOD i) Bairo, cavara 1, 2, and 4	Z	5.0E-37 AF149773.1		3.63	2	5 25242	12335
Homo saplens glycine C-acetylransrerase (2-amino-3-ketocutyrate-CoA ugase) (CCA I), IIINIVA	NT	7657117 NT	Γ	4.02			11160
AV750211 NPC Homo sapiens cDNA clone NPCBGHU8 5	EST_HUMAN	5.0E-37 AV750211.1		1.03		5 22035	8956
EST178035 Colon carcinoma (HCC) cell line Homo sapiens CUNA 3 end	EST_HUMAN	5.0E-37 A4307123.1			32742	19393	6218
EST178035 Coton carcinoma (HCC) cell line Homo sapiens cuiva 5 end	EST_HUMAN	5.0E-37 AA307123.1		4.3	32741	19393	6218
Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mKNA, partial cos	N,	6.0E-37 AF202723.1		4.5		25641	12984
Human olfactory receptor offr17-201-1 (OR17-201-1) gene, citactory receptor offr17-20 (OR17-21) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds	TN	6.0E-37 U78308.1	6.0E-37	2.3	<u> </u>	25576	12864
Homo saplens protocadherin alpha 10 alternate isoform (PCUH-alpha 10) mitivis, complete cos	NT	6.0E-37 AF169689.1	6.0E-37	0.59	35251	21714	8634
repetitive element;	EST_HUMAN	7.0E-37 AI536702.1	7.0E-37	1.89	37831	24206	11134
tm87g03 x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' strrilar to contains L1.b3 L1		-			٦	7	
PTR5 repetitive element;	EST_HUMAN	7.0E-37 AI817700.1	7.0E-37	8.66	37706	24073	10994
wk25b11.x1 NCI_CGAP_Bm25 Homo septens cDNA dano IMAGE:2413341 3' similar to contains PTR5.22		-			٦	7	
EST380899 MAGE resequences, MAGJ Homo sapiens cDNA	EST_HUMAN	7.0E-37 AW968823.1	7.0E-37	3.04	31320	7	5228
DKFZp434E0422_r1 434 (synonym: ntess) Homo saptens cunk cione unrzzpasacoazz o	EST_HUMAN	7.0E-37 AL042800.1	7.0E-37	4,92			1313
genes	NT	8.0E-37 X37344.1	8.0E-37	6.2	34870	21160	8068
H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14					٦	$\neg$	
RC1-CN0008-210100-012-a09_1 CN0008 Homo saplens cDNA	EST_HUMAN	8.0E-37 AW840840.1	8.0E-37	7.08		19183	5998
MER29 repetitive element;	EST_HUMAN	8.0E-37 B=350127.1	8.0E-37	3.48	32449		5940
ht09g01.x1 NCI_CGAP_Kid13 Homo sepiens cDNA done IMAGE:3148266 3' similar to contains MER29.b3		-			T	Т	
MER29 repetitive element;	EST_HUMAN	8.0E-37 B=350127.1	8.0E-37	3.48	32448	19135	5949
htogot xt NCI_CGAP_Kid13 Homo sapiens cDNA done IMAGE:3146266 3 similar to contains MER29.63						T	
CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA	EST_HUMAN	8.0E-37 B=698077.1	8.0E-37	1.7	T	Т	5383
Homo sapiens chimerin (chimeerin) 2 (CHN2) mRNA	NT	757979	8.0E-37	1.4	29824	7	3436
73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional	EST_HUMAN	9.0E-37 W 22618.1	9.0E-37	3.57		╗	12619
We80b07x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3	EST_HUMAN	8.0E-37 AW 009277.1	9.0E-37	2.27		П	7639
ws80b07x1 NCI_CGAP_Co3 Homo capiens cDNA clone IMAGE:2504245 3	EST_HUMAN	9.0E-37 AW 009277.1	9.0E-37	2.27	34087	_	7539
Homo sapiens Sad1 unc-84 domain protein 2 (SUNZ) mRNA, partial cds	NT	1.0E-36 AF202723.1	1.0⊑-36	2.76		$\neg$	13131
Homo sapiens chromosome 21 segment HS21C013	NT	1.0E-36 AL163213.2	1.0E-36	5.76		7	12836
Homo sapiens Ren GTPess activating protein 1 (KANGAP1), mKNA		11418177 NT	1.0E-36	2.83		7	12340
Homo sapiens PP3227 protein (PP3227), mRNA		11545901 NT	1.0E-36	10.8		П	12048
UI-HF-BNO-ale-c-03-0-UI.r1 NIH_MGC_50 Homo sapiens cUNA clone IMAGE:30/82// 5	EST_HUMAN	1.0E-36 AW 504143.1	1.0E-36	3.55	٦	┑	11682
CM3-NN0061-140400-147-h12 NN0061 Homo sepiens CUNA	EST_HUMAN	1.0E-36 AW 897638.1	1.0E-36	2.55	37895		11180
RC3-CT0279-040500-017-e10 CT0279 Homo sapians cDNA	EST_HUMAN	1.0E-36 AW855868.1	1.0E-36	0.64	37177	23569	10534
		V	Value	oignai	ē Z C	Ö	Ņ.
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Single Exon Probes Expressed in Placenta

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8933	8409	6127	5055	3267	2154	13184	12797	11856	8227	8185	8185	6798	6676	2 2	\$360 0	3999	2021	1105	1105	<u>ფ</u>	392	7728	5985	333	2581	2074	2074	868	6416 6	2495	Prabe SEQ ID 1
22012	21490	19306	18183	16441	15290	25770	26770	24844	21309	21267	21287	19953	19835	18703	17603	17156	15162	14270	14270	13620	13629	20790	19170	16206	15706	15214	19214	22621	19585	15622	SEQ ID
15998	35019		31158		28417			38541	34829	34791	34790	33353	33224		30485	30162	28287	27329	27328	26667	26668	34279	32492			28333	28332	36192	32947	28741	ORF SEQ ID NO:
3.59	1.12	0.89	2.34	1.03	6,95	4.19	1.44	10.07	2.32	0.47	0.47	3.72	0.6	0.9	0.6	. 6.71	1.32	2.53	2.53	0.89	0.89	0.72	.0.7	4.02	1.54	3.42	3.42	0.56	0.68	2.97	Expression Signal
		9 1.0E-37			Γ		4 2.0E-37						5 2.0E-37			1 2.0E-37							Г								Most Similar (Top) Hit BLAST E Value
1.0E-37 AA171408.1	I.0E-37 BE546032.1	7305360 NT	1.0E-37 BF371719.1	1.0E-37 AW 862082 1	1.0E-37 AL 163281.2	7 11417972 NT	-	AF-1760	2.0E-37 BF204032.1	2.0E-37 BE537764.1	2.0E-37 BE537764.1	2.0E-37 AA346720.1	7 11990617	2.0E-37 BI-035327.1		4503210 NT	20E-37 AL163247.2	2.0E-37 AU131202.1	2.0E-37 AU131202.1	20E-37 D89790.1	2.0E-37 D89790.1	3.0E-37 AI749952.1	3.0E-37 AL138274.1	3.0E-37 AW981150.1	3.0E-37 AW961150.1	3.0E-37 AL048956.1	3.0E-37 AL048956.1	4.0E-37 AA843806.1	4.0E-37 AW 794502.1	4.0E-37 AA702794.1	Top Hit Acession No.
EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	T	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	_	EST_HUMAN	NT	NT	N.	EST HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Top Hit Database Source
zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sepiens cUNA cione invakez o ruccer o simuar co contains L1.t2 L1 repetitive element;	601072418F1 NIH _MGC_12 Homo sepiens cDNA clone IMAGE:3430308 5	Mus musculus otogelin (Ctog), mKNA	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens CUNA	RC3-CT0347-210400-016-h03 CT0347 Homo septens cDNA	Homo sapiens chromosome 21 segment HS21CU81	Home septens pessedille (zebratish) homelog 1, containing SKC I domain (FESI), mKNA	Homo sapiens pescadillo (zebratish) homolog 1, containing or C i domain (PEC), mining			(601067534F1 NIH_MGC_10 Homo sapiens cUNA cione IMAGE:3453657 5	601067534F1 NIH_MGC_10 Homo sapiens cUNA clone IMAGE:3453557 5	EST62831 Fetal heart II Homo sepiens cDNA 5 end	Homo saplens mouse thiamin pyrophosphokinase nomolog (1PK1), mKIVA	601458531F1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:3862086 5	Homo saplens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (UDX1) mikina	Hamo sapiens cyconitane P150, sublemily XXVIII, (see out 27 hydrox)reso, concentrations and subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subj	Homo sapiens chromosome 21 segment Hozarowa 27 hodowy for carefronting to	AU131202 N I 2KH3 Homo sapiens cuna cione N I 2KH3UUZ100 0	AU131202 NT2RP3 Homo sapiens cDNA cione N 12RF3002166 5	Homo sapiens mRNA for AML1, complete cds	Homo sapiens mRNA for AML1, complete cds	a(34c)5x1 Barstead colon HPLNB7 Homo sapiens cLina cione invadez 237.3555 3 similiar to POGO ELEMENT.;	DKFZp547G067_r1 547 (synonym: nibri ) Homo sablens conva color on rupos color o	EST373222 MAGE resequences, MAGF Homo sapiens cUNA	EST373222 MAGE resequences, MAGF Homo sepiens ou NA	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone UKFZp434L2418	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens GUNA cione UK FZp434L2410	ak09c02.s1 Scares_parathyroid_tumor_NbHPA Homo saprens cUNA clote IMAGE:14094423	RC6-UM0014-210200-021-H05 UM0014 Homo sapiens GUNA	z80b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cUNA clone INAGE: 44c0103	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

	EST_HUMAN	3.0E-38 H85494.1	Γ	211	35470	21930	8861
	EO TOMAN	3.0E-38 H85494.1				Г	8851
CW3-F10161-140100-241-140110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-10110-1-1010-1-10110-1-1010-1-1010-1-1010-1-1010-1-1010-1-1010-1-1010-1-1010-1-1010-1-1010-1-10	EST HUMAN	3.0E-38 BF3/3664.1			Γ	Γ	7763
	ES: HOMAN	3.0E-38 AW 302461.1	Г		33937	3 20471	7393
Homo sapiens chromosome zi segineni mozi o roc	Z	3.0E-38 AL163300.2	Γ		33463	25836	6893
GUTTS/GGGET NIH_MGC_21 Hondo subterior CONA Civile INACCESCATE C	EST_HUMAN	3.0E-38 BE278301.1	Γ	0.61		17871	4736
COCCION TO DATE TO DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPANION DE LA COMPA	SWISSPROT	3.0E-38 P53538			30120		3958
SSC72 PROTEIN	SWISSPROT	3.0E-38 P53538			30119	П	3958
Homo sapiens HIKA interacting protein 4 (anax-like) (HIKIT+), mikika		7649807		1.49	ÿ	16948	3787
	NT	3.0E-38 AI-003530.1		4.42			2167
Homo sapiens chromosome 12 open reading traines (v. 2001), in the case training	INT	11435947 NT		1.15	27403	14346	1183
B. taurus mitochondrai asparate aminoratisterase irinina, complete Cos	NT	Z25466.	F		26381		121
B. taurug mitochondrial asparata amin'oranisterasa monto, complete Cho	NT	4.0E-38 Z25466.1			26380	13351	121
601450148F1 NIH_MGC_55 FIORID SEPTENS CONN GOID INFO CONN CONN CONN CONN CONN CONN CONN C	EST_HUMAN	5.0E-38 BE871610.1			33748	20305	7172
Homo sapiens Kiblik gene (parua), exor o		5.0E-38 AJ237740.1	5.0E-38	0.98	28774	15650	5288
Homo sapiens derodinase, iodotnyronine, type ii (DIOZ), tariscript variant 2, military	NT	7549804 NT	5.0E-38	0.77			3971
11-	NT	-	5.0E-38	0.94		16957	3796
1	NT	5.0E-38 AJ237740.1	5.0E-38	4.57	28774		2525
ES 1383908 MAGE, resequences, WAGE name suprems covex	EST_HUMAN	5.0E-38 AW971819.1	5.0E-38	0.9			745
Homo sapiens adenyosuccinale lyase (AUSL), mixina		11418164 NT	6.0E-38	1.79	31861		13160
Homo sapiens UNA for Human r ZWi, complete cus	Z	6.0E-38 AI3002059.1	6.0E-38	6.66	32025	26468	12704
Homo sapiens chromosome 12 open reading framo a (C (2007-3), illinous	NT	11435947 NT	6.0E-38	4.27		25147	12189
Hamo septens hypothetical protein FLJ20128 (FLJ20128), mr.vvA	NT		6.0E-38	0.59			7482
Homo sapiens zinc tinger protein LNF28/ (LNF28/), MNNA	NT	11426114 NT	6.0E-38	0.98		_	5708
Homo sapiens zinc finger protein CNF28/ (CNF28/), MINNA	NT	11425114 NT	6.0⊑-38	0.98	32192		5706
601465722F1 NIH_MGC_65 Home sapiens cuiva cone image: 3008540 0	EST_HUMAN	BI-033033.1	6.0E-38	1.98			3107
EST384920 MAGE resequences, MAGE Homo sapiens CUVA	_	7.0E-38 AW972825.1	7.0E-38	1.7	28515	П	2254
Homo sepiens DNA for Human r ZAW, complete cus		8.0E-38 Al3002059.1	8.0E-38	1.44		26049	13210
Homo sepiens Grb2-associated binder 2 (KIAAU5/1), mRNA	N <sub>T</sub>	11436955 NT	8.0E-38	1.37	27470	7	12735
602018401F1 NCL CGAP Bm6/ Homo sabiens CUNA CIONA CIONA CEL 4100552 0	EST_HUMAN	8.0E-38 BF346221.1	8.0E-38	1.21		$\exists$	2567
Homo sapiens Grb2-associated binder 2 (NIAAUS/T), ITT/NA		11436955 NT	8.0E-38	1.96	27470	7	1249
Rattus norvegicus mutidomain presynaptic cytomatrix protein Piccolo (LUCcorreo), mixiya		10048482 NT	9.0E-38	1.72	32398	╗	5898
CM3-FT0096-140700-243-d07 F10096 Homo sapiens culva	EST_HUMAN	1.0E-37 BE771814.1	1.0E-37	1.94		$\neg$	12871
Human somatic cytochrome c (HC1) processed pseudogene, complete cos	L	1.0E-37 M22878.1	1.0E-37	2.19	37652	24019	10937
	<u>L</u> _	, ,	Value	Signal	D NO:	NO:	Ņ.
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Exon D	Probe
	Citible Double	الم					

Page 284 of 550 Table 4 Single Exon Probes Expressed in Placenta

					,		
Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10177	7 23214		1.84	3.0E-38	3.0E-38 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21 C048
11598	П		1.88	3.0E-38	3.0E-38 AL 163248.2	NT	Homo saplens chromosome 21 segment HS21C048
12990	7	27403	1.23	3.0E-38	11435947 NT	NT	Hamo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2	П	٦	1.96	2.0E-38	2.0E-38 AL163248.2	NT	
141	_1		3.66	2.0E-38	5902097 NT	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	. [		13.95	2.0⊑-38	2.0E-38 A4437353.1	EST HUMAN	zw30d01.r1 Soares overy turner NbHOT Homo expiens cDNA clone IMAGE:770785 5' similar to SW: MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;
1678	$\neg$		13.95	2.0⊑-38	2.0E-38 A.4437353.1	EST_HUMAN	ZWG0d01.r1 Scares overy turner NbHOT Homo septens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2:MANNOSIDASE;
3622	16786		0.92		2.0E-38 A =070670.1	T	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	П	30824	18.99		4557887 NT	NT	
5252	2 18339	31312	0.68	2.0≦-38	2.0E-38 A4437181.1	EST_HUMAN	2x61d09.rf Scares_testis_NHT Home suprens cDNA cione IMAGE: 705129 3 SIMIIII DE INCIGE 17957 GB17957 GLYCINE RECEPTOR SUBUNIT, ALPHA 4;
5836	7	I	0.75		2.0E-38 Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5836	8 19026	32332	. 0.75		2.0E-38 Z26634.2	NT	Homo saplens mRNA for ankyrin B (440 kDa)
7897	7 20949	34457	1.47		2.0E-38 AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HIBARH11 5
8680			4.47		2.0E-38 BE165980.1	EST_HUMAN	MR3+HT0487-150200-113-g01 H10487 Homo septens CUNA
9098	8 22175	35719			2.0E-38 F06450.1	EST HUMAN	HSC18F031 normalized intent brain culva Homo sapiens culva cione ciliono
9165	5 22243	35786	1.26		2.0E-38 AF069755.1	NT	Homo sabiens orphan G protein-coupled receptor FIG20 (FIG20) mixture, compared cuts
9422	2 22496		1.36		2.0E-38 BE222256.1	EST_HUMAN	GAG POLYPROTEIN.:
10665	5 23699	37309			2.0E-38 D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11781	1 24771		4.86		2.0E-38 BE712790.1	EST_HUMAN	QV2-HT0698-080800-293-e05 HT0698 Homo sapiens cDNA
11939	9 24925	38826	2,86		2.0E-38 AF180501.1	NT	Homo sapians leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11939	9 24925	38627	2.86		20E-38 AF190501.1	N T	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR8) mRNA, partial ods
12244	4 25186		6.21		2.0E-38 AV726988.1	EST_HUMAN	
12246	6 25187		1.26		2.0E-38 AB012723.1	N <sub>1</sub>	Homo sapiens gene for kinesin-like protein, complete cds
12546			3.36		2.0E-38 M55630.1	NT	
12559	9 25381	32073	4.81	Γ	2.0E-38 H55641.1	EST_HUMAN	
12632	2 25426		2.87	Γ	S74906	3	E1 beta=byruvate denydrogenase beta (promoter) (numan, placetta, Genorito, 1204 iti)
131/4	4 20/62		1.00	205-30	18104201411	91.41	House a consideration of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s

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Table 4
Single Exon Probes Expressed in Placenta

Limite arbitrary Manager Last seaso (Last seaso)	N	1 N   2070741	96-⊒0.0	1.53	_	25479	12720
at36b04.x1 Barstead colon HPLRB7 Homo saplens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.t1 LTR7 repetitive element;	EST_HUMAN	A175015	5.0E-39		8 29247	1	3050
Horno sapiens X-linked arradionic econderma dyspiesia prount gane (CDX), www.z. with materials report	NT	5.0E-39 AF003528.1	5.0E-39	1.64	27259	2 14201	1032
763403 XT NCI_CGAP_LUZ4 Homo sapiens curva came invasce.32043040 summer or ref. 101.00.00 CE00828;	EST_HUMAN	6.0E-39 BE670394.1	6.0E-39	2.24		25697	13064
	EST_HUMAN	6.0E-39 BF331829.1	6.0E-39	2.4	37758	7 24124	11047
Homo sepiens chromosome 21 cegment HSZ1CUZ/	NT	7.0E-39 AL:163227.2	7.0E-39	,	28421	П	2160
POL PROTEIN:	EST_HUMAN	8.0E-39 Al323404.1	· 8.0E-39	1.8		15020	1876
Homo sapiens estrogen receptor-pinding institutions could close IMAGE: 2384461 3' similar to TR-P87890 P87890	NT	4758229 NT	8.0E-39	1.3	27652	14579	1425
Homo capiene A i Pase, H+ transporting, lysosoma (vacuosa prouxi pump) long (A i roc) ilining	N		8.0E-39			П	55
zm27f07.r1 Stratagene pancreas (#93/208) Homo sapiens curva cione invade: 020000 0	EST_HUMAN	9.0E-39 A4112438.1	9.0E-39	1.64	38801	25096	12116
Homo sapiens chromosome 21 segment HS21C084	NT	1.0E-38 AL:163284.2	1.0E-38	4.79	/	25877	12403
1 :	EST_HUMAN	1.0E-38 BE350127.1	1.0E-38	6.31	36236	22665	9610
Home sapiens hypothetical protein FLJ 10000 (FLJ 10000), mixina.	NT	11422250 NT	1.0E-38	0.58	35987	22429	9354
Homo sapiens mkina for kinanosia protein, pardal cos	NT	1.0E-38 AB014512.1	1.0E-38	2.55		20635	7563
Mus musculus otogelin (Otog), mRNA	NT	7305360 NT	1.0E-38	4.69	32673		6151
Mus musculus otogelin (Otog), mRNA	NT		1.0E-38	4.59	32672	19327	6151
Homo sapiens chromosome 21 segment HS27CU80	NT	1.0E-38 AL163280.2	1.0E-38	1.89	31355		5268
Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mKNA	NT	8922543 NT	1.0E-38	1.08		17854	4719
Homo sapiens chromosome 21 segment HS21C003	NT	I.0E-38 AL163203.2	1.0E-38	2.18			4444
Homo sapiens chromosome 21 segment HS21C003	NT	1.0E-38 AL163203.2	1.0E-38	2.15	30563	17584	4444
Homo saplens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products	NT	4505016 NT	1.0E-38	0.6	30858	17579	4439
Homo sapiens mRNA for KIAA1442 protein, partial cas	NT	1.0E-38 AB037863.1	1.0E-38	0.93	30405	17416	4271
Homo sepiens cyclin K (CCNK) gene, exon /	NT	1.0E-38 AF270831.1	1.0E-38	1.69			2564
Home septens KIAA0173 gene product (KIAA0173), mKNA	NT	7661969 NT	1.0E-38	1.33			2077
Homo septens guanine nucleotide binding protein-like 1 (GNL1), mKNA	NT	4885288 NT	1.0E-38	2.62	28310	П	2055
	EST_HUMAN	1.0E-38 A\401570.1	1.0E-38	1.98		14282	1117
	COLL		Value			Ş	Š
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similer (Top) Hit BLAST E	Expression Signal	ORF SEQ	S	Probe SEQ ID
Single Exon Floues Expressed in Flaverica	באסוו הוסטפי	Singi					١.

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Table 4
Single Exon Probes Expressed in Placenta

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1543	2   2	9826	8505	702	7702	7526	808	4523	2692	2030	4	1566 6	057	85			12236	12236	8	8			٦	$\exists$		8267	П		$\neg$	400	
14695	24759	22866	21686	20767	20767	20599	18803	17662	15812	16171	1	14713	14223	₹ 3	14095	25212	26180	25180	13287	13287	13287	25588	25494	22695	22595	21340	19136	19138	16826	13756	SEQ ID
27774	T	П	٦				31868		28928	28279							38349	38348	26299	26298	26297		٠	36166	38165	34864	32451	32450	29835	26782	ORF SEQ ID NO:
							4.45	1.74	1.89	4.48		33.59	3.8	11.65	7.78	5.72	6.59	6.59	11.96	11.86	11.98	2.56	6.36	0.46	0.46	1.02	0.6	9.0	6.0	4.39	Expression Signal
																										4.0E-39	4.0E-39	4.0≦-39		4.0€-39	Most Similar (Top) Hit BLAST E Value
1.0E-39 A.1006345.1	2.0F-38 D86964.1	2.0E-39 AI686660.1	2.0E-39 AF-078779.1	2.0E-39 AL 163202.2	2.0E-39 AL-163202.2	2.0E-39 AA080867.1	2.0E-39 AA508880.1	2.0E-39 BF370207.1	2.0E-39 AL163248.2	2.0E-39 A/\720574.1		2.0E-39 AW372318.1	2.0E-39 AF-000573.1	2.0E-39 AI525119.1	2.0E-39 BE409203.1	3.0E-39 H37903.1	3.0E-39 AI084557.1	3.0E-39 AI084557.1	3.0E-39 AA631949.1	3.0E-39 AA631949.1	3.0E-39 AA631949.1	4.0E-39 BE836452.1	11418177 NT	4.0E-39 D84116.1	4.0E-39 D34116.1	4.0E-39 A\1682949.1	11422113 NT	11422113 NT	4.0E-39 AL163210.2	4.0E-39 AB015610.1	Top Hit Acession No.
NI:	- 1	EST_HUMAN	NT	NT	NT	EST_HUMAN		EST_HUMAN	NT	EST_HUMAN		EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	7 NT	NT	NT	EST_HUMAN	NT	NT	ΝT	<u> </u>	Top Hit Databese Source
Homo saplens KVLQT1 gene	Human mRNA for KIAA0209 gene, partial cds	tu35e03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253052 3	Rattus norvegicus putative four repeat ion channel mRNA, complete cds		Homo sepiens chromosome 21 segment HSZ1CUUZ	2n06(02.r1 Strategene hN I neuron (#837233) Homo septens culviv cione liwiw GE 34000 I 3	ng86f03.s1 NCI_CGAP_Pro Homo sapiens cuiva cione image:341083	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens CUIVA	Homo sapiens chromosome 21 segment HSZ1CU48	THR repetitive element;	mw21g02.s1 NCI_CGAP_GCB0 Homo septens cDNA clone IMAGE:1241138 3' similar to contains THR.13	PM0-BT0340-211288-003-d02 BT0340 Homo sapiens cDNA	Homo sapiens homogentisate 1,2-dioxygenase gene, comprete cos	promina-7.D01.r bytumor Homo saplens cUNA 5	601301607F1 NIH _MGC_21 Homo saprens cUNA Crone IMAGE:3056289 0					fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clore CN 2-1	fmfc16 Regional genomic DNA specific cUNA library Homo sapiens cUNA ciure CN 2-1	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cUNA	Homo sapiens Ren GTP ase activating protein 1 (RANGAPT), mKWA	Homo sapiens DNA for prostacyclin synthese, exon 2	Homo sapiens DNA for prostacyclin synthäse, exon 2	ge22g04. g1 Strategone conzo orain S11 Homo septens CUNA crone IMA/SE. ID20490 S SITURE W COTTRAINS OFR.b1 OFR repetitive element;	Home saplens EBNA-2 co-activator (100kb) (P100), mkNA	Homo sapiens EBNA-2 co-activator (100kU) (p100), mr.NA	Home septens chromosome 21 segment HS21CU10.	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds	

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Table 4
Single Exon Probes Expressed in Placenta

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44430	7894	7894	4033	3106	4466	4081	3885	1480	1263	1263	669	11165	8762	7521	6965	5781	6781	5747	5474	5474	4824	4782	4782	1763	1561	1543	Probe SEQ ID NO:
1	20946	20946	17189	16282	17608	18467	17044	14633	14420	14420	13761	24238	21841	20694	20193	18973	18973	18939	18673	18673	17957	17917	17917	14912	14714	14695	Exan SEQ ID NO:
	34453	34452		29298		30242	30043	27718	27485	27484	26785			34069			32278	95228	31687	31686	30943	30904	30903	28007	27791	27775	ORF SEQ ID NO:
	2.21	2.21	3.43			3,99		15.75	16.02	16.02		1.4	1.04	2.15	1.85		,	1.2	0.82	0.82	9.13	9.32	9.32	1.14	5.98	2.83	Expression Signal
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7.0E-40 AL:163246.2	7.0E-40 U80325.1	7.0E-40 U60325.1	8.0E-40 BE396541.1	8.0E-40 AA078165.1	4507848 NT	9.0E-40 AE033070.1	4503764 NT		4765145 NT			4759051 NT	1.0E-39   O46530	1.0E-39 D78132.1	11436736 NT	1.0E-39 AJ278170.1	1.0E-39 AJ278170.1	1.0E-39 T80876.1	11417342 NT	11417342 NT	7657020 NT	1.0E-39 AW851895.1	1.0E-39 AW951995.1	1.0E-39 H55224.1	7657020 NT	1.0E-39 AJ006345.1	Top Hit Acession No.
<b>፯</b>	NT	NT	EST HUMAN	EST_HUMAN	NT	NT	NT NT	2 NT	SNT	SNT	ONT	NT	SWISSPROT	NT	6 NT	NT	NT	EST_HUMAN	2 NT	2 NT	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	ONT	NT	Top Hit Database Source
Homo sapiens chromosome 21 segment Hoz I CO40	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete ods	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds	OUTCOACOL I MILL MICO TO LINUM COCHANICA COMPANICATION CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR	ATIONAL CHARMONOR ( THE CONTACTION OF THE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERV	Homo sapiens uniquium specimo protesse i a (isopopulación i a) (con i a) iniquia.	Homo sapiens mixing for Nixy 1244 protein, parient was	Homo septens fragule A mental relationation in (river) fritten	mRNA	Homo sapiens Act-pinging protein (Actor 1) Haves	Homo sapiens AE-binding protein (AEBB2) BIONA	Homo sapiens UDP-glucose pyropnosphorylase 2 (UGP2), mixtur	Homo sapiens ribosomal protein S6 kinasa, suku, polypepude 3 (Nr 30003) ilinuwa	RIBONUCLEASE KO PRECURSUR (KNAVE NO)	Homo sepiens mRNA for res-related GTP-binding protein, complete cos	Homo sapiens tubby like protein 3 (10LF3), MKNA	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)			(TM) and short cytoplesmic domain, (semaphorin) 5A (SEMA5A), mRNA	Tomo sepiens sema domain, seven uromouspurum repeate (ypo e ana ypo e may).  (TM) and chort cytoplasmic domain, (semaphonnin) 5A (SEMASA), mRNA.	Homo sepiens UKrcp434rc11 protein (UNICC1454rc11), HIDVAN	ES1364065 MAGE resequences, MAGE Homo saprens CUVA	ES 1364065 MAGE resequences, MAGE nomo sapiens conva	CHR220163 Chromosome 22 exon Homo sapiens CUNA cruie V22_200 0	Homo septens UKFCP454F2T1 protein (UNFCFF5#F211), illinux	Homo septens KVLQT1 gene	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

			-7	7	7	П		П		Т	٦	П	Т	٦	T	٦		Т					7		٦	٦			<u> </u>
817	335	11544	10899	9412	9169	8575	6777	6592	4993	425	10955	9255 9255	9255	8181	8070	4508	2175		1926	2670	10182	10182	7075	7076	6275	8	2788	2788	Prabe SEQ ID NO:
13996	13548		╗	П		П	19932	19752	18122	17396	24036	22332	22332	21263	21152	17647	15310		16068	15791	23218	23219	20128	20128	19449	19242	15904	16904	Exon SEQ ID NO:
<b></b>		38276		36050	35790		33328	33137								30635		1	28173	28907	36812		33545	33544			29012	29011	ORF SEQ
5.58	3.91		,	1.6	1.27		7.06	0.66	0.83		1.95				0.84	7.2	6.81		3.81	2.75	6.09	6.09	3.04	3.04	1.38	1.85	9.91	9.91	Expression Signal
								3.0€-40								4.0€-40		1					6.0E-40		6.0E-40		6.0⊑-40	6.0E-40	Most Similer (Top) Hit BLAST E Velue
2.0E-40 AW303868.1	2.0E-40 A1223036.1	6005813 NT	D86964.	3.0E-40 AF078779.1	3.0E-40 AF078779.1	5454167 NT	11417342 NT	4506736 NT	3.0E-40 AA055118.1	3.0E-40 AI925949.1	4.0E-40 AW841585.1	4.0E-40 BE009416.1	4.0E-40 BE009416.1	4.0E-40 AA742809.1	4.0E-40 AU127831.1	7682117 NT	4.0E-40 AF-003528.1		4.0E-40 AI686005.1	5.0E-40 AL163285.2	6.0E-40 AV/653028.1	6.0E-40 AV/653028.1	11439783 NT			6.0E-40 BE504766.1	6.0E-40 A.\361275.1	6.0E-40 AA361275.1	Top Hit Acession No.
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Con en cont	Homo sapiens serine unaphine protein whase (IVON), illinux	Human mRNA for KIAA0209 gene, paruat cos	Rattus norvegicus putative four repeat ion channel miniva, complete cus	Rettus norvegicus puizave icur repeat ion chemine minito, cumpiero cus	Homo sapiens HBV associated factor (XAP4) mXIVA	(TM) and short cytoplasmic domain, (serial money of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the Carlotte of the 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ciona invasci245073 3 \$1111111 \$111.00000 010000 Pt01 Pt01 Pt01 Pt01 Pt01 Pt	Homo sapiens chromosome 21 segment nozi Coo	3	AV653028 GLC Homo sapiens cuna cione occuperva s	Homo sapiens rany acid desamase i (1905), iiin 105	Homo septens farry actio desaurase 1 (FADC1), IDNIVA	Homo septens KIAA0211 gene product (KIAA0211), mr.wA	hz40g01.x1 NCI_CGAP_GC6 Homo sapiens cDNA cione liviA GE. 32 10400 3	EST70527 T-cell lymphoma Homo saplens cDNA 5' end similar to similar to zinc finger protein family	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

			ſ		4 61000	10024	00
wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2453895 3	EST HUMAN	7 0E-41 AI934364.1			Ī	1	
wp04h04.xt NCI_CGAP_Kid11 Homo sapiens conv. Conic intro-Catagogae a	EST_HUMAN	7.0E-41 A1934364.1		262		ſ	3
Homo expires chromosome 21 segiment noz rovo	Z	8.0E-41 AL163203.2		1.6		1	818
1	EST HUMAN	9.0E-41 VV01598.1		0.59	5 30064	7	3906
INTO 10222 1 1035-002 510 0 1012 S Homos seniors oDNA clora IMAGE 284602 5	EST_HUMAN	1.0E-40 EF334112.1	Γ	6.94	2	7 26032	12687
Momo capiens chomosomie zi seguiena i exticorio	NT.	1.0E-40 AL163246.2		1.88	9		12079
	EST_HUMAN	1.0E-40 AA614255.1		1.49	8 38684	24978	11993
nn09h03 s1 NCI CGAP P/3 Homo sepiens cDNA clone IMAGE:1116861 similar to TR:G1136406			Ī		3000	0/8#7	CRRII
	EST HUMAN	1 DE-40 AA614255.1		. 140			1
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Table 4

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Table 4
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OU 144004 FT : INIT MICE OF THIR SEPTETS WHEN STATE MICE OF TOWN OF	ESI HUMAN	1.0E-41 BE869735.1	Γ	1.05	29470	6 16450	3276
Homo saplens nuclear factor of activated 1 -cells, cytopasmic 2 (NFA I C2), minixA	BNT	11420516 NT		1.2	7	8 25747	13148
EST84555 Colon adenocarcinoma IV Homo sapiens CUNA 3 end	EST_HUMAN	2.0E-41 AA372637.1		2.87		П	11775
Homo sapiens KIAA0433 protein (KIAA0433), mKNA	BNT	11417118 NT	2.0E-41	0.56	36242	コ	9617
Homo sapiens KIAA0433 protein (KIAA0433), mKNA	8 NT	11417118 NT	2.0E-41	0.66	36241		9617
ZING FINGER PROTEIN 136	SWISSPROT		2.0E-41 P52742	1.65		5 22253	9176
EST31723 Embryo, 12 week i Homo sapiens curva o eno	EST HUMAN	2.0E-41 AA328265.1	2.0E-41		34891	3 21370	8288
	<u>1</u>	2.0E-41 M86944.1	2.0E-41	1.36		21341	8259
Human B-cell specific transcription factor (BSAP) mixiva, complete cus	NT	20E-41 M96944.1	20E-41	1.36	34858	П	8259
Hemo capiens homolog of Nedd5 (nivedd5) mkina, complete cas	NT	2.0E-41 AF038404.1	2.0E-41	9.27	34409		7850
Homo sepiens integrin, beta 8 (II GB8) mKNA	BINT	4504778 NT	20E-41	0.98	33314	19919	6763
not2c07.51 NCL_CGAP_Phot Home capteins curve close invested a similar to guarded in the printing L-PROLYL CIS-TRANS ISOMERASE A (HUMAN);	EST HUMAN	2.0E-41 AA584575.1	2.0E-41	0.6	32132	18850	5656
Homo saplens chromosome 21 segment H321Cub/	NT	2.0E-41 AL163267.2	2.0E-41	1.23			4744
Homo sapiens chromosome 21 segment HS21COS/	NT	2.0E-41 AL163267.2	2.0E-41	1.23	30862		4744
Homo sapiens son of seveniess (Drosophile) homolog 1 (SUS1) MKNA		5032106	2.0E-41	0.69		17100	3941
15	EST_HUMAN	2.0E-41 A4449549.1	2.0E-41	0.69	٦	$\neg$	3406
Human ribosomal protein L23a mRNA, complete cds	NT	2.0E-41 U43701.1	2.0E-41	11.99	Ī		2889
G.gorilla DNA for ZNF80 gene homolog	NT	2.0E-41 X39631.1	2.0E-41	5.52			2347
Human mRNA for KIAA0207 gene, complete cds	NT	2.0E-41 D86962.1	2.0Ε-41	1.26			2293
EST35818 Embryo, 8 week I Homo saplens cDNA 5 end	EST_HUMAN	2.0E-41 A4331940.1	2.0E-41	2.17		П	2013
Human ribosomal protein L23a mRNA, complete cd3	N	2.0E-41 U.43701.1	2.0E-41	31.25	27827	14744	1871
601762940F1 NIH_MGC_20 Homo capiene cDNA clane IMAGE:40/26081 5	EST_HUMAN	3.0E-41 BF125922.1	3.0E-41	1.43		٦	12783
ef17f10.s1 Scares_tests_NHT Homo saplens cDNA clone IMAGE:T031947 3	EST HUMAN	3.0E-41 A4609768.1	3.0E-41	1.98		П	12196
QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA	EST_HUMAN	3.0E-41 AW 994941.1	3.0E-41	1.36		П	12119
QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cUNA	EST_HUMAN	3.0E-41 AW884841.1	3.0E-41	1.36		П	12118
y/75d08.r1 Scares breast 2NbHBst Homo sapiens cDNA Clone IMAGE: 1545/0 5	EST_HUMAN	3.0E-41 R54765.1	3.0E-41	0.71	٦	٦	7987
Homo saplens mRNA for KLAA1387 protein, partial cds	NT	3.0E-41 AB037808.1	3.0E-41	1.23			651
H. capiens mRNA for putative p64 CLCP protein	NT	3.0E-41 X37689.1	3.0E-41	11.76			609
complete cds)	NT	3.0E-41 AB026898.1	3.0E-41	4.03	30575	17595	4455
Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,						П	
Horno saplens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds	NT	3.0E-41 AB030176.1	3.0E-41	1.8	٦	П	970
	EST_HUMAN	4.0E-41 BE887118.1	4.0E-41	1.61	31942		13110
AV708431 ADC Homo saplens cDNA clone ADCARE02 5	EST_HUMAN	4.0E-41 AV708431.1	4.0E-41	1.3		25917	12900
Top Hit Descriptor	Top Hit Detabase Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
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Table 4

Single Exon Probes Expressed in Placenta

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20430	20254	19978	19978		13694		13364	П	18779	15494	П	П	П	22561	21746	14128	25904		26035	15311	13670	22450	22450	21797	25241	22673	17824	16450	Exxin SEQ ID NO:	
33892	33691	33386	33385			26683		31824	31824					36124						28439	26/02	36012				36243	30811	29471	ORF SEQ	
1.55	257	0.94	0.94	1.14	3.06	1.56	6.34	1.6	1.65	3.6		3.24	3.24		0.5	2.23	2.91		30.00	8.63	5.34	2.81	2.81	1.19	1.67	1.57	9.46	1.05	Expression Signal	
	7 5.0E-42		4 5.0E-42	4 5.0E-42	5.0E-42					Г											Γ	Τ					1.0∈-41		Most Similar (Top) Hit BLAST E Value	
5.0E-42 AI-071569.1	2 11417957 NT		2 11433063 NT	5730038 NT		BE21791	5.0E-42 AJ271735.1	6.0E-42 AB028990.1	6.0E-42 AB028990.1	6.0E-42 AW 238656.1		6.0E-42 AF012872.1	6.0E-42 AF012872.1	7.0E-42 AI204358.1	7.0E-42 R 10963.1	7.0E-42 AL163285.2	8.0E-42 AW 088062.1		8.0E-42 A.4493896.1	8.0E-42 AB026898.1	0.0E-42 A -003000.1	11560151		9.0E-42 BE179191.1	11526291	1.0E-41 AI217868.1	6678468 NT	1.0E-41 BE869735.1	Top Hit Acession No.	
NT	7 11	SNT	3 NT	BNT	NT	EST_HUMAN	NT	NT	NT	EST_HUMAN		NT	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN		EST_HUMAN	NT	1	2	Z	EST HUMAN	3	EST_HUMAN	NT	EST HUMAN	Top Hit Database . Source	
ndino sepietis mumu izquira cascuminoam rocponicon, processi su secondario sepietis mumu izquira cascuminoam rocponicon, processi su secondario sepietis se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se constituino se	Homo sapiens myoutouarin related protein 3 (wir wins), ""Ness II delta? isoform mRNA, complete	syndrome) (UBE3A), mRNA	Homo sepiens uniquim protein ligase E.A. (numen pepilium a virus accessorated protein, menus syndrome) (UBE3A), mRNA	Homo sepiens SET domain and mainter transposase rusign gene (SET inverty inverte handings	Homo Sapiens SE I comain and mainter unitsposses insert year (SE TRANS) THOMAS	hydren xi NCI_CGAP_Luz4 Homo sapiens curink dore invided 3 1 2002 3	Homo sapiens Ad pseudoaudosomai regiun, sagunent 172	Homo saplens mRNA for KIAA 1067 protein, parual cas	Homo sapiens mikiNA for KIAA 1007 protein, paruai cas	repetitive element;	xx20/08.x1 NCI_CGAP_HN10 Homo septens cDNA done IMAGE:2741799 3' similar to contains L1.t1 L1	Homo saplens phosphatdylinositol 4-kinase 230 (pi4K230) mKNA, complete cas	Homo sapiens phosphatidylinositol 4-kinase 230 (plan230) mrkva, complete cus	qf58g12.x1 Soares_testis_NHT Homo sapiens cUNA cione invace: 1,34276 3	y/38g04,r1 Soares fetal liver spieen 1NFLS Homo septens CDNA cione INA CE. 149 174 3	Homo sapiens chromosome 21 segment HOZ1CUSO	OFR repetitive element;	xc97a04.x1 NC]_CGAP_Bm35 Homo saplens cDNA clone IMAGE:2592174 3" similar to contains OFR.C2	18078P EXPRESSED SEQUENCE TAG MRNA;	complete cds)	Want DNA DIEC1 to ORCTI 4 cene region section 1/2 (DI EC1 ORCTI 3 ORCTI 4 genes.	Home services homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Homo sapiens hypothetical C2H2 zinc finger protein Ft. 192504 (Ft. 192504), mRNA	HC0-H10513-210300-032-g01 m10613 mono sapiens cover	Homo sapiens hypothetical protein FLUZU434 (FLUZU434), ITINIXA	qf75c10.x1 Soares_testis_NHT Homo sapiens culva cione invalor:1700000 3	Mus musculus tubulin alpha 6 (Tubab), mikiya	601445647F1 NIH_MGC_65 Homo sapiens CUNA Cione IMAGE3645603 3		

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Table 4
Single Exon Probes Expressed in Placenta

					06		
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
8978	8 22057	35599	288	5.0E-42	5.0E-42 AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10832			0.55	5.0E-42	11431168 NT	NT	Homo sepiens 3-hydroxyarthranilate 3,4-dloxygenase (HAAO), mKINA
10832	7	37488	<b>0.55</b>	5.0E-42	11431168 NT	NT	
11246	$\neg$		1.77	6.0E-42	8923162 NT	NT	Homo sepiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772			5.6		4.0E-42 AF055086.1	NT	Homo sapiens MHC class 1 region
772			5.6		4.0E-42 AF055066.1	Z	Homo sepiens MHC class 1 region
1091	7	27312	1.82		4.0E-42 AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cas
4311			1.39		X59417.1	NT	H. sepiens PROS-27 mRNA
4343			1.1		AF24621	NT	Homo sapiens SNARE protein kinase SNAR mr.NA, complete cas
4364			4.67			NT	Homo saplens regulatory factor X, 4 (Influences HLA class II expression) (NFA+) (IIINNA
4706	8 17841	30825	17.64	4.0E-42		ZT	Homo septens zinc tinger protein 177 (ZNP177) mizuka
5285	Т		0.93	Γ	/601035 NI	2	Tollio seperis DN EL OCTOZOCE Promi (DN E. COTTETT)
10884	23988	37697	232		4.0E-42 AW818530.1	EST HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiers cDNA
10884	П		2.32		4.0E-42 AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo saplers cDNA
11240	П		1.43	П	4.0E-42 Al435225.1	EST_HUMAN	ti11d02x1 NCI_CGAP_Pen1 Homo septens cDNA clone IMAGE:2130147 3
11698		38387	1.69		4.0E-42 BF035327.1	EST HUMAN	60146853TF1 NIH MGC 66 HOME SEDIENS CUIVA CIDITE INVAGE. 3002400 3
1512	2 14665	27750	3.79	Γ	2.0E-42 BF376834.1	EST HUMAN	RCQ-IN0079-110900-024-507 IN0079 Homo sapiens cuiva
2468	6 15593	28718	1.6		2.0E-42/AV690218.1	EST_HUMAN	A VOSUZIO GAL HOMO SEPIENO CUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUNA CIUN
2483	3 15610	-	4.24		2.0E-42 AW898344.1	EST_HUMAN	KC3-NNOU/G-2/0400-011-niu NNOU/G Flooring Sapielis CORK
2496	6 15623	28742			2.0E-42 AW 250059.1	EST HUMAN	2819283.3pnme NIH_MGC_/ none septents colver claims winder. ze rezest a
5875	5 19065	32372	11.82		2.0E-42 AW955368.1	EST HUMAN	ES 135/438 MAGE resequences, MAGC Homo septems cons
6876	6 19065	Γ	_	Ī	2.0E-42 AW955368.1	EST HUMAN	ES 1307436 MAGE resequences, MAGE INGIS S1 Homo septems cDNA clone IMAGE:18534173'
6892	2 20044	33452	0.9		2.0E-42 AI052586.1	EST_HUMAN	DWS3003.X1 Coares_lear_liver_splean_liver_c_c_or notice septed a coare claim invoc.
10046	6 23084	36685		Γ	2.0E-42 BE538919.1	EST_HUMAN	SUIDSTEAST IN IT MIGC TO TOMO Septems COVA COME INVOCESTATION
10260	0 23295	36892	0.64		2.0E-42 P81649	SWISSPROT	ABONUCE RACE SACRESA
10260		36893	0.64		20E-42 P81848	SWISSPROT	RIBONUCLEASE X3 (KNASE X3)
12037	7 25019	38723	1.53		2.0E-42 AL163246.2	3	Homo sapiens chromosome 21 segment Hoza Cu4o
762	2 13932	26977	1.75		X57147.1		Human endogenous retrovirus PHE. 1 (ERV9)
1067	14233	27292	2.2		1.0E-42 AW 295809.1	EST_HUMAN	UI-H-BIT-erin-e-04-0-UI-ST NCI_CGAP_SubS Homo sapiens cons done immoci
1125		27345	1.74	1.0E-42	AJ251818.1	NT	Homo septens partial C9 gene for complement component C9, exchi
1125			1.74		.0E-42 AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
	- 1				A DE 10 A E DE 7 4 6 6 4	Z-1	Homo septens NADH-ublquinone oxdoreductase AGGG subunit precursor nomolog mixNA, nuclear gene encoding mitrochondrial protein, complete ods
	10000	04417	11.00	Γ	2007 100.		

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						Single	e Exon Proper	Single Exon Propes Expressed in Placella
_ g _ g	Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
Т		33	27400	11 00	1 0=-40	1 0E-42 AE087166 1	NT I	Homo saplens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete ods
Т	<u> </u>	14884	27977	1.15	1.0E-42	23219	ZT	Hamo sapiens rec (LOC51201), mRNA
Т	28 7	15227	28349	1.18	j	1.0E-42 AF110296.1	NT	1
Т	2609	15733	28849	1.42		5174458 NT	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
1								Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated
	3029	16205	29228	9.15	1.05-42	4505524 NT	NT	products
	3799	16960	29984	3.31	1.0E-42	7662027 NT	NT	Homo sapiens KIAA0255 gene product (KIAA0255), ITKINA
	3895	17054		1.11	1.0€-42	5031610 NT	NT	Homo sapiens Goigi vesicular membrane danicking protein pio (oc. i i) movey
	4036	17192		66.0		1.0E-42 AL163267.2	NT	Homo sapiens chromosome 21 segment no210007
	4361	17504		3.47		1.0E-42 All.163280.2		Homo sapiens chromosome 21 segment riozitouov
	4716	17851	30834	0.61		AW813617.1	EST HUMAN	RC3-S10197-101099-012-803 S10197 Figure septems CONS
Г	4867	18000	30984	2.37		5803122	Z	Tomo superior procession in include a poly
Γ	4867	18000	Γ	2.37	7.05-42	1	1	Long applient removing heavy (1997) mRNA
Τ	4801	18031	Γ	6.13	Ī	1000/0004	ECT LINAM	A01304125E1 NIH MGC 21 Homo sepiens cDNA done IMAGE 3638310 5
Ţ	1	74507	Τ	1.29	Τ	1.0E-42 DI-4000 1.1		Homo sanjens chromodomain protein. Y chromosome like (CDYL) mRNA
T	10201	22020	26962	27.00	T	8 0E-43 AV/736R24 1	EST HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
<b>T</b>	8 8	13855		20.77		8.0E-43 AV736B24.1	EST HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
_	78	13900	1	5.12		8923276 NT	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
_	718	13900	26939	6.12	8.0E-43	8923276 NT	NT	Homo sapiens hypothetical protein rLJ2029/ (rLJ2029/), mknA
	718	13900	26940	5.12		8923276 NT	NT	Homo saplens hypothetical protein HLJ2U29/ (FLJ2U29/), IRINNA
	5816	19006	32312	0.72	]	8.0E-43 H13952.1	EST HUMAN	1 Notes placenta No2Hr Homo sapiens CUIVA cione livix GE. 140 174 0
T	3731	16892	29898	7.48	T	7.0E-43 A\V246442.1	EST HUMAN	um89h01 x1 NCI CGAP Brn25 Home sablens cDNA clone IMAGE:2466985 3' cimilar to TR:015475
	8968	22047		3.98		7.0E-43 A1336748.1	EST_HUMAN	016475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element;
	1374	14529		11.62		6.0E-43 AA491890.1	EST_HUMAN	ne72d06.s1 NCI_CGAP_Ew1 Homo septens cDNA clone IMAGE:309803 similar to go:Lubuva oub RIBOSOMAL PROTEIN L30 (HUMAN);
_	2657	15780		4.03		6.0E-43 AV708201.1	EST_HUMAN	AV708201 ADC Homo sepiens cDNA clone AUCACCTU 3
	4983	18092	31068	252.27		6.0E-43 AI421540.1	EST_HUMAN	#29604X1 NOI_CGAP_Bm23 Homo captens cuna cione image::2007316 3 similar to switching_15856 PRE-MRNA SPLICING HELICASE BRR2;
	6441	19608	32971	263	6.0E-43	9955973 NT	NT	Homo sapiens ATP-binding cassette, sub-family C (CF I MANY), member 3 (ADCCS), warswript variant MRP3B, mRNA
Г		Į	ſ					

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Table 4
Single Exon Probes Expressed in Placenta

8371 8371 10521	105 83	8 8	3 8	~_ ಜ	-	1200	3	6499	5373	60	Ţ.	14213	11001	10651	10609	900	200	3 8	8381	<u>.</u>	7043	AA35	2908	5,	إ	11383	10056	7048		Probe SEQ ID NO:	
-	111 25227	21 23550	1		71 21482	2000	I	Т	1	895 15987	Т	Т	٦		09 23643	22/00	Т	Т	81 21462	Т	20000	Т	Т	Т	Т	╗	36 23094	48 20101	1	NO:	
_	7	3/164	T		2 34975	1	1			7 27227				5 37295	37251	. 302/2	Τ	Ţ	34986	T		T	-	26736	5		\$ 36696	33518		ORF SEQ	
	2.7	1.02		л 18	5.18					4.4				1.02	2.6	4.00			0.64						1.82	2.45	1.77	1.50		Expression Signal	
_		4.08-43	Ī			Ţ		$\exists$			T						Τ	Ī		T	T	T	Ī							Most Similar (Top) Hit BLAST E Value	
	4.0E-43 R20950.1	INI JOSCOCO	800.508	4 0F-43 A1244341 1	4.0E-43 AI244341.1			6996009 NT	4.0E-43 A1056338.1	4.0E-43 AF003528.1		6.0E-43 W/29011.1	5.0E-43 AW 863007.1	5.0E-43 All.049110.1	5.0E-43 Al733244.1	0.0E-10/1400200.1	A // 486388 4	5.0E-43 H74277 1	5.0E-43 AA442271.1	5.0F-43 AA442271.1	6.0E-43 Al613509.1	5.0E-43 A1613509.1	5.0E-43 AV732578.1	5.0E-43 AA382780.1	5.0E-43 AL163213.2	6.0E-43 AL119158.1	6.0E-43 A-X195154.1	6.0E-43 AW 468897.1		Top Hit Acession No.	
-	EST_HUMAN	N. I	TINT	EST HUMAN	EST_HUMAN		BNT	- 1	EST_HUMAN	NT		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	1010000	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	Ŋ	EST_HUMAN	EST_HUMAN	EST HUMAN		Top Hit Database Source	
th92b12.x1 Soares NSF F8 9W OI FA F ST Homo sapiens colve clore investigation of strings of		vc06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10	Homo sepiens zinc finger protein 161 (ZNF161), mRNA	g/76e02x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1865354 3' similer to contains MER10.t3	MER10 repetitive element;	qi76a02.x1 NCI CGAP KId3 Homo sepiens cDNA clone IMAGE: 1865354 3' shrilar to contains MER10.13	Homo sapiens protocadherin beta 6 (PCDHB6), mRNA	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA	oy47h03.xt NCI_CGAP_Bm23 Homo captens cDNA clone IMAGE:1669013 3		Homo sapiens X-linked anhidrotitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	55a4 Human retina cDNA randomly primed sublibrary Homo sepiens cDNA	MR2-SN0007-290400-004-c02 SN0007 Homo septens CUNA	DKFZp434D0119_r1 434 (synonym: https3) Homo septens GUNA clone UKFZp434U0118		052c10.x5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591	aa33d08.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:815055 5'	yu49g12.r1 Soares fetal liver spicen 1NFLS Homo sepicns cDNA clone IMAGE:220510 5	zv54a03.r1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:757420 5'	2054a03.r1 Scares testis NHT Homo sapiens cDNA clone IMAGE:757420 5	tw22e07.x1 NCI_CGAP_Brn52 Homo saplans cDNA clone IMAGE:2260452 3'	w22e07.x1 NCI_CGAP_Brn52 Homo septens cDNA clone IMAGE:2280452 3'	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'	EST96033 Testis I Homo saplens cDNA 6' end	Homo sapiens chromosome 21 segment HS21C013	DKF2p761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKF2p761L1712 5	G529641 DB1, COMPLETE CDS. ;contains element PTR7 repetitive element;	WENT Source NhHMPH S1 Homo sablens cDNA clone IMAGE:665410 5' similar to TR:G529641	hd30b04x1 Scares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2810981 3' similar to contains	Top Hit Descriptor	

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			I			ſ	[
Homo sepiens Sp4 transcription factor (SP4) mKNA	BNT	4507168 NT	1.0E-43		33292		6744
Homo sapiens Sp4 transcription factor (SP4) mRNA	BINT	4507168 NT				П	6744
Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PUK3) mKNA	4 NT	4885544 NT	1.0E-43			18723	5526
602022313F1 NCI_CGAP_Bribt Hamo sapiens curva cione invasce: + 101000 0	EST_HUMAN	1.0E-43 BF348283.1		4.73	29009		2786
Homo sapiens chromosome 21 segment Hoz 10084	Z	1.0E-43 AL! 163284.2		4.12	27985		1742
Homo sapiens Res-like & Fromoting protein (RADZA) Belle, example to and a	N.T	1.0E-43 AF154836.1	Г	2.95	27918	14833	1681
Homo sapiens Nas-like & Creationing protein (Napaziv) Benis, exams to and a	Z	1.0E-43 AF154836.1		2.95	27917	14833	1681
	EST HUMAN	2.0E-43 T03007.1				24535	11476
Turner indescribe State of Land Springs of No. 4000 EBACR 3'and similar in INIT-1		2.0E-43 U43701.1		3.16		21584	8503
United the complete in the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the com	EO HOMAN	2.0E-43 AW 207390.1			33973	ľ	7426
INITIA BIT of COOL II ST NOT COAP Sub3 Homo serdens cDNA clone IMAGE:2721712.3'	EU TOMAN	2.0E-43 BE222/18.1		1.2	Γ	П	6604
hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:31/3/50 3 similar to contains element	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					$\neg$	
	EST_HUMAN	2.0E-43 BE222778.1		1.2	33152	19764	6604
hu53a08.x1 NCI_CGAP_Bm41 Homo septens cDNA clone IMAGE:3173750 3' similar to contains element						7	
	EST_HUMAN	2.0E-43 A   190764.1	2.05-43	7.24		13410	188
Homo septens on I contain and thanks decisions on the Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of Contains of	N	5730038 N I	3.0E-43	1.42	38712	25010	12026
none sapiers similar to druming concerns the concerns of the concerns (SETIMAR) mRNA	N	11420217 NI			36709	23106	10068
idili Sepiralia in production of the content of the sepiral (I OCS3648) mRNA	2	IN 12/100/	3.05-43		35639	22099	8020
Long regions troubled or order (HSA011916) mRNA	EST HUMAN	3.0E-43 AV468824.1	3.0E-43	4.39	Γ	Г	8357
ea88111.51 Stratagene fetal retina 937202 Homo sapiens CUNA cione IMAGE:835413 3 Stritturi di contami e Trub di Trub constitue alemant:							
Human ribosomal KNA upotroam binding transcription (actor (opin) getre, parest cas	3	3.0E-43 U55487.1	3.0E-43	5.09	33428		6887
Mus musculus otogelin (Otog), mkina	NT	7305360 NT	3.0E-43		33017		6487
Mus musculus otogelin (Otog), mknyk	NT	7305360 NT	3.0E-43	1.56	33016	19654	6487
Human I BANS I gene for information bytanese, promote region and soon i	Z	-	3.0E-43 D34613.	0.94	32515	19198	6014
TRYACT TO A transportation of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of	EST_HUMAN	3.0E-43 AA548154.1	3.0E-43		30532	17548	4405
ALEGADO 44 NCI OCAB D.7 Homo socione con a chore IMAGE: 1017419		3.05-43 368002.1	3.UH-43		Γ	Г	3662
AML1-EV-1=AML1-EVI-1 fusion protein (rearranged translocation) [numan, leukemic ceil line Son 1, initivo Numan, 5038 nti	<del>-</del>	2					
MSR1 repetitive element;	EST_HUMAN	3.0E-43 RB3422.1	3.0E-43	1.1	28377	16055	2120
yp82f01.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:193945 5' similar to contains		-				٦	
H. sapiens gene encoding La autoantigen	ZT	3.0E-43 X97869.1	3.0E-43		27971	П	1730
spliced	3	3.0E-43 AF223391.1	3.0E-43	3.46		14399	1240
Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively							
	Source	į	Value	ę.	Ç	O	Ö
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Exon SEQ ID	Probe SEQ ID
Single Exon Prodes Expressed in Placerita	e Exon Probes	Singi			•		•

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Single Exon Probes Expressed in Placenta

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	Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	7106	18533	31488	1.19	1.05-43	1.0E-43 R19751.1	EST_HUMAN	yg40e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34732 5' strillar to SP:8D38_MOUSE P28656 BRAIN PROTEIN DN38 ;
	8117	T	34720	0.6	1.0E-43	.0E-43 AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
-	8256	П		2.17		1.0E-43 AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA211) gene, partial cds
	9037	П	35659	28.54		1.0E-43 AW 963676.1	<u>L</u>	EST375749 MAGE resequences, MAGH Homo sapiens CUNA
	10498	П		0.66	1.0E-43	1.0E-43 AW853228.1	1	EST365299 MAGE resequences, MAGE Homo capiens CUNA
	11206		37912	5.81	1.0E-43	1.0E-43 AI984861.1	THUMAN	
	11647		38418	3.05	1.0E-43	24378	NT	Homo sapiens calcium channer, voitage-dependent, alpina ile suburiii (CACAA) ile, illinivo
	12248			2.29		1.0E-43 AL137984.1	EST_HUMAN	UKFZp/81U1015_71 /61 (Synonym: namyz) nomo sapianis cultin ciuna enti episte i e i e i e i e i e i e i e i e i
	12550	Г		3.16		1.0E-43 A)875416.1	EST HOMAN	Wideboury I INCL Config. 120 Long septembers Chang receptor 1 (CELSR1), mRNA
	12805	Τ		5.21	T	9 0E 44 A POCCIO VV 30 0	EST LIMAN	
	913	14088	27154	6.32		8.0E-44 AI222985.1	EST_HUMAN	T_GBC_S1 Homo sapiens
	8736		1	2.86		8.0E-44 X94354.1	NT	
	10545			0.5		11423497 NT	NT	Homo sapiens small proline-non protein 20 (Spopson) mBNA
	10545	23580		0.5		423497	2	16
	11436	Т		2.87		8.0E-44 Y10488.2	N	Lomo seniene myosin mRNA partia cds
	/BALL	Т	T	200	T	0.0E 44 L.0130.1	TIN	Homo saplens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
	12544	25735	31946	2.17			NT	Homo capiens putative nuclear protein (HRIHFB2122), mRNA
	12945	П		1.85	8.0E-44		NT	
	13126	П	31946	2.29		11418086 NT	1	Homo sapiens putative nuclear protein (HRIHF02122), mr.ivA
	676	13862		1.13		7.0E-44 R06035.1	EST_HUMAN	
	2307		28573	1.19	ľ	5031886 NT	NT	Homo sapiens Liw domain-containing pretering delistication beduter in abund (Lin / minute)
	3031	16207	29228	4.44		7.0E-44 Al-048729.1	2	Hollo Sapletis fill trade in the first region
	3031	16207	Γ			7.0E-44 AF-048729.1	Z	Homo sapiens minisatellite missa repeat egivii
	3965	Γ.	Γ			7.0E-44 AL 163284.2	i	Homo sociene chomosome 21 Inknown mRNA
	4366	Ι.	Γ			0E-44(AI-231919.1	2	Homo sepiens chromosome 21 unknown mRNA
	4300	Т	3/000	3 20		7 0F-44 All160839 1	EST HUMAN	AU159839 Y79AA1 Homo saplens cDNA clone Y79AA1000496 3*
	330	10404	T		T	6.0E-44 Z:0946.1	EST HUMAN	HSAAADEYU P, Human foetal Brain Whole tissue Homo sapiens cDNA
	314	Ţ	T			5.0E-44 AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
	342	П		242		5.0E-44 A.1289880.1	NT	Homo sapiens KIAA0851 gene (pertiel), XT3 gene and LZT FL1 gene

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Single Exon Probes Expressed in Placenta

607/269/14F1 NIT_MOC_44 HOLID September Color Guille Transcription	EST_HUMAN	2.0E-44 BE389058.1		1.8	35437	21898	8819
Homo sapiens vesicle rensport-related protein (NAAVes 17), maya	ONT NT	7706370 NT				21703	8623
Homo sapiens vesicle transport-related protein (Albade 17), initiativa	ONT					3 21703	8623
Homo sapiens giutemate receptor, metabotropic 3 (GKM3), mRNA	BNT				34122	20644	7572
Homo sepiens glutamate receptor, metabotropio 3 (CKM3), mRNA	6 NT	11419226	2.0E-44	3.8	34121	20644	7572
Homo capiens general transcription factor 2-I (GTF2I) mRNA, alternatively spliced product, complete cds	N <sub>1</sub>	2.0E-44 AF038968.1		2.18	31507	18515	6996
Homo saplens chemokine (C-C motif) receptor 9 (CCR9), mKNA	1 NT	11449901 NT	2.0€-44	1.75	П	19395	6220
PM4-SN0016-120500-003-e.04 SN0016 Homo sapiens CUNA	EST_HUMAN	20E-44 AW864379.1					4692
Homo saplens DNA for amyloid precursor protein, complete cos	NT	2.0E-44 D87675.1		1.34	29740		3559
Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mixina	3 NT	5901933 NT		2.3			2676
Human mRNA for integrin alpha subunit, complete cds	ŇŢ	D25303.1		0.94	28879		2642
Homo capiens tumor necrosis factor (ligand) superfamily, member 10 ( INFSF10) MIXINA	2NT	4507592 NT	2.0E-44	1.28			2605
Homo sepiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cos	TN	2.0E-44 AI-070661.1		50		_ {	2219
P22069 OXYSTEROL-BINDING PROTEIN.;	EST_HUMAN	2.0E-44 BE466325.1			27628	14554	1400
Homo sapiens RAB36 (RAB36) mRNA, complete cas	NT	2.0E-44 AF133588.1		8.82	27568	14496	1340
Homo sapiens transmembrane trafficking protein ( IMP21), mKNA	NT	5803200 NT	2.0E-44	3.61		П	1234
Homo sapiens transmembrane trafficking protein (10022), mKNA	NT	5803200 NT	2.0E-44	3.61			1234
Homo sapiens DEAD/H (Asp-Giu-Ale-Asp/His) box polypeptide 1 (UUX1) mknA	5 NT	4826685 NT		1.43		П	1074
Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (UDX1) mRNA	5 NT	4826685 NT					1074
Sus scrofa domestica submadilary apomuoin mRNA, complete cds	NT	3.0E-44 AF-005273.1				٦	9719
601510547F1 NIH_MGC_71 Homo sapiens cDNA clane IMAGE:3912010 5	EST HUMAN	3.0E-44 BE884820.1				П	7970
2018b05.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE: 608777 5	EST_HUMAN	3.0E-44 AA169851.1			29350	П	3167
Homo sapiens keryopherin elpha 6 (importin elpha 7) (KPNA6), mRNA	NT	6912477 NT	٦	1.5	7	П	1827
Homo saplens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds	NT	4.0E-44 U30878.1		5.64	38247	П	11513
RC3-HT0585-010400-023-d08 HT0585 Homo saplens cDNA	EST_HUMAN	4.0E-44 BE176618.1	4.0E-44	0.71		П	9079
Human fibrillin (FBN1) locus polymorphism	NT	4.0E-44 L21948.1	4.0E-44	0.86		╗	8468
601508601F1 NIH_MGC_71 Home sapiens cDNA clone IMAGE.3910152.5	EST_HUMAN	4.0E-44 BE883178.1	4.0E-44	0.87	34187	Т	7639
ti11d02x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:21301473	EST_HUMAN	4.0E-44 A 435225.1	4.0E-44	0.89		Т	5128
Homo sapiens chromosome 21 segment HS21C103	NT	4.0E-44 AL163303.2	4.0≅-44	4.27	29678	╗	350
AU124571 NT2RW4 Homo sapiens cDNA clone NT2RM4000218 5	EST_HUMAN	5.0E-44 AU124571.1	5.0E-44	1.39			9584
tn40d02x1 NCI_CGAP_Brn25 Homo septens cDNA clone IMAGE:2170083 3 similar to contains OFR. n OFR repetitive element ;	EST_HUMAN	5.0E-44 AI568523.1	5.0E-44	4.12	34673	21154	8072
Top Hit Descriptor	Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	SEQ ID
	Ton Hi		Most Similar			n i	7

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Single Exon Probes Expressed in Placenta

repetitive element;	EST_HUMAN	6.0E-45 AI875425.1		236	5	3 14735	1583
wb99c06.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2313802 3" similar to contains L1.t1 L1		-				┑	Ţ
EST90893 Synovial sercoma Homo sepians cuiva o end	EST HUMAN	8.0E-45 AA377985.1		1.03	0 34902		8298
Homo sepiens TRK-tused gene (NOTE: non-standard symbol end name) (TFG) minutes	8 NT	5174718 NT	8.0E-46	9.63	5 31283	П	5193
	NT	5174718 NT	8.0E-45	3.9		7	2591
Homo capiens mRNA for KIAA0995 protein, partial cos	NT.	9.0E-45 AB023212.1		1.41			6787
Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRINA	INT	8922391 NT		0.98	30822	1 17836	4701
Homo sapiens hypothetical protein FL/10379 (FL/10379), mR/NA	NT		9.0E-45		9 30821		4701
RC1-CT0198-150998-011-CU8 C10198 Homo sapiens CUNA	EST_HUMAN	AW8469			38575		11890
IRC1-CT0198-150999-011-CUS CT0198 Homo sapiens CDNA	EST_HUMAN	1.0E-44 AW846967.1		3.21	38574	0 24878	11890
Homo sepiens Sush domain (SCK repeat) containing (propagal), mixwx	N.	10092664 NT			38505	0 24809	11820
AV714608 UCB Homo sapiens curva cione UCBD TEUS S	EST HUMAN	AV7146		4.13	3	4 24333	11264
qx88g07.x1 NCI_CGAP_GC6 Homo sapiens cuina cigne invasce.2009020 3	EST_HUMAN	1.0E-44 A 337183.1		0.56	5 35848	7 22305	9227
Homo saplens chromosome 21 segment H321C0U9	NT	1.0E-44 AL163209.2			7 35468	8 21927	8848
EST379147 MAGE resequences, MAGJ Homo sapiens conva	EST_HUMAN	1.0E-44 AW967073.1		0.91	35071		8460
	EST_HUMAN	1.0E-44 AW967073.1		0.91	1 35070	21541	8460
Homo sapiens alpha satellite UNA, Mi monomer type	3	1.0E-44 AJ130755.1		0.68	31315		5221
Homo sapiens alpha satellite UNA, M1 monomer type	NT	1.0E-44 AJ130755.1		0.68	31314	╗	5221
ag01c09.s1 Soares_NhHMPu_S1 Homo sapiens cuiva cione images o i 1804 3	EST_HUMAN	1.0E-44 AA455869.1		3	T.	16979	3819
	Z	1.0E-44 AF198779.1		1.74	29043	15932	2818
JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,							
Homo septens transcription factor IGHM chhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,					T	Т	
zw63d02 r1 Scares_total_fetus_Nb2Hr8_9W Homo sapiens cUNA cione invisce: (13700 9 similar to contains THR.13 THR repetitive element;	EST_HUMAN	1.0E-44 AA434554.1	1.0E-44	6.17	28564	15431	2299
ontains THR.63 THR repetitive element;	EST_HUMAN	1.0E-44 AA434554.1	1.0E-44	6.17	28563	15431	2299
- E2-22 - Comparison of the Nh2HER Ow Homo senions cDNA clone (MAGE: 773763 5' similar to		1.0E-11/02003:5		0.00		14/20	1000
Homo septens chromosome 21 segment HS21C103		1 DE-74 OF 183303 2		908		Т	1224
RC1-BN0039-110300-012-b01 BN0039 Homo septens cDNA		AWGGARGS 1	١		T	Т	3 8
RC1-CT0249-030300-026-h12 CT0249 Homo saplens cDNA	EST HUMAN	AW8531:			1	T	20.0
Homo saplens Misshapen/NIK-related kinase (MINK), mRNA	TN					П	53
Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	NT	7657334 NT			26306	Т	83
Homo sepiens neuronal cell edhesion molecule (NRCAM) mRNA	NT	4826863 NT	2.0E-44	1.56		╗	12730
TCBAP (E2795 Pediatric pre-B cell acute lymphobiastic leukemia Baylor-HGSC project= i CBA notino septensi cDNA clone TCBAP2795	EST_HUMAN	2.0E-44 BE244902.1	2.0E-44	4.59		25122	12152
	Source	No.	BLAST E	Signal	D NO:		N I
. Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	0	SEO D	Probe
The cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperation of the cooperati	Oligio Exort 10000	ري. نو					

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Datebase Source	Тор Hit Descriptor
4087	17242		3.77	6.0E-45	6.0E-45 AW157670.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo saplens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
12911	П		1.89	6.0E-45	8213		Homo saplens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
916	7		1.71	6.0E-46	6.0E-46 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2058		28313	4.42	5.0E-45	5.0E-45 BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA
3081			2.87	5.0E-45	5.0E-45 A1523766.1	EST HUMAN	tg94f07.x1 NCI_CGAP_CLL1 Homo septens cDNA clone IMAGE:2116453 3' stimiter to SW:PAX1_MOUSE   P09084 PAIRED BOX PROTEIN PAX-1.;
							zt/2d03.s1 Sogres_testis_NHT Homo sapiens cDNA done IMAGE:727877 3' similar to contains element
5629	18823	- 31897	8.95	5.0E-45	5.0E-45 AA397781.1	EST_HUMAN	TAR1 repetitive element;
6143	٦	32664	1.09	5.0E-45	5.0E-45 Y18933.1	ZT	Homo sapiens MCP-1 gene and enhancer region
6143	19321	32665	1.09	5.0E-45	5.0E-45 Y18933.1	NT	Homo septens MCP-1 gene and enhancer region
6190		32714	0.92	5.0∈-45	5.0E-45 AB022318.1	NT	
6100		32715	0.92	5.0E-45	5.0E-45 AB022318.1	NT	Homo saplens mRNA for Inducible nitric oxide synthase, complete cds
6318	_	32847	0.87	5.0Ε-45	11496268 NT	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6318		32848	0.87	5.0E-45	11496268 NT	NT	Homo sepiens zine finger protein 277 (ZNF277), mRNA
8471			1.12	5.0E-45	11418704 NT	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9241			1.46	5.0E-46	4769223 NT	NT	Homo sepiens programmed cell death 5 (PDCD5), mRNA
11897		38688	25	5.0E-45	8923698 NT	NT	Homo sapiens golgin-like protein (GLP), mRNA
1167		27386	6.3	4.0E-45	4.0E-45 X95826.1	NT	
2365	15496	28622	2.16	4.0E-45	4.0E-46 BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cUNA clone IMAGE:3538425 5
0167	3000		2	4 25 45	4 05-45 4 228220 1	TOT HIMAN	no26e07.c1 NCI_CGAP_Pr1 Homo sapiens cDNA clons IMAGE:1009284 similar to contains etement L1 repetitive etement :
12166	26089	31659	1.36	4.0E-45	35947		Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3411	П		0.83	3.0E-45	3.0E-45 T/71480.1	EST_HUMAN	yd35f07.r1 Scares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5
4199			1.03	3.0E-45	3.0E-45 T/71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo saptens cDNA clone IMAGE:110245 5
6366		32895	1.34	3.0E-45	6753651	3	Mus musculus dynein, exon, heavy chain 11 (Dnahc11), mRNA
6366			1.34	3.0E-45	6753651 NT	1	
8645	П		1.76		3.0E-45 AV723976.1	EST HUMAN	AV723976 HTB Homo sepiens cDNA clone HTBAAG01 5
8991		35610	4.31	3.0E-45	4758451 NT	3	Homo sapiens golgi autoantigen, golgin subfamily e, 2 (GOLGA2) mRNA
10515	23550	37169	7.62		3.0E-45 AL163227.2	3	Homo saplens chromosome 21 segment HS21C027
10515			7.52		3.0E-45 AL163227.2	Y	Homo sapiens chromosome 21 segment HS21C027
13040	26078		3.45		3.0E-45 X89211.1	3	H.sapiens DNA for endogenous retroviral like element
2572	15697		3.12		20E-45 AL163218.2	3	Home saplens chromosome 21 segment HS21C018
3097	1	29287	0.92		2.0E-45 AU243213.1	N	Horno sepiens partial 5-HT4 receptor gene, exons 2 to 5

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Table 4
Single Exon Probes Expressed in Piacenta

Commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of the commence of th	EG TIOMS	8.0E-40 AVV 240804. I	Γ	6.89	3/335	7 23730	10697
2822449 5 Mill MGC 7 Hamo septens cDNA clone IMAGE:2822449 5	DOT LI MAN	B.OC-40 M. 100ZOS.Z			T	Τ	8835
Homo satiens chromosome 21 segment HS21C009	2	3	1		Ī	Т	100
Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	3 NT	8910293 NT				T	043
Homo sapiens calcium channel, votage-dependent, alpha il subuni (CACIVA II), nuava	7NT	11418157 NT	1.0E-45	4.02	31963	7 25686	13047
nomo sapiens nan Gilnase acuramis protein i (nances i), misura	ZNI		1.0E-45	6.42	7	26387	12668
nome sapens ripoureuces process research ( Executor ), many research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research and research a	NI NI			19.43	_	2 25384	12562
From separa prises C. apria prises present Prises C. J. 1995	2				32117	25263	12369
THE CONTROL PRINTS OF A PARTIES PRINTS PRINTS IN LAND WAS A PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF THE PRINTS OF TH	2	AB0022				2 22787	9722
OUISTIAZONI NIM JWOCZ / I HONO Reptetia como camo minochio intercenta	EST_HUMAN	1.0E-45 BE887843.1			35950		9321
Homo sapiens DIVA for emyoto precursor protein, complete due s		1.0E-45 D87675.1				1	8806
	NT	11422236 NT			34823	21302	8220
Homo septems percondumate organisation of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr	NT				34822	21302	8220
Homo sabiens niben protein (NIBAN), Inciva	S N			1.56	31181	18209	5081
And Port Spaces letter like Spice in Inc. In Indian Sapieta Control Control Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice in Inc. Spice	EST_HUMAN	H57443		1.05		17981	4848
601289116F1 NIH_WGC_o nomo sepiens convo cione impost. so isoso o	EST_HUMAN	1.0E-45 BE396633.1		6.4	30716	17736	4699
Homo septens mixINA for NIAATO91 protein, peruei cas	Z	1.0E-45 AB048811.1	1.0E-45	0.69	29836		3664
Homo sapiens chromosome 21 open reading frame 1 (V2 i Griv), illivivo	NT	8559558 NT	1.0€-45	0.85		16746	3581
Human pro-e2 chain of collegen type At (COLTIAA) gene, complete cas	NT	U32169.1	1.0E-45	. 10.41			3172
Homo sapiens Langerinas celi specific c-type iscar (L-vivocchin), mivo	NT	7657290 NT	1.0E-45	1.66	27423	14363	1201
Homo sapiens KAPTA, member of KAR oncogette variety (INATIO), mento	N		1.0E-45	1.02	26714	13679	485
	EST_HUMAN	1.0E-45 BE389855.1	1.0E-45	1.00			422
601284360F1 NIH_MGC_44 Homo septens out to close introduction of	EST_HUMAN	1.0E-45 BE389855.1	1.0E-45	1.22		13617	126
Homo sapiens calcium chartret, voltage-dependent, alpha in outrem (concernit),	Z	11418157	2.0€-45	2.73		25710	13087
XD 72803.XT NCI_CGAP_CV40 Homo sapiens colvin ciolle invocazi recordo		2.0E-45 AW270280.1	2.0E-45	3.35	38482	24784	11794
XP / 2803 XT NCI_CGAP_CV40 Floring septens CDVA cibile INVOCE:2745088 3'	EST_HUMAN	2.0E-45 AW270280.1	2.0E-45	3.35	38481	24784	11784
TR:G1144569 G1144569 R-SLV1.;	EST_HUMAN	2.0E-45 AA458770.1	2.0E-45	2.71	38177	24510	11450
	E01   1018511	2.0E-45 DE834300.1	V.011-40	12,00	3//84	79907	11042
1/30_HT092_190800-201-e02 HT0923 Homo sapiens cDNA	L	2.0E-45 A1030700.1	2.00-45	0.01	Γ	Т	9784
Insering of CGAP Kid8 Home sapiens cDNA clone IMAGE:2232552 3	EST LINAN	2.0E-45 AW834834.1	2.0E-45	0.91	Γ	Т	8610
	L	2.UE-40 DE /02 104.1	2.0E-40	1.1	Ī	Г	7786
	THIMAN	DE 70.00 A	200 10		Τ	Т	9
Human eosinophil Chercot-Leyden crystal (CLC) protein (hysophospholipase) gane, promoter and exon 1	NT	2 0E-45 1 01665.1	2.05-45	5.45	33108	10910	R I
	Source		Value		5		N Ö
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit.	Expression	ORF SEQ	Exon SEQ ID	Probe SEQ ID
	On Bio Cyclin 10000	01.8					

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Table 4
Single Exon Probes Expressed in Placenta

							0.0
Probe SEQ ID	SEQ ID	ORF SEQ	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Тор Hit Descriptor
2513	15639	28760	7.67	8.0≅-46	8.0E-48 A1433261.1	EST_HUMAN	ti32708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similer to gb:J00314_me2 TUBULIN BETA-1 CHAIN (HUMAN);
2	535	20764	7.67	a 0⊑ .aa	8 0E-48 A1433261 1	EST HUMAN	ti32/08.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similer to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);
8244	21326		272	8.0Ε-46	8.0E-46 BE167244.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4703	17838		4.79	7,0E-46	7.0E-46 BE386165.1	EST_HUMAN	601277282F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3818118 5
4928	18058		1.33	7.0E-46	7.0E-46 BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6167	19343	32689	4	7.0E-46	22708	TN	Homo sepiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6623	19783	33171	1.8	7.0E-46	7.0E-46 BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cUNA clone IMAGE:4042735 5
12706	25469		2.6	7.0E-46	7.0E-46 AL163248.2	NT	Homo saplens chromosome 21 segment HS21C046
2812	15028	250037	6.87	6.0E-46	6 0E-46 AI884381.1	EST HUMAN	wm3108.x1 NCI_CGAP_Ut4 Home septens cDNA cone IMAGE:243/3/3 3 similar to contains with 13:2 MER18 repetitive element;
1					-		wm31f08.x1 NCI_CGAP_Ut4 Homo saptens cDNA clone IMAGE:2437676 3' eimitar to containe MER19.2
2812	15926	29038	6.87	6.0≿-46	6.0E-46 A1884381.1	ES I_HUMAN	INFERENCE A NO. COAD KIER Home series cONA close IMAGE: 2232835 3' similar to TR: 060363 060363
6257	19431	32778	11.57	6.0Ε-46	6.0E-46 A1635448.1	EST_HUMAN	SA GENE.;
7000	3	33007	0 00	8 OF -46	8 0F-48 AW513244 1	EST HUMAN	x642604.x1 NCI_CGAP_UI1 Homo sapiens cDNA clone IMAGE:27066543' similar to gb:L08069 DNAJ  PROTEIN HOMOLOG 2 (HUMAN);
7541	20614	34091	0.67		6.0E-46 BF509740.1	EST_HUMAN	UI++BI4-apg-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo capiens cDNA clone IMAGE:3087298 3
11673	23901		2.14		6.0E-46 BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Hamo sapiens cDNA clone IMAGE:3880995 5
209	13432		5.31		6.0E-46 AL163210.2	N-T	Homo sapiens chromosome 21 segment HS21C010
3017	16781	29798	1.17		5.0E-46 BE677194.1	EST HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo septens cunA cione IMAGE:3270408 3
3617	16781	29797	1.17		5.0E-46 BE677184.1	EST HUMAN	neg38f07x1 NCI_CGAP_Kid11 Home sepiens cDNA clone IMAGE:3259757 3' similar to TR:075202
6874	20026	33436	1.52		5.0E-46 BF5904421	EST_HUMAN	075202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7080	20174				5.0E-46 BF347229.1	EST_HUMAN	802021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5
7244	20327		0.75		5.0E-46 AW 682253.1	EST_HUMAN	QV4-ST0212-120100-075-109 ST0212 Homo septens CUNA
7544	20616	34093	0.59	T	5.0E-46 BE549744.1	EST_HUMAN	7038005.X1 NCI_CGAF_LU24 Tigning septents cDNA clone IMAGE: 1104500.3' similar to ob:X53741 mail
658	13844		3.95		4.0E-46 AA601143.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
							hi86c03.x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:3008836 3' similar to gb:X14008_rna1
1740	14889	27981	2.89		4.0E-46 AW770544.1	EST_HUMAN	LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;

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Table 4

Single Exon Probes Expressed in Placenta

					90		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27982	299	4.0E-46	4.0E-46 AW770544.1	EST_HUMAN	hl86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' sirrilar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2788	$\neg$		7.4	4.0E-46		NT	
5553			21	4.0E-46		NT	
5553	ī		2.1	4.0E-46	4.0E-46 M36852.1	NT	Human Ig germline gamme-3 heavy-chain gene V region, partial cds
12851			1.36		4.0E-46 AB002059.1	NT	
2359	П		0.94	3.0E-46	7657203	ZT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
4513	Π		1.21	3.0⋶-46	4506376	NT.	Homo septens mitogen-activated protein kinase kinase kinase (IMAF4K3), mikina
4898	18028	31015	1.11	3.0⊑-46	3.0E-46 273660.1	NT	H.sapiens tg lambda light chain variable region gene (7c.11.2) germline; tg-Light-Lambda; VLambda
4898	18028	31016	1.11	3.0E-46	3.0E-46 273860.1	Z,	H. sepiens Ig lembda light chain variable region gene (7c. 11.2) germilne; Ig-Light-Lambda; VL.embda
	$\neg$			П			w/49c04_x1 NCI_CGAP_Lu19 Homo saptens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
8949	Т	T	12.43	Τ	0.0E-40 700 1402.1	LO LO TONO	Himse AD smyloid mRNA complete cds
9770	Т	Γ	0.01	T	3.0E-40 E00000.	111	Unimon AD amidoid mRNA complete cds
9206	Г		0.61	Γ	3.UE-46 LU883U.1	1	I HAIRGI FOR MILITARY A COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE COMPRISON OF THE
11873	24861	38556	1.78	Γ	3.0E-46 (231765.1	2	THE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
200	14027	27000	12.65		2 DE-46 AA468646.1	EST HUMAN	repetitive element;
558	丁		3.78		2.0E-46 AA678246.1	EST_HUMAN	zzzra11.s1 Soares_fetal_liver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3
	ヿ	$\neg$		-		1	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L444lke ribosomal protein
1671	14823	27906	5.63	T	2.0E-46 C/8027.1	2	259e02.rl Scares_testis_NHT Homo sapiens cDNA done IMAGE:726650 5 similar to SW:RSP1_MOUSE
5089	18217	31188	1.26		2.0E-46 AA399286.1	EST_HUMAN	Q01730 RSP-1 PROTEIN:
7653	П	34197	7.1		9910569		Mus musculus sperm tall associated protein (Stap), mixina
8280	21342	Į.	1.29		BE86916	EST_HUMAN	801445137F1 NIH MGC 65 Homo sepiens CUNA Cione IMAGE 3949297 O
11524	24580		1.82		7657233 NT		Homo saplens small acidic protein (IMAGE 140052), ritkina
12294			1.4		2.0E-46 BF028854.1	EST HUMAN	601766225F1 NIH MGC 53 Homo sapiens CUNA Cione IMAGE: 308077 6
12555	25931	_	1.57		2.0E-46 H48391.1	EST_HUMAN	VISION L. Coares tetal liver spices TNFLS Homo capitals CDNA clone IMAGE: 408015 A
12596	3 25401		3.31		2.0E-46 AA001786.1	EST HUMAN	INIAGE:#20010
12934	25923	31864	4.26	Γ	AW2772	EST_HUMAN	xq/shu3.x1 Not CGAP_Lu34 none sapiens colve cone inimediateles) (CDC10) mRNA
1261	1 14418				4502694 NT	NT	Homo sapiens cell division cycle for (noninologous in Cockio of 3: celevisiae) (Cockio) illinore
2356	15487	7 28619	4.88		1.0E-46 AW978518.1	EST HUMAN	ES ISSUOZO MAGE ISSEQUENCES, MAGE FIGURE SEQUENTS CONTA

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Table 4
Single Exon Probes Expressed in Placenta

	171	OUT TO INDUSTRUCT	Γ	0.00	3 30038	3 22953	9913
	ZI :	ADDA0804 1	T		Τ	Т	9913
Homo sapiens RECQL5 bela mRNA for DNA helicase recQ5 beta, complete cds	TN	6 0E-47 AB042824 1	T		1	Т	3 3
	EST_HUMAN	6.0E-47 AI695189.1	٦		T	Т	0476
HSU77054 Human Homo sapiens culna cione N7	EST_HUMAN	6.0E-47 U77054.1				П	8890
Hamo sapans chromosome zi seginani nozioceo	NT	6.0E-47 AL163246.2		3.04	7 28851	3 15737	2613
13	EST_HUMAN	7.0E-47 AV683284.1		1.99	2		12962
Homo sapiens minute for occurrently what of the occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurrence occurre	Z	8.0E-47 AB041926.1	Γ	0.77	29882	5 16876	3715
Homo sapiens mixiva for GCN lettilly kinaso wilkik. 2 complete cds	Z	8.0E-47 AB041926.1		0.77	3 29881	5 16876	3715
Homo sapiens sow to coning pawaeri nunci and obtained ords	Z	8.0E-47 AJ229043.1				16265	3089
Homo caplens protein phosphatase 2, regulatory subunit 8 (858), epsilon isoform (PPP2R5E) mRNA	5 NT	5453955 NT		1.5	29007	1 15897	2781
Homo sapiens HLA-C gene, exan o, individual 18323	NT.	¥18536.1	8.0⊱-47	32.2	28101	П	1851
Hamo septens HLA-C gents, exon s, individual 19923	ZT	8.0E-47 Y18536.1		32.2	28100		1851
Homo sapiens SEC14 (S. cerevisiae)-like a (SEC14E), illinian	UT	11417966 NT	9.0E-47	1.64	31675		12874
(LOC83093), mRNA	NT	11432209 NT	9.0E-47	1.4	38110	24449	11388
Loron seriens similar to although productase family 1, member B1 (aldose reductase) (H. sapiens)		11425439 NI	9.0E-47	0.86	33039	19672	6506
HYPOTHETICAL 12.4 KD PROTEIN.;	EST_HUMAN	9.0E-47 AW770928.1	9.0E-47			18175	6047
Incomo sapienis Au pasadusadrian region, express. 172 Incomo sapienis Au pasadusadrian region, express. 172 Incomo sapienis Au pasadusadrian region, express. 172	2	9.0E-47 AJ271735.1	9.0⋶-47	3.7		13966	787
AV/103// UCO notice september (1/2)	EST_HOMAN	1.0E-46 AV715377.1	1.0E-46	1.99		25764	13176
002072204FT NCL_CGAP_DINO7 DOING SQUARE SCHOOL COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR C	EST_HUMAN	1.0E-46 BF531102.1	1.0E-46		32106	25233	12323
6020/2264P1 NCI_CGAP_bmo/ Homo septema >DNA clong IMAGE-4215398 5	EST_HUMAN	1.0E-46 BF531102.1	1.0E-46		32105	25233	12323
Homo sapiens C I LZ gene	3	1.0E-46 AJ245621.1	1.0E-46	1.61			11410
7:92b01.x1 NCI_CGAP_Ov18 Homo sapiens cuina cione image: 3043703 3	T_HUMAN	.0E-46 BF194707.1	1.0E-46			П	11102
MER22 repetitive element;	L	1.0E-46 BF196247.1	1.0E-46	0.64	33285	19902	6746
7p48e07.x1 NCI CGAP Lu24 Homo saplens cDNA clone IMAGE:3567852 3' similar to contains element		8923762 NI	1.0E-46	5.34	32810	26818	6098
Homo sepiens centaurin-alpha 2 protein (1190/2/2/195), mRNA			1.0E-46	5.34	32609	25818	8098
7692b01x1 NCI_CGAP_OVIS Homo sapiens CLIVA CEXTS IMFAGE. 3043703 3	EST HUMAN	1.0E-46 BF194707.1	1.0E-46	5.89	32313	П	5817
Homo sapiens mRNA for KIAAU980 protein, partial cos	_	1.0E-46 AB023197.1	1.0E-46	3.13		╗	4995
np78b02.s1 NCI_CGAP_Pr2 Homo sapiens curva cione invasce: 1132333 stitlica to guinario i i i i i i cosperio MT-11 mRNA. (HUMAN);	EST_HUMAN	1.0E-46 AA631912.1	1.0E-46	212	29511	16494	3321
	EST_HUMAN	1.0E-46 H97330.1	1.0E-46	3.53	28725	15600	2473
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
		- Gright					

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Table 4
Single Exon Probes Expressed in Placenta

4933	<b>1</b>	4503	4503	4467	1712	1623	1598	066	990	152	9033	9033	7540	7540	6694	6136	6136	4482	4073	3376	836	841	558	558	11936	8818	8677	8677	8971	1432	11035	6707	Probe SEQ ID NO:
18083	1	3 17643			2 14863	3 14775			0 14162	2 13377	П				П	П	$\neg$	П		16548	14141	П	13751		24922	П		┪		14585		19865	Exan SEQ ID NO:
		3 30629		7 30585	3 27952	5 27859	1	27222	2 27221	7 26409	2 35655			3 34089				30603		3 29562	27202		26779	26778		П	$\neg$		33625	27660	•	33255	ORF SEQ ID NO:
		1.67	1.67	1.61	4.49	1.61	0.95	2.45		1.21	0.77		0.88	0.88	1.71		4.68		6.61	0.97	10.04		209	2,09	1.98	0.83	222	2.22	0.82	7.03	5.68	5.73	Expression Signal
						Γ			Γ																					4.0€-47		5.0E-47	Most Similar (Top) Hit BLAST E Value
AW9651	7 5174648 NT	2.0E-47 AA569592.1	2.0E-47 AA569592.1	7 4504866	20E-47 AA524514.1	7662109 NT	20E-47 AI969279.1	2.0E-47 AL163209.2	2.0E-47 AL163209.2	7 4505318 NT	AW9637	3.0E-47 AW963796.1	3.0E-47 A1819755.1	3.0E-47 AIB19755.1	3.0E-47 A1222413.1	3.0E-47 AW408800.1	3.0E-47 AW 408800.1	3.0E-47 M12959.1	3.0€-47 (193181.1	4504116 NT	AL 16328	3.0E-47 N57483.1	3.0E-47 BE907634.1	3.0E-47 BE907634.1	4.0E-47 AW615509.1	4.0E-47 AWB93777.1	4.0E-47 BE616483.1	4.0E-47  BE616483.1	4.0E-47 BE938896.1	4657556	5.0E-47 M78590.1	11423972 NT	Top Hit Acession No.
EST_HUMAN	8 NT	EST_HUMAN	EST_HUMAN	_	EST_HUMAN	•	EST HUMAN		3	NT I	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT T	NT	NT	TN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	3	EST_HUMAN		Top Hit Database Source
EST377239 MAGE resequences, MAGI Homo saplens cDNA	Homo sepiens Rev/Rex activation domain binding protein-related (KAB-K) mKNA	ni23g07.s1 NCI_CGAY_PTI Homo sepiens cuna cione invasce.si 1405.		-13		Homo sapiens RIAAV420 gene product (RIAAV420), III/IAAC GOOJEO/79,	wq86502 x1 NCI_CGAP_GC6 Homo sapians CUNA cigns INIA-GC.2473031-3	Homo sapiens chromosome 21 segment nozi uvve	Homo sapiens chromosome 21 segment nozi cono	Homo sapiens myosin prospinatase, targer subunit 2 (WITT 12), Timbres	EST375869 MAGE resequences, MAGH Homo sapiens CONA	EST375869 MAGE resequences, MAGH Homo sapiens CUNA	W)11h08.x1 NCI_CGAP_NG12 Homo sapiens curva cigns invade. 2402000 0	W) 11h08.X1 NCI_CGAP_NoT2 Homo sapiens CUIVA Cicilis IMAGE: 202550 3	qh04e07.x1 Soares_NFL_T_GBC_S1 Homo septems cDNA cone IMAGE: 1843/193	UI-HF-BMO-adx-d-07-0-UI-r1 NIH_MGC_38 Homo sapiens cunn cione invince: 3003203 3	UI-HF-BM0-edx-d-07-0-UI-1 NIH_MGC_38 Homo sapiens cuiva cione liwa GE:3003203 S	Human T-cell receptor active alpha-chain mKNA from JM cell line, complete cos	Homo septens nuclear dual-specificity prospharase (SETT) rivova, parual dua	Homo septens glutamate receptor, tonouropic, valinate 1 (Chart) minuto	Homo septens chromosome 21 segment 1921 (Volume) month	1)54b04.s1 Soares_multiple_scierosis_2NbinNor Homo sapiens culva cicine immor	601487639F1 NIH_MGC_70 Homo septems CDNA clone INVACE 3777377 3	601497639F1 NIH MGC 70 Homo septens culva cione liwa circober 21 3	D84252 VIRAL INTEGRATION SITE PROTEIN INT-8. [1]:	RC3-BN0034-220300-015-105 BN0034 Home septens CUNA	601280486F1 NIH_MGC_39 Homo sapiens cUNA clone IMAGE:3622437 o			Homo septens E1A binding protein p300 (EF300) mK/VA	EST00738 Fetal brain, Strategene (catred30200) Homo saptems CUNA clone nin burni	Homo sapiens CDC3/ (cell division cycle 3/, S. cerewsiae, nombeg) (CDC3/), III/N/N	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

1280	1210	1370	113/8	88	300	8008	5797	6797	3646	1643	150	10564	6908	7189	5187	3926	3926	1437	12394	12357	9690	8915	8151	8161	7876	6097	6097	5902	5245	Probe SEQ ID NO:	
7		14436	Т	T	Т	19404	18987	18987	16809	14785	20000	1		20054	18309	17085	17085	14590	26076	26073	22739	21994	21233	21233	25854	19278	19278	19093	18366	NO: SEQ ID Exon	
			36080	T	Ī	32751	32291	32290	29823	27879		37205		33464	31275	30081	30080	27663		31653	36308	35533	34764	34753		32608	32607	32407		ORF SEQ ID NO:	
	1.65	1.75				0.57	1.1	1.1	- 0.73				4.24	10.76	24		1.1		1.87	3.36	1.27	1.76	1.98	1.98	1.34	1.32	1.32	8.0	0.71	Expression Signal	
	5 8.0E-48		Τ	T	1										Τ						2.0⊑-47								2.0E-47	Most Similar (Top) Hit BLAST E Value	
	4501800 NT		0.0000	0.05 49 85203813 1	9.0E-48 AU123240.1	9.0E-48 AI833168.1	9.0E-48 BE888198.1	9.0E-48 BE888196.1	9.0E-48 BF359947.1	9.0E-48 AF223391.1		.0E-47 L30115.1	.0E-47 AW664548.1	1.0E-47 A 880886.1	1.0E-47 AW813906.1	1.0E-47 BE280477.1	1.0E-47 HE2804//.1	1.0E-47 AI333429.1	2.0E-47 AL 163209.2	2.0E-47 R42423.1	11526136 NI	2.0E-47 AF071771.1	2.0E-47 D87675.1	2.0E-47 D87675.1	2.0E-47 L09731.1	2.0E-47 BE778475.1	2.0E-47 BE778476.1	2.0E-47 AF073921.1	2.0E-47 AI041128.1	Top Hit Acession No.	9.9.0
	O NT	-	NIT COM	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HOMAN	2		NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EG! HOWAN	EST HUMAN	Z	EST_HUMAN	N	N.	1	3	3	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	Top Hit Detabase Source	
hk61b03.x1 NCI_CGAP_Lym12 Home sapiens cDNA cione IMAGE:3001133 3 similar ar got.xom/or	rigino sapera aminosalysas a (ACC) 1), minoro	Line and an incomplete (ACVI) mRNA	Homo seriens aminoacylase 1 (ACY1), mRNA	601310479F1 NIH MGC 44 Hama saptens cDNA clone IMAGE:3632063 6'	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 6'	O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN.	601511/14F1 NIT NIGO I FORDE LA COLLA COLLA INACE 3377889 4' similar to TR-060844	SUTSTATE VIII WOO 74 Units september 100 A change IMAGE 3013108 5	CM2-W110100-3 07100-230-0-0-0 min vivo indine editors (MAGE:3013108 5)	spliced	Homo saplens calcium channel alpha1E subunit (CACNA1E) gana, exons 7-49, and partial cds, alternatively	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5 region	hi84a11.x1 Soares_NHC_1_GBC_S1 Homo sapiens cuna cione invascezzaroarz 3 similia to gomecono KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	RAS-RELATED PROTEIN RAP-1A (HUMAN);	120000 A Register and API RBB Homo saplens cDNA clone IMAGE:2355588 3' similar to gb:M22995	BDS STAART 199AAN 047 h09 STA407 Home senions CDNA	001100261 11111_NOC_5 Tempo content of NA close (NA GE:3138893.5)	4p99103X1 35453_1544_1519 Sablens cDNA clone INAGE:3138893 5	Homo sapiens chromosome zi sogment i oz i ovos	repetitive element;	wooden at Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE: 29966 3' similar to contains OFR	Companies STG family member 3 (BTG3) mRNA	Homo sapiens DNA for amyon precursor process, comprese cos	Homo sapiens DNA for amyotic precursor protein, complete cos	Homo sapiens 6-hydroxydyctemine 1D receptor pseudogene with an Aiu repeat insertion	601463932F1 NIH_MGC_67 Homo sapiens culva cione invage: 3007407 3	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3667467 5		ov61h03x1 Soares_testis_NH1 Homo sapiens cunA cione invace: 104 1043 3	Top Hit Descriptor	

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Table 4

Single Exon Probes Expressed in Placenta

					Singi	באטוו דוטטפג	Single Exon Floores Expressed in Flacenia
Probe SEQ ID NO:	Exon SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	8.0E-48 AW768477.1	EST_HUMAN	
\$	П		0.68	8.0E-48	4116	NT ·	Homo saplens glutamate receptor, tonotropic, kainate 1 (GRIK1) mRNA
55 55	1		2.58	7.0E-48	7.0E-48 AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
29 4	Т		18.69	7.0E-48		NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1527	Т	27761	1.98	7.0E-48	6912719 NT	NT	Homo sepiens tousled-like kinase 1 (TLK1), mRNA
1667	14819	27902	5.39	7.0E-48	5730038 NT	NT	Homo septens SET domain and mariner transposase fusion gene (SET IVAK) mrava
6885	19843	33233	24.01	7.0E-48	11416831 NT	Ι'	Homo sapiens histidy-tRNA synthetase (HARG), MXNA
12125	25105	38809	2.98	7.0E-48	7.0E-48 R18623.1		yg37b02.rl Soares imant brain TNIB Homo saprens cultiva cione invisice. 34747 3.
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9741	22808	T	1.87	٦	11427428 NT	Z,	Homo saplens hypothetical protein FLJ11006 (FLJ11006), mRNA
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3384	18465	29569	1.48		7689 <u>1</u>		Homo sapiens phosphodiesierase I.A. calmodulin-dependent (FDC I.A.) IIIININA
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350	16672	29682	0.93	T	3.0E-48 AF1/2453.1	2	hi14b12 x1 NC) CGAP GU1 Homo sablens cDNA done IMAGE:2972256 3' similar to SW:DCRB_HUMAN
3721	1 16882	29888	0.9		3.0E-48 AW664531.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B.;
4362			0.63		3.0E-48 AA009541.1	EST_HUMAN	ZIO4g03_r1 Spares_fetal_liver_spleen_1NFLS_S1 Homo sapiens curva cione IMAGE: 425044 o
6015		32516	2.08		3.0E-48 BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens CUNA
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Table 4

Single Exon Probes Expressed in Placenta

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Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11114 24186	37818	8.1	3.0E-48	P514170.1	EST_HUMAN	UHH-BW1-eni-e-10-0-UI.s1 NCI_CGAP_Sub7 Homo septens cDNA clone IMAGE:3082267 3
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		1.7	2.0E-48	AA631940.1	EST_HUMAN	
$\neg$						TCBAP1D3842 Pediatric pre-B cell ecute lymphoblastic leukernia Baylor-HGSC project=1 CBA Homo
Г	F	0.99	2.0E-48	BE246095.1	EST_HUMAN	espiens CUNA cione i CEAP 3842
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6935 19121	32434	0.64	2.0€-48		LΗ	no18g01.s1 NCI_CGAP_rne1 Hamo septens culviv cume INVIVEL. 1 VIV. 2 3
7688 20753	34236	3.99	2.0E-48		ZT	Homo sapiens mixiva for KIAA tou i protein, paruai cos
7688 20753	34237	3.99	2.0€-48		NT	Homo sapiens mixiNA for NIAA1601 protein, partial cos
7703 20768		3.54	2.0Ε-48	11496238	NT	Homo exptens v-rel avian reticuloandothelosis viral oncogene nomolog A (nuclear radus of kappa layin polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
╗		1.13		AV743451.1	EST_HUMAN	AV743451 CB Homo sepiens oDNA clane CBCCGG10 5
12109 25089		1.38		AW291799.1	EST_HUMAN	UI-H-BI2-agi-b-11-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens curva cione invace
12320 13244	26245	298		AA465007.1	EST_HUMAN	200003.r1 Soares overy tumor womo! Homo sapiens GUINA cicine ilwayoro iovoco
12674 25990	31771	1.25		BE737164.1	1,-	601306064F1 NIH MGC 39 Homo septems cultiva citate invade: 3005162 5
57 13295	26311	2.33		7706534	NT	Homo sapiens displain resistance associated overexpressor process (Locos 1777), 111 Nov.
		4.67	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
٦	27323	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activetor (100kD) (p100), mkNA
1101 14288					Z	Homo sapiens EBNA-2 CO-activator (100KD) (P100), minuxx
1324 14481		4.01		-	Z	Homo sapiens KNA binding mour protein o (KDMb) mKNA
1968 15111				AL163302.2	NT	Homo sapiens chromosome 21 segment HSZ1C1U2
3577 16742				AL163248.2	NT	Homo sapiens chromosome 21 segment Hozi Cu4o
5240 18362				M10976.1	N.	Human endogenous retroviral DINA (4-1), complete retroviral seguirant.
6417 19588				AI889077.1	EST_HUMAN	SIMILARITY TO U73941;
				A1889077.1	EST_HUMAN	Id17c01.X1 NCL CGAP_Co16 Homo saplens cDNA clone IMAGE:2070904 3 similar to 1 K:014508 O14508 SIMILARITY TO U73941;
		0.87		Y18000.1	3	Homo seplens NF2 gene
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26245         2.0E-48         2.0E-48           14206         27323         1.52         1.0E-48           14272         27137         4.67         1.0E-48           1521         3.0E-48         1.0E-48	EXCIT SEQ ID NO: Signal Properties No: Signal Properties No: Signal Properties No: Signal Properties No: Signal Properties No: Signal Properties No: Signal Properties No: Signal Properties No: Signal Properties No: Properties No: Signal Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: Properties No: 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Single Exon Probes Expressed in Placenta

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Indino suprems processario (arconino, macropari) 26S estimble ATPasa A (PSMC4) mRNA	Z		7.0E-49	1.21	26638		142
	3	<u> </u>	7.0E-49	1.21	26637		142
OD/BBUS TINCL CUAR GCD1 FIGHTO SEPTEND PARTY VIOLET TO THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY	EST_HUMAN	8.0E-49 AA872183.1	8.0E-49	2.08			12097
element contains element PTR5 repetitive element;	EST_HUMAN	8.0E-49 AI623722.1	8.0E-49	3.65	37804	24169	11096
ISSB412 XI NCI CGAP Utal Hamo septens oDNA clone IMAGE:2230871 3' similar to contains Alu repetitive		-	0.02		27006	2020	40101
Homo sapiens gene for activin receptor type IIB, complete cds	ZI.	R OF 49 ARODREST 1	8 OF 40	0.03	T	Т	246
Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds	Z I	123850	8 OF 49		T	Т	61/8
Mus musculus T-bax 20 (Tbx20), mRNA	N.	10048417	8 OF 40		T	Т	01/0
Mus musculus T-box 20 (Tbx20), mRNA	NT	10048417	8 OF 49	3.07	1	Т	2004
Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds		8 0E-49 4B026497 1	8 OF 49	0.07		Т	1700
15d8 Human retina cDNA randomly primed sublibrary Homo sapians cDNA	EST_HUMAN	1.0E-48 W26785.1	1.0E-48	1.41		7	3 3
	NT		1.0E-48	4.23	T	1	1000
Homo sapiens B cell linker protein (SLP65), mRNA	TN	11429808 NT	1.0E-48	4.23	1	T	10581
601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5	EST_HUMAN		1.0E-48	4.74	1	Т	9781
Homo sepiens mRNA for KIAA1245 protein, parual cos	N.	1.0E-48 AB033071.1	1.0E-48	6.79	1	٦	9468
Homo sapiens Chediak-Higashi syndrome 1 (Choi) move	NT	4502838 NT	1.0E-48	0.99	36053	22488	212
	Source		Value	<u>.</u>	Ç		Ņ.
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Exen D D	Probe SEQ ID
	Single Exem : 10000	J. J. J. J. J. J. J. J. J. J. J. J. J. J					

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Table 4
Single Exon Probes Expressed in Placenta

					9.19		
Probe SEQ ID NO:	NO:	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11557	24612	. 38291	3.39	6.0E-49	6.0E-49 AW 452218.1	NAMUH_TS3	ULH-BI3-alo-e-05-0-ULS1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088048 3
11961	24946	38650	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pencreas tumor III Homo sapiens CUNA o end
11961	П			6.0E-49	6.0E-49 AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
12670	7		10.54	6.0E-49	6.0E-49 AA707667.1	EST_HUMAN	zj29c08.s1 Soares_fetal_]Iver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:451694 3
730		26951		5.0E-49	5.0E-49 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
730	13912	26952	. 5,84	5.0E-49	5.0E-49 AL163210.2	NT.	Homo sapiens chromosome 21 segment HSZ1CV1U
1836	14983	28082	10.18		6.0E-49 AA172121.1	EST_HUMAN	如28c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:e10860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN.;contains LTR7.均 LTR7 LTR7 repetitive element;
2808	П		7.1	5.0E-49	5.0E-48 U17714.1	3	Homo sapiens putative tumor suppressor S i 13 (S i 13) mRNA, complete cas
3348	16519	. 29533	7.59	5.0E-49	11436355 NT	NT.	
					4 0E-40 AW180533 1	EST HUMAN	Jd08b01.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2676593 3' cimilar to WP:B0350.2B   CE06703 :
7395	20473	T		T	4.0E-49 Z26634.2	TN	Homo sapiens mRNA for enkyrin B (440 kDa)
7395	7	1			4.0E-49 Z26634.2	NT	Homo sepiens mRNA for enkyrin B (440 kDa)
7422			0.68	4.0E-49	11525737 NT	Z 7	Homo saplens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acety/galactosaminyitransrerase o (GalNAc-T8) (GALNT8), mRNA
7422	-1				11525737 NT	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosemine:polypeptide N-acetylgalactosaminyliranstarase 8 (GalNAc-T8) (GALNT8), mRNA
7892	7					TN	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
9065		35680	0.47	П		NT	Homo saplens copine III (CPNE3), mKNA
9065	55 22144	35691	0.47	Γ	11425374 NT	11	Homo sapiens copine III (CTNES), MXNX
12614	14 26145	1	2.74	Ţ	4.0E-49 AA210798.1	EST_HUMAN	Homo saplens clutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12615	15 25413	3	2.93		4.0E-49 AF240788.1	NT.	
6	574 13766	26789	0.91	ľ	3.0E-49 X68968.1	Z	H. septens mixina for exercising N3k4HB Homo sentens cDNA clone IMAGE 360584 5' similar to contains L1.33 L1
2713	13 15831		2.73		3.0E-49 AA016131.1	EST HUMAN	repetitive element;
5098	П	31198	2.68		3.0E-48 U.46999.1	শ	Human type IV collegen (COL4A6) gene, exon 40
7577	77 20649	34127	9.83		3.0E-49 H39479.1	EST_HUMAN	EST25e12 WATM1 Homo sepiens cDNA clone 25e12
11582	82 24636	38316	1.41	Γ	3.0E-49 AA337561.1	EST_HUMAN	ES 1425/2 Endometrial tumor Homo septens CUNA o end
6	678 13864				2.0E-49 BE165980.1	EST_HUMAN	MR3-HIU467-130200-113-901 F10467 Floring septems CDNA - Fragilla CE '262574 5'
3294	16468	3 29487	1.16		2.0E-48 N26446.1	EST TOWAN	ATTACABLE OF LINES AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND AND THE LAND

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Single Exon Probes Expressed in Placenta

27	Ţ,	S.	2652	<u></u>	7	7		6534	5109	12508	12148	11590	11304	10331	9183	8874	7453	7453	7372	7372	6208	6202	6476	184	1584	823 223	12626	8291	6876	3659	Probe SEQ ID NO:
2764 15879	T	1	╗	7	737 13919	737 13919		34 28215	П			П	╗	31 23366	٦		33 20530			П	٦					┑	╗	Т	٦	9 16822	Exan SEQ ID NO:
15879 28988	T	T	٦		9 26960	9 26959	8 26426	5	7	9		38325		6 36975	35809	3	0 34004	34003	33916	٦					27816	7				29832	ORF SEQ ID NO:
2.42	Ī			8 4.32	0 1.92	1.92	5 4.18	0.63	0.92	1.82	1.26	2.91	1.32	1.23	1.48	0.71	209	209	278	278	1.09	0.85	4.68	2.83	77	9.1	2.09			0.86	Expression Signal
T	T				Г					Г		П				1.0E-49								П				•			Most Similar (Top) Hit BLAST E Value
D80334.1			7706394 NT	4501890 NT	8.0E-50 X95097.2	8.0E-50 X95097.2	8.0E-50 AL163202.2	9.0E-50 BE295758.1	9.0E-50 AF101475.1	11418322 NT	BE1693	11427386	1.0E-49 AV751477.1	1.0E-49 AL043129.2	1.0E-49 BE409340.1	9994184 NT	1.0E-49 N25884.1	1.0E-49 N25884.1	1.0E-40 BE398110.1	1.0E-49 BE398110.1	1.0E-49 AW984640.1	1.0E-49 H18291.1	1.0E-49 BF131007.1	1.0E-49 BE255216.1	4557887	1.0E-49 BF035327.1	2.0E-48 AF163864.1	20E-49 M86033.1	2.0E-49 AV717938.1	2.0E-49 AF026564.1	Top Hit Acession No.
N I	NT	NT NT	NT NT	N T	Z	3	3	EST_HUMAN		ZINT	EST_HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	A NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	Top Hit Database Source
	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA		Homo seplens p47 (LOC51674), mixina	Homo sapiens actinin, eiphē 1 (ACTIVI) IIINVA	Homo septens mixing for viri receptor 2	Homo sepiens mixing for Vir receptor a	Homo septens chromosome 21 segment risz i Cuuz	601176250F1 N/H_MGC_17 Home sapiens curve cione invivor: 300 1300 3		Homo Babians Cagnerin E.G. LAG Seven-pass G-type recopiling (CECCOM), illustration	MRO-H 10407-010200-005-702 H 10407 Homo septems CDVV	Homo sapiens brefeldin A-imbited guanine nucleotude-exchange protein i (pro i), illinora	AV761477 NPD Homo sapiens cuna cione NPUAWEUS	DKFZp434D24Z3_F1 434 (synonym: niesa) nomo sapæits cultiva cicule unit a promuenta o	601300992F1 NIH_MGC_21 Homo septens curva clone transcer accorded to	Homo sepiens RNA binding motif protein / (LOCS)1120), mrova	yw78g12.s1 Sogreg_piacenta_tosweeks_Zwortrousey nomo sepietts cutes units invocation of similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);	yw78g12.s1 Sceres, piacenta, accumentation of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 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18) mKNA	801459531F1 NIH_MGC_66 Hamo sapiens cUNA clone IMAGE::3852085 5	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spuced	EST02558 Fetal brain, Stratagene (cat#936206) Homo saptens cUNA clone HFBCY50	AV717938 DCB Homo septens cDNA clone DCBALBUT 5	Homo sapiens RNA binding protein II (RBMII) gene, complete cds	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

					Silic	6 LY011 L 1006	Lypecoca III - Income
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	
6	634 13819	26843	1.07		7.0E-50 BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo saplens cDNA
6923	П	П	0.73		7.0E-50 EF091922.1	EST HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sepiens cUNA
6923	П		0.73		7.0E-50 EF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cUNA
7457	- {		0.74		7.0E-50 AA627822.1	EST HUMAN	nq59e12.91 NCI_CGAP_Co8 Home sapiens cUNA cione (MAGE:1148208 3: SITEIRE DE COSSET OUS RIBOSOMAL PROTEIN L6 (HUMAN);
10993	П		23.18		7.0E-50 AI872137.1	EST_HUMAN	apiens cDNA dor
4482	П	П	0.67		8.0E-50 EE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cUNA cione IMAGE:3995977 5
9409	21480	<u>-</u>	3 28		6.0E-50 EE044078.1	EST HUMAN	n839n04X1 NOT COME OF FROM SEPTEMBER VOTES COME INVISCOUNTS OF SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEP
11053	7	37765	3.32		6.0E-50 AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
11053	П				6.0E-50 AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo seplens cUNA 5 end
<b>16</b>	1835 14982	28080			5.0E-50 EF332938.1	EST HUMAN	CMC-BIO/AK-SCOODO-SOS FOR BTO/OS Long serions CDNA
Ta	1835 14982	2 28081	1.34		6.0E-60 6F332838.1	E O L	n/45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5
9294	94 22370	<u> </u>	5.27		5.0E-50 AA557683.1	EST_HUMAN	repetitive element;
12080		38777	1.78		5.0E-50 AA403053.1	EST HUMAN	z62b01.r1 Soeres_testis_NHT Homo sapiens cDNA clone IMAGE://z6889 o similar to Inc. G1335769 GAG-POL POLYPROTEIN.;
					4.0E-50 AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sepiens cDNA done IMAGE:1104520 3' smilar to gb:x53741_in81 FiBULIN-1, ISOFORM A PRECURSOR (HUMAN);
ıμ	3536 16701	1 29712	2.08		4.0E-50 AL163248.2	3	Homo sapiens chromosome 21 segment Ho210046
92	6491 19657	7 33020	0.92	Γ	11440683 NT	1	Homo sapiens cysteinyi-urive synthesise (LANO), rinven
73	7383 20461	33924	1.02		4.0E-50 BE087536.1	EST_HUMAN	IOITO Papiario
16	1992 15134	4	9.4		3.0E-50 M18048.1	S	Human endogenous regovirus 7 i ve-ric
မ္ဘ	3371 16543	3 29557	0.92	Τ	3.0E-50 AA746142.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo saplens cDNA clone 4151935 similar to CMYA5
<del></del>	3846 17006	30008	0.9		3.0E-60 AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
2					11418317 NT	NT	Homo capiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
g)	П			3.0E-50	11419317 NT	TNT	
92	6904 20219	9 33648	1.71	3.0⊑-50	11421514 NT	NT .	
				5 3.0E-50	3.0E-50 AF233436.2	N T	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-USF1a mXNA, competed ods
	$\neg \uparrow$	$\neg$			VE235478 2	2	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
	7822 20877	343//		30.00-00	3.0E-00 FM 233430.E		

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Single Exon Probes Expressed in Placenta

					Rillo	Silligie Exoli Liopes Expresses	2 Lyprosocu III e Idooriuu
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ	Expression Signel	Most Similar (Top) Hit BLAST E Value	Fop Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8782	21861	35404	0.66	3.0E-50	6601589 NT	NT	Homo seplens enkyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10023	╗	36657	1.08		3.0E-50 AB048818.1	NT	
10032	╗	36870	1.03		11418514 NT	NT	Homo saplens t-complex 10 (a murine top homolog) (TCP10), mKNA
10737		37380	1.04		3.0E-60 AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11364	٦	38080	1.51		36956	NT	Homo saplens Grb2-associated binder 2 (KIAA0571), mRNA
11752	7	37564	8.19		3.0E-50 AJ245621.1	NT.	Homo sapiens CTL2 gene
13217		31922	1.35		3.0E-50 AB011399.1	NT	Homo saplens gene for AF-6, complete cds
799			7.94			NT	21
1104		27327	6.16		57752	NT	Homo septens midline 1 (Cpitz/BBB syndrome) (MICT) mRNA
1474		27713	33.77		2.0E-50 AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, atternatively spliced
4376	17519	30499	0.76		2.0E-60 D86424.1	TV	Mus musculus mkiva for nign-suitur keraun pictein, pa iiai cus
5329	Г	Γ	7.37	Τ	ZUE-SUIABUTASTA.T	POT LINAN	ATTIONES NOTORNO Homo series schille clone NT2RM2001609 5
200	Т	35136	103	T	2 OF 50 AR038162 1	NI	Homo saplens TFF gene cluster for trefoil factor, complete cds
851	21592	35127	1.03		2.0E-50 AB038162.1	TN	Homo saplens TFF gene cluster for trefoil factor, complete cds
8650	7	35288	7.21		2.0E-50 X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8650			7.21		2.0E-50 X06956.1	NT	
10088		36728	1.6	2.0E-50	9910293 NT	NT	
10088	23126	36729	1.6		9910293 NT	NT	Mus musculus keratin complex 2, gene 5g (K/TZ-5g), MKNA
11960	24945		1.39		2.0E-50 AF023861.1	T	Macaca mulatta cyclophilin A mkina, complete cos
474	13669	26701	2.17		1.0E-50 AL163209.2	NT	Homo sepiens chromosome 21 segment Hoz 1 Cuuy
2438	15566		10.11		1.0E-50 AJ271735.1	NT	Homo sapiens Xq pseudosurosomai region, segment iliz
10398	23431	37038	1.65		1.0E-50 D11078.1	NT	Homo sapiens RGHZ gene, retrovirus-like element
6104	19284	32617	1.04		9.0E-51 AW511225.1	EST_HUMAN	
6354	19624		0.58		9.0E-61 AA744837.1	EST_HUMAN	ny67h03.s1 NCI_CCAP_GCB1 Homo sapiens CUNA clone IWA GE: 120301 3
8872	21951	35487	0.7		9.0E-61 AI791154.1	EST_HUMAN	ab23904,55 Strategene lung (#837210) Homo sapiens cuna come invade: 641 boo 3 similar co SW PSM HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
9525			1.29	Г	9.0E-51 AA043738.1	EST HUMAN	ZK61g09.r1 Soares pregnant utarus NbHPO nomo sapiens curva cione invade: 400002 o
9700	22749	36317	89.0		9.0E-51 AI791154.1	EST_HUMAN	ab23904.x5 Strategene lung (#937210) Homo septens cUNA cione IMAGE:341050 3 cimilar co SW.PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
9700			0.68		8.0E-51 AI791154.1	EST_HUMAN	
11764		П	1.97		9.0E-51 H89078.1	EST_HUMAN	yw24g06,r1 Morton Fetal Cochlea Hemo sepiens cDNA clone IMAGE: 263210 6

Page 314 of 550
Table 4
Single Exon Probes Expressed in Placenta

Ī	Γ	Γ	Τ	Γ				Ė						اِـ	_		$\int$		63						_		5	=	Probe SEQ ID NO:
9885	8337	9337	7 2	7032	6900	6124	8124	6113	4428	4426	3562	2036	1657	11885	4471	4376	4282	4282	3447	3354		$\neg$	7321	4690	4559	4559	12069	11764	
22926	22413	22413	18531	20168	20216	19303	19303	19283	17568	17568	16727	15177	14710	24970	17611	17518	17427	17427	16615	16526	22626	20885	20403	17825	17697	17697	25050	23960	Exxn SEQ ID NO:
36508		1	Γ	Γ			Ī			30547	29743	28287	27790	38674			30417	30416	29633	29541		34387	33865	30812	30678	30677	38768	37580	ORF SEQ
20.5											14.65	5.93	0.94	1.36	1.44	1.18	1.37	1.37	0.82	1.27	1.06	211	0.71	5.38	1.11	1.11	1.84	1.97	Expression Signal
0.00-01			T	Γ	I					Γ		6.0E-51	6.0E-51							Γ	Г				8.0E-51	8.0E-51			Most Similar (Top) Hit BLAST E Value
1001000141	-					AF0/008	G.UE-61 AF070083.1	6.0E-51 XU1 /88.1	9910553 NT			7657268 NT	6678763 NT	7.0E-51 AF161449.1	7.0E-51 AW295603.1	11421595	7.0E-61 AL079628.1	7.0E-51 AL079628.1	7.0E-51 AWZ74720.1	7.0E-51 AW889219.1	8.0E-51 AU138590.1	11439587	AF0642	8.0E-61 AA610842.1	4503932 NT	-	9.0E-51 AA885514.1	9.0E-51 H8907B.1	Top Hit Acession No.
2141	S NT	NT.	5 0 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A NI	ON	2	1 -	2	3 NT	3 2 1	6 NT	NT	SNT	3	EST HUMAN	3	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN			EST_HUMAN	NT	Ž	EST_HUMAN	EST_HUMAN	Top Hit Database Source
	Homo sapiens B9 protein (B9), mRNA		Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA	Home seriens rerebral cell adhesion malecule (LOC51148), mRNA	Lorgo senions non-kinase Cdr42 effector protein SPEC2 (LOC56990), mRNA	Light series ribosomal prohin S6 kinese. 70kD, advocatide 1 (RPS6KB1) mRNA	Homo saniens mitogen-ectivated protein kinase kinase 1 (MKK4) gene, exon 4	Lamo seriene milionen-entivated nicitein kinase kinase 1 (MKK4) gene, exon 4	S. Gooding of	Turno saprens source centrer family a (fecilitated chicose transporter) member 9 (SLC2A9), mRNA	Homo sepiens KIAA0929 protein Msv2 interecting nuclear target (MINT) homolog (KIAA0929), mRNA	Hamo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) hamalog (KIAA0929), mRNA	Homo sepiens pulsave DIVA binding protein (Waso), illinois	Homo sepiens Hor Cool miniva, perual cos	UI-H-BWO-sip-b-05-0-UI-S1 NCI_CASAP_Supo Homo sepiens cuiva durie impage	tomo appens immunogiopulin superiarinis, interiore a (1997-5), illivara	OKFZp434B22Z9_r1 434 (synonym: nies3) Homo sapiens CDNA Giorio DNI Epro-Hozzzzo V	UK-CP434B222B 11 434 (Synonyiii, Iness) Humb sabasia sensa vana bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira sabasia sensa bira 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minino, cumpleto cos	HETEROGENEOUS NUCLEAR RIBONUCLEORROTEN A1 (HUMAN) HETEROGENEOUS NUCLEAR RIBONUCLEORROTEN A1 (HUMAN)	Homo sapiens glycine emonocensierase (L-a giiilii a giycine culturiora aso) (Cristian to chi Y10871 met	Homo sapiens glycine antomotensierase (L-aginine-grycine antomotensiarase) (GATM) mRNA	SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : SW:CAYP_CANEA P10463 CALCYPHOSINE : 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Table 4
Single Exon Probes Expressed in Placenta

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17586 20613 22719 26227 26227 25578 13585 13889 13889 14873 14973 17753		П	3.0E-51 AA211296.1	EST_HUMAN	zq87g01.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649008 3
20813 22719 26227 26227 25578 13585 13889 13889 13889 14873 16987		П	3.0E-51 AL159142.1	NT	Novel human gene mapping to chomosome 22
22119 26227 25578 25578 13585 13889 13889 13889 14873 16987	304 2.3		3.0E-51 R15914.1	EST_HUMAN	ya47c08.rl Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);contains LTR5 repetitive element;
2627 25578 13585 13889 13889 14873 16987		П	3.0E-51 M29063.1	Y	Humen hnRNP C2 protein mRNA
25578 13585 13889 13889 13889 14873 16987 17753	0.61		3.0E-51 AW583777.1	EST HUMAN	Homo sepiens X-linked anhidrotte ectodermal dyspiasia
13585 13889 13889 13889 14873 18987 17753	6.56		3.0E-61 AF003528.1	N	regions
13889 13889 14873 16987 17753	619 1.98	2.0E-51	4507798 NT	NT	Homo sepiens ubiquitin protein ilgese E3A (human papi syndrome) (UBE3A) mRNA
13889 14873 18987 17753			2.0E-51 BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5
1,4873 16987 17753			2.0E-51 BE391063.1	EST_HUMAN	601286694F1 NIH_MGC_44 Homo sepiens CUNA cione ilviAGE:360/463 3
16987 17753	965 16.76		2.0E-61 AA233352.1	EST_HUMAN	2/30g05/i Stratagene N Z neuronal procursor 93/230 Homo septents curve review to TR; G233226 G233226 RTVL-H PROTEIN, contains LTR7/ID LTR7 repetitive element;
17753		П	2.0E-51 AI492415.1	EST_HUMAN	ti27g03.x1 NCI_CGAP_Kid11 Homo septens cDNA clone IMAGE:2131/323
			2.0E-51 AW 137826.1	EST_HUMAN	UI-H-BI1-edj-d-02-0-UI-S1 NCI_CGAP_Sub3 Homo sa
6326 18439 31408		0.66 2.0E-51	2.0E-51 Al381620.1	EST_HUMAN	b/6c/8x1 Soares_NFL_1_GBC_S1 Homo septents culvix clotte InvixoE_2052024 9 stituted to 11x1-95107   P53107 PF20.;

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Table 4
Single Exon Probes Expressed in Placenta

_			2000	200	12 20 0	117000484	ECT LINAN	601470446F1 NIH MGC 67 Homo saplens cDNA clone IMAGE:38/3503 5
		2021	20020	0.73	3 OF B4	2 OE 84 AE210027 1		Homo sapiens diacydlycerol kinasa iota (DGKI) gene, expn 23
	1462	2003/		5.25	2.00-01		1	Homo saplens cell recognition molecule Caspr2 (KIAA0868), mRNA
	7615	20685	34161	1.29	2.01-01	8467	L	THE OTHER AND THE PROPERTY CASES. THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
	8896	21975	36512	1.61	2.0E-51	2.0E-51 EE901994.1	HUMAN	601676/8/F1 NIM MGC. 21 Homo septems culvi diotre trance. 39-9010 3
	8688	21975	35513	1.61	2.0€-51	BE901994.1	EST_HUMAN	601676/87F1 NIH_MGC_21 Homo sapiens curva cione imakise isasso is s
	9236	22312	35854	1.03	2.0∈-51	11037064 NT	NT	Homo sapiens disrupted in echizophrenia 1 (DISC1), mKNA
					200	1017070 1	EST LINAN	ts74a07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2236980 3" similar to SW:1RKC_HUMAN   0149989 NT-3 GROWTH F4CTOR RECEPTOR PRECURSOR :
	2003		28/30	4 98		2 0E-51 RE165080 1	EST HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
	818	22858	36439	0.69	$\prod$	2.0E-51 AB007926.1	NT.	Homo sapiens mRNA for KIAA0457 protein, partial cds
	10648	T	37293	1.58		2.0E-51 AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
	10690	23723	37329	1.07		2.0E-51 AA378559.1	EST_HUMAN	EST91296 Synovial sercoma Homo sapiens cDNA 5 end
	11610	18752	31789	5.82	2.0⊑-61	2.0E-61 (\1732851.1	EST HUMAN	0634709,25 NCI_CGAP_KI35 Homo sepiens cDNA clane IMAGE:1325509 3 stimilar to 5W:NME1_MCUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
	11610	1	31780	5.82		2.0E-51 AI732851.1	EST_HUMAN	6534799.X5 NCI_CGAP_K65 Homo sapiens cDNA clone IMAGE:1325609 3" similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
								Hamo sepiens myeloid/lymphoid or mixed-lineage leukernia (trithorax (Drosophila) hornolog); translocated to,
	12860	25571	31992	1.62	2.0E-51		NT	(MLLT4), mRNA
	117	13348	26375	10.94		4503528 NT	1	Homo septens eukaryotic translation initiation factor 44, isolorim 1 (ELF4A1) minitary
	1523	14676		37.16		1.0E-51 AV742248.1	EST_HUMAN	
	4918	18048	31036	0.82		1.0E-51 AF111168.2	NT	Homo sepiens serine paimitoyi transferase, subunit ii Qene, complete cus, attu utwickii genes
	5505		31720	3.7		1.0E-51 718862.1	EST_HUMAN	b12056t Testis 1 Homo sapiens CUNA cione b12000
	7827	20882	34384	1.03	Γ	1.0E-51 AI572532.1	EST HUMAN	1639g02.x1 Soeres NhHMHU S1 Homo septens CUNA ctone INVACE. 2009 100 3
	8087	21169	34884	0.51		1.0E-51  BF434359.1	EST_HUMAN	7:96502.xf NCI_CGAP_Ov18 Homo sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione IMAGE:3644091 3 similar to Incine sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione sepiens cDNA cione
	12076	7		1.97	٦	1.0E-51 AV760590.1	EST_HUMAN	AV760590 MDS Home sapiens cDNA clone MDSCBB02 5'
	12610			9.43		9.0E-52 AA777621.1	EST_HUMAN	z95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE: 448500 3' similar to contains THR.t3 THR repetitive element;
	į	Т						nw21g02.81 NCI_CGAP_GCB0 Homo capiens cDNA done IMAGE:1241138 3' similar to contains THR.t3
	156	13381	26412	11.42		8.0E-52 AA720574.1	EST HUMAN	THR repetitive element;
	1526	7		2.39		8.0E-52 X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
	1686	14838	27922	2.85	8.0E-52	11968028 NT	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
						-		

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Table 4

Single Exon Probes Expressed in Placenta

					1 20020	120	707
Homo sapiens mRNA for KIAA1249 protein, partial cds	NI	2 0E-62 0E033075 1	T		T	Т	0/0
Human-endogenous retroviral DNA (4-1), complete retroviral segment	ZI	2 0E-52 NA10976 1	T		T	Τ	300
Human endogenous retroviral DNA (4-1), complete retroviral segment	NT	M10976			28790	Т	2
Homo sapiens nypometical protein in the root of the trees of the trees of	2NT	11437042 NT	3.0E-52	. 11.41	3	╗	4924
Harmo sepiens gene ioi Arto, compare ora	N	4.0E-52 AB011399.1		1.3	1	П	13141
Trujilo especia o visa i racinali i avvis	2	4.0E-52 AB002059.1		12.79	2	25642	12887
	2	114181//NI		3.44	-	25304	12429
Lights september Ran GTPassa antivisting protein 1 (RANGAP1), mRNA	N/	j.	Γ		35347	П	8731
Linear Malancia (17 hots) dehidrogenese 4 (HSD1784), mRNA	EST HOMAIN	BE6220			34830	21310	8228
Rentance 72 Home series cDNA cione IMAGE:3915836 5	1	4506132INI			31575	18603	5401
Library sphere phosphoritory pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA	2		4.0E-52		31574	18603	5401
Westbuck I Not 1997 1997 1997 1997 1997 1997 1997 199	EST HUMAN	4.0E-52 AI766814.1 EST	Γ	0.81	30980		4862
Figure 3 Local Mindulating traders and more MAGE:24004593		-		0.77	30203	17193	4037
Homo adplents recomposition by the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c	N.T	-		1.63	28072		1829
Homo sapiens on 3-curtaining protein of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the statement of tools in the	2	AF25731	Г	1.66			1695
Homo septens For Direction Services Services R1 mRNA complete cds	NI	11437365 NT		0.48	36218		9592
n. sepiral a num source no anno a 1 (EBGA) mRNA	2	278898		2.27	30682	17700	4562
TRO IEO GET CAN CONE TNO IEIN I NECONO CON	EST_HUMAN	6.0E-52 BE048172.1	Γ	2.36	38214	24543	11484
E'S							
	EST HUMAN	6.0E-52 AI208794.1		1.05	32341	19035	5845
partial cds	TN	6.0E-62 AF109907.1		7.1	27970	14879	1729
Homp saplens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and contributed						П	
QV3-B10537-271288-048-007 B10037 FULL BLANCE COMPANY CAR and \$171 gene	EST_HUMAN	6.0E-52 EE072409.1	6.0E-52	0.63		7	1214
contains All reputitive element;	EST_HUMAN	7.0E-52 W/58471.1	7.0E-52	1.86	35836	22293	9215
THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S	2	77476580171	8.0E-52	0.76	34233	20751	7686
Homo sopiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA	N.		8.0E-52	0.76		20751	7686
Homo saplens hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13536), mixtus	Z	11968028 NT	8,0E-52	8.75	27923	14838	4101
					T	11000	4
Homo capiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	NT	11988028 NT	8.0E-52	8 75		14838	101
Homo saplens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	NT	11968028 NT	8.0E-52	2.85	27823	14838	1686
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
Olligia Lyoli Lionga Lybrosoca III i manima		Circle					

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Table 4
Single Exon Probes Expressed in Placenta

			ſ			Г	
	Z	1.0E-52 S61070.1		2.6	29315	16302	3126
pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1,						Т	
Homo sapiens ary/sulfatase D (ARSD), transcript varient 1, mRNA	TN				T	٦	2600
Homo sapiens glutamate-ammonia ligase (glutamine symmase) (GLUL) mikina	NT	4504026 NT	1.0E-52	18.76	27630	14656	1402
Zu/75h12.s1 Scares_testis_NHT Homo sapiens cDNA Gone IMAGE: (438/83	EST_HUMAN	1.0E-52 AA634445.1		1.89	28764		546
Q16859 CARBOXYLESTERASE;	EST_HUMAN	2.0E-52 AI808985.1		5.72		26437	12658
	EST_HUMAN	2.0E-52 AW 236297.1	2.0E-52	5.9	31541	26194	12234
Home sapiens Lim domain whase & (Limite), history MAGE-3700036 3' similar to contains Air	Z	11417990	20E-52	3.26		24904	11918
17	ES HUMAN	W 70260.1	2.0E-52	1.46		24714	11634
AV/103// DCB Home sapiens culvy clone DCBAIECG of		AV715377.1	2.0E-52		38225	24550	11491
THR repetitive element;		20E-52 AI831462.1	2.0E-52	3.14	38210		11481
wi49c04.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2	1010011	C. OC. JOSEPH TOTAL	20202	3.17	20200	24040	1140
w/49c04x1 NCI_CGAP_Lu19 Homo saplens cDNA clone IMAGE:2408150 3; similar to contains 1 Firebz	EST HI MAN	19214601	3 On -83	314			
Homo septems SE I domain and mariner transposase itusion gene (SE IMAR) IIINAA	NT	5730038 NT	20E-52	4.6	36966	23356	10321
	NT	5730038 NT	2.0E-52	4.6	36965	23356	10321
	N <sub>1</sub>	4758789 NT	2.0E-52	1		22842	9680
2/45g05.s1 Soares_fetal_liver_spicen_INFLS_S1 Harmo sapiens cunA cione IN/ACE: 4532/23	EST_HUMAN	2.0E-52 AA778785.1	2.0E-52	0.96	35759	22246	9136
Macaca mulatta beta-tubulin mRNA, complete cos	NT	2.DE-52 AF147880.1	2.0E-52	8.71		21933	8854
Homo septens transducin (beta)-like 1 ( IBL1) mRNA	NT	5032158 NT	2.0E-52	0.69	34559	21046	7998
Homo sapiens transducin (beta)-like ( (TBL1) mRNA	NT	5032158 NT	2.0E-52	0.69	34558	П	7896
os45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5	EST_HUMAN	2.0E-52 AI792146.1	2.0E-52	0.76		٦	7081
Homo seplens mRNA for KIAA1081 protein, partial cds	NT	2.0E-52 AB029004.1	2.0E-52	0.96	33415	П	8853
Homo sapiens interleukin 21 receptor (IL21R), mRNA	NT ,	11141868 NT	2.0E-52	1.98	33026	П	6497
IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cUNA	EST_HUMAN	2.0E-52 AW848041.1	2.0E-52	3.24	32317	7	6821
qa56e05,s1 Soares_NhHMPu_S1 Homo sapiens cDNA Gone IMAGE:1590784 3	EST_HUMAN	2.0E-52 AI141802.1	2.0E-52	1.4	31217		5126
qa56e05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA done IMAGE:1890784 3	EST_HUMAN	2.0E-62 AI141802.1	2.0E-52	1.4	31216	_	5126
Novel human gene mapping to chromosome 20, similar to membrane transporters	NT	2.0E-52 AL137188.3	2.0E-52	3.41	31190	7	5082
	EST_HUMAN	2.0E-52 BF677892.1	2.0E-52	11.46		15911	2796
bb66b07.y1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE:3030421 5' similar to gb:X16483 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);	EST_HUMAN	2.0E-52 BE207575.1	2.0E-52	1.6	28818	15693	2568
	Source	No	BLAST E Value	Signal	D NO:	NO.	N 0
Top Hit Descriptor	Top Hit	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ		Probe
a says cooks are a second	Cilibra Exott 10000	. Girls					

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Table 4

Single Exon Probes Expressed in Placenta

		10000000	ſ		3/2021	3 18483	02/20
QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA		3 OF 53 BE 160025 1	T		T	Τ	3 5
Homo sapiens MIL1 protein (MIL1), mRNA		11526297	T		T	Т	
Homo sapiens 26S proteasome subunit 9 mRNA, complete cds	NT	3.0E-53 AF001212.1			1	T	5544
11.2-UM0081-240300-055-DU3 UM0081 Homo sapiens curva	EST_HUMAN	3.0E-53 AW 803563.1		0.75		٦	4713
MXZZGV/ XI OOBIOS DIGGING CHUIT IN TOO THE SHOP OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF	EST HUMAN	3.0E-63 AW 060836.1		1.18	29988	5 16985	3825
complete cds)	Z	3.0E-53 AB028898.1		2.34	28955	6 15844	2726
[Homo sapiens DNA, DLEC1 to ORCITA gene region, section 1/2 (DLEC1, ORCITE, ORCITE games,						7	1
601810969F1 NIH_MGC_48 Homo sapiens CUNA CICIE INVACE #000977 C	EST_HUMAN	4.0E-53 BF128701.1		2.89		7	11489
601810969-1 NIH MIGC 48 Homo sapiens GUNA CICIE IMAGE AGENT I	EST HUMAN	4.0E-53 BF128701.1			38221	П	11489
HSCSID041 normalized great oran color advises color clare colors	EST_HUMAN	4.0E-53 F13080.1		0.94	7	$\neg$	9366
INDEPORTANT INC. CONT. DO DOTTO September CONT. Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Contro	EST_HUMAN	4.0E-53 (A)613037.1	4.0E-53	0.67	_	3 22871	9616
Homo sapiens chiquiosque a la seguiena con la core interes 2778327 31	NT	4.0E-63 AL163285.2	Γ		26302	13289	8
Homo sapiens chromosome zi weginerit nozi coco	N	4.0E-53 AL163285.2		2.07	26301	13289	8
Ü	EST HUMAN	5.0E-53 AW 813563.1	Γ	1.83		25360	12528
Homo sapiens chromosome 21 segment nozi Cook		5.0E-53 AL1632822	Γ	0.92	31377	18411	5293
18	NT	4758543 NT		4.46	30351	17363	4214
THR repetitive element;	EST_HUMAN	7.0E-63 AI421782.1	7.0E-63	7.06		26046	12958
tf44f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone tMAGE:2089077 3' similar to contains THR.f1						Т	
601904771F1 NIH_MGC_54 Homo sapiens CUNA clone IMAGE:4132/83 o	EST_HUMAN	7.0E-53 BF238465.1	7.0E-63			П	12480
Homo saplens core binding factor alpha1 subunit (CBFA1) gene, excit 3	NT	9.0E-53 AF001446.1	e.c-∃0.e		1	7	4511
Homo sapiens protein kinase, camir-dependent, regulatory, type II, beta (Francisco) IIII (1997)	NT.	4506064 NT	9.0E-53	0.69		╗	3891
Homo sapiens 5-3 exoniboruclease 2 (ARN2), minna	3	11421401 NT	1.0€-62	1.31		$\neg$	12135
Homo sapiens 5-3' exombonuclease 2 (XHN2), mXNA	TN	11421401 NT	1.0E-52	1.31	38819	$\neg$	12135
Homo septens processome (prosome, mecropair) subulist, ped type, a (t contact) mission	NT	11426321 NT	1.0E-52	1.72			11075
Homo septens protein tyrosine phosphalase ril CAAA (IT IT CAAA ) ITTNIAA, Cumples was	NT	1.0E-52 U48296.1	1.0E-52	2.12	37720	П	11004
	NT	_	1.0E-52	1.06		П	10814
di08g05.y1 Morton Felal Cochlea Homo saplens culvia cione ilvia GC.24631433	EST_HUMAN	1.0E-52 AW020370.1	1.0E-52	0.68		-1	10804
Reitus norvegicus putative four repeat ion channel mixiva, complete cus			1.0E-62	0.77	36029	7	9390
Homo seplens chromosome 21 segment HS21CU2/	NT	7.2	1.0E-52	1.18		П	866
protein (naip) and survival motor neuron protein (smn) genes, complete cds	NT	.0E-52 U80017.1	1.0€-52	0.59	34576	21084	8014
Homo sapiens basic transcription fector 2 p44 (bir2p44) gene, partial cds, neuronal apoptosis inhibitory					7	Т	1
Human aldolase C gene for fructose-1,6-bisphosphate aldolase	Z		1.0E-62 X07282.1	207	1	Т	7500
Human PMS2 related (hPMSK2) gene, complete cas	NT		1.05-62	233	1	П	6523
Human P-glycoprotein (MDR1) gene, exon 4	NT	1.0E-52 M29426.1	1.0⋶-52 1	4.43	31626	18648	5448
Top Hit Descriptor	Database Source	No.	(10p) Hit BLAST E Value	Signal Signal	ID NO:	SEO D	SEQ D
	Top Hit	•				Exan	Proha
Olligie LAUI Flouds LAPIscook III I Roome	LACIT PTODES	High					

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Table 4

Single Exon Probes Expressed in Placenta

6012/2863F1 NIH_MGG_ZO Homo septens CUNA Crone IMPAGE.301403 F3	EST HUMAN	8.0E-54 BE386785.1		1.29	26465	13435	212
Homo sapiens IQ motif containing G i Pase activating protein 1 (IQGAPT) mRNA		4506786 NT		5.86	31593	25803	6417
Homo sapiens glutamate receptor, ionotropic, kainate 1 (GKIK1) MKNA	SNT	4504116 NT	9.0분-54	0.61			3324
	EST_HUMAN	1.0E-53 AW 245422.1	1.0E-53	1.47		$\neg$	12228
H.sapiens mRNA for hnRNPcore protein A1	NT	1.0E-63 X78536.1	1.0E-53	4.73			9290
II9571.seq.F Human felal heart, Lambda ZAP Express Homo saplens CUNA 5	EST HUMAN	1.0E-53 AA249072.1	1.0E-53				8120
	EST_HUMAN	1.0E-63 BE012071.1	1.0E-63	0.87		20475	7397
CM4-NN1029-150800-543-e02 NN1029 Homo septens cDNA	EST_HUMAN	1.0E-53 BF364201.1	1.0E-53				6831
60/176725F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:3531919 5	EST_HUMAN	1.0E-63 BE296386.1	1.0E-63	1.06	31178		5078
complete cds)	N.T	1.0E-53 AB026898.1	1.0E-53	2.99	29875	16663	3496
Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,		-				╗	
Homo sapiens Xq pseudoautosomal region; segment 2/2	NT	1.0E-53 AJ271736.1	1.0€-53	2.2		╗	1477
7560502x1 NCI_CGAP_Lu24 Homo sapiens cDNA cione IMAGE: 3231627 3 similei fo I K. Lu4wua Lu4wua MYOSIN HEAVY CHAIN.;	EST_HUMAN	2.0E-53 BE550195.1	2.0⋶-53	0.69	37517	23895	10862
2822665.5prime NIH_MGC_7 Homo sapiens CUNA cione IMAGE::2822000 0	EST_HUMAN	2.0E-53 AW 245676.1	2.0€-63	3.47		22663	9608
15429.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens CUNA 5	EST_HUMAN	2.0E-53 AA095652.1	2.0E-53	0.48		21278	8196
EST387707 MAGE resequences, MAGN Homo sapiens cDNA	EST_HUMAN	2.0E-53 AW975598.1	2.0E-53	1.01	34658	21138	8055
PM1-CT0396-170800-001-g03 CT0398 Homo sapiens cDNA	EST HUMAN	2.0E-53 BF334740.1	2.0E-53	2.46	31767		5542
PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA	EST_HUMAN	2.0E-53 BF334740.1	2.0€-53	2.46		18739	5542
Human Krueppel-related DNA-binding protein (TF34) gene, partial cds	3	2.0E-63 M61873.1	2.0€-63	2.59			4170
Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNAZD1) gene, exon 6	N	2.0E-53 AF083822.1	2.0Ε-53	1.20	29508	16490	3317
	NT	7705687 NT	2.0∈-63	0.79	29483	18484	3290
Homo sapiens ATPase, H+ transporting, lysosomal (vacuoiar proon pump) 31kU, vacuoiar proonta (rass. subunit E; V-ATPase, subunit E (ATP6E), mRNA	NT	4502316 NT	2.0E-53	12.68		15726	2601
Homo septens brution s tyrosine kinase (b i n), вірпа-С-дывсьвывае к (GLX), стт-пке пывення рокані (L44L) and FTP3 (FTP3) genes, complete cds	NT	2.0E-53 U/8027.1	2.0E-53	6.26	28662	15535	2404
Home sapiens nyaiuronic acid receptor (TAX), mr.vvA	NT	7705394 NT	2.0€-53	3.29	28325	15209	2068
EST77525 Pancreas tumor III Homo septens cUNA 5 end	EST_HUMAN	2.0E-53 AA366556.1	2.0E-63	11.25		13665	470
	Z	11426423 NT	3.0E-63	1.18			12361
Homo sapiens FGFR1 oncogene partner (FOP), mRNA	NT	5901853 NT	3.0E-53	9.77		$\Box$	9257
Harno sepiens bone morphogenetic protein 5 (BMP5), mkna	NT	10835090 NT	3.0E-63	0.85	35683		9060
GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]	NT	3.0E-53 S72043.1	3.0E-53	10.97	35116		8499
H. sepiens graf gene	NT	3.0E-53 Y10388.3	3.0∈-53	0.76	33777	П	7247
H. sepiens graf gene	NT	3.0E-53 Y10388.3	3.0E-53	0.76	33776	20330	7247
Top Hit Descriptor	Top Hit Detabase Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID

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Table 4
Single Exon Probes Expressed in Placenta

_ G			37652 28483 27211 27211 28096 28097	37652 28483 27211 28096 28097	30704 31073 31073 37652 28483 27211 28096 28097	30764 30704 31073 31073 37652 28483 27211 27211 28096 28097	20542 20542 30764 30704 31073 31073 31073 31073 21073 21073 21073 21073 21073 21073 21073 21073	28570 28571 28542 30265 30704 31073 31073 28483 28483 28095	2667 2867 2954 3070 3107 3107 2848 2848 2809	2866 277 2876 3176 2866	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2								
4.58 3.26 3.26	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					5 5	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 6	4 6									30 20 20 20 20 20 20 20 20 20 20 20 20 20	
4.0E-54 AA306794.1 4.0E-54 D38521.1 4.0E-54 D38521.1 4.0E-54 D38521.1 4.0E-54 AI935086.1 3.0E-54 AA313487.1													7.0E-54 7.0E-54 Al16018 6.0E-54 AB0036 6.0E-54 6.0E-54 6.0E-54 AV7647 6.0E-54 AV7647 6.0E-54 AV80846 6.0E-54 AV88383 5.0E-54 P51623 4.0E-54 A3083 4.0E-54 A3385 4.0E-54 A3385 4.0E-54 A3385	7.0E-54 7.0E-54 7.0E-54 A116018 6.0E-54 AB0038 6.0E-54 AV7547 6.0E-54 AV7547 6.0E-54 AV7547 6.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 5.0E-54 AV813 6.0E-54 AV813 6.0E-54 AV813 6.0E-54 AV813	7.0E-54 N27177 7.0E-54 7.0E-54 A116018 6.0E-54 AB0038 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541 6.0E-54 AV7541	7.0E-54   Y10545 7.0E-54   Y10545 7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54   7.0E-54	7.0E-54 AA8125 7.0E-54 V127177 7.0E-54 A16016 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036 6.0E-54 A50036	8.0E-54 7.0E-54 AA8125 7.0E-54 V10545 7.0E-54 V10545 7.0E-54 A116016 6.0E-54 AB0036 6.0E-54 AB0036 6.0E-54 AV7647 6.0E-54 AV9846 6.0E-54 AV9813 5.0E-54 P51622 4.0E-54 A39852 4.0E-54 A39852 4.0E-54 A39852 4.0E-54 A39852	8.0E-54  8.0E-54  7.0E-54 N27177  7.0E-54 N27177  7.0E-54 A116014  7.0E-54 A16014  7.0E-54 A16014  6.0E-54 A80036  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 A00846  6.0E-54 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Table 4
Single Exon Probes Expressed in Placenta

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Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA	NT					Т	10213
Homo sepiens Janus Kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	7 NT	11429127 NT	T		I	Т	310
Homo sapiens mRNA for brain ryanodine receptor, complete cos	NT	2.0E-54 AB001025.1			1	Т	g
mRNA	NT	11426544 NT	2.05-54	8.33	6  33810	3 20356	7273
Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1),					T	Т	
Homo saplens mRNA for KIAA0895 protein, partial cds	NT	2.0E-54 AB023212.1			7	ℸ	6950
Homo sepiens mRNA for KIAA0995 promin, perual cos	S	2.0E-54 AB023212.1			٦	٦	6950
Homo sapiens EVIS nomolog mKNA, complete cus	즉	2.0E-54 AF008915.1		1.63		7	6796
Homo saplens mxNA for NAA1091 proem, paruar cus	3	2.0E-64 AB046811.1		11.29	7 32488		5982
Homo sapiens minna for NAA 109 I promin, parina ous	3	2.0E-54 AB046811.1			32487	2 19167	5982
Homo septens NAAUTOU gene product (NAAUTOU), HINNEY		11426657		3.99	32379	2 18071	5882
Z4SC11. Y1 NCL_CGAT_BM3Z nomin septents CDNA cique swinger-426 1910 0	EST_HUMAN	2.0E-54 BE047864.1		1.21	3 32209		5720
Homo sepiens small inducible cytokine sublamily A (Cys-Cys), illetilized 17 (20 mm) mm.	Z	4769069			31833		5591
Homo capiens syncyun precursor, mixtus, complete cus	Z	AJ=20816		7.1		17701	4563
Homo sapiens chaperonin occuranning i rodifipies socialis o (occis) mission	NT	4502642 NT		1.74	*	1 17464	4321
RIBOSOMAL PROTEIN L23 (HUMAN):	EST_HUMAN	AA63292	2.0E-54	6.1		8 16802	3638
n/45g09.s1 NCI_CGAP_Pr9 Homo septens cDNA clone IMAGE:895488 similer to gb:X53/// buS		Ţ			]	7	
Homo sapiens mRNA for phospholipase C-bera-10 (FLCB) gene)	NT	2.0E-54 AJ278314.1	2.0E-54	0.6		٦	3392
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Homo septens chromosome 21 segment nozitouto	NT	2.0E-54 AL163210.2		2.25		╗	2666
gu92g03, y1 Schneder fetal train 00004 Homo septens SUNA digital invase2/63/04 5 silling to SW:CUL1 HUMAN Q13616 CULLIN HOMOLOG 1;	EST_HUMAN	2.0E-64 AW 163175.1					2604
	Z	4507184 NT	2.0Ε-54	1.54	27625	14550	1396
Homo sapiens Killer cell lectin-like receptor subramily of member 1 (nuncil), illustro	S	-	2.0E-54	1	П	П	659
	EST_HUMAN	3.0E-54 AW748965.1	3.0E-54	3.16			12379
ES 1366629 MAGE resequences, WAGE nomo sapiens cova	EST_HUMAN	3.0E-54 AW954559.1	3.0E-54	1.32		Į	12336
27012.7 Soares tests NH I Homo septents curve construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the Construction of the	EST_HUMAN	3.0E-54 AA393362.1	3.0E-54	2.86	38421		11650
602019408F1 NCI_CGAP_Brn67 Home sapiens culvia done invador 4 130121 5	EST_HUMAN	3.0E-54 BF345600.1	3.0E-54	4.01	38053	$\neg$	11341
Homo sapiens golgi autoantigen, golgin subilamily a, o (GOLGAO), miniwa	NT	34806	3.0E-64	1.77		╗	11277
al92c08.s1 Soares_parathyrod_tumor_nother A nome sapiets convolution invoce	THUMAN	3.0E-64 A-844061.1	3.0E-54	1.34			7548
alszcob.s1 Soares parantyrod umor junna numo sapiana con a construction of	1_	3.0E-54 A.844061.1	3.0E-54	1.34	34098	20620	7548
Homo sapiens BMX non-receptor tyrosine kinase (bmx) mkrva		4502434 NT	3.0E-54	1.36	32527	19207	6024
	Source		Value	ğ	Ĉ		Ņ.
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Exon SEQ ID	Probe SEQ ID
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Table 4
Single Exon Probes Expressed in Placenta

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Table 4
Single Exon Probes Expressed in Placenta

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22342	22342	25851	18027	16199	13852	13757	13594	25719	25205	19887	25244	24563	21620	15515	16287	15287	15221	15221	14696	14626	14626	13873	16004	26298	24560	24560	23462	23278	23278	22585	22321	NO: SEQ ID Exon
Segon	Γ			29222	26880		26630	П		33279		•			28413	28412	28342	28341		27711	27710	26908	26310		38237	38236	37069	36873	36872		35865	ORF SEQ
0.40				0.89	3,98	1.08	1.69		4.18	0.68	1.82	2.31	9.85	3.02	8.36	8.36	2.19	2.18	1.72	2.16	2.15	32.17	2.24	1.73	1.3	1.3	1.13	1.53	1.53	0.91	23	Expression Signal
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ministrational control protein (CS3786) mRNA	ES (3/0004 NAGE resognatives, waste Y chromosome family 1 member A1 (RBMY1A1) mRNA	Homo sapiens pescelulio (zeutarisir) richiwice i, concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore concerning chore chore concerning chore concerning chore concerning chore concerning chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore 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chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore chore	Homo sapiens SNAF35 nomologue (SNAF31 Combbing BROT Armein (PES1) mRNA	Homo sapiens Strates and nongree (Strate Low), Indiana	Homo sepiens nei (onioken)-iko z (ivercz), ilinive	Homo sapiens microal for Kiladuot i protein, parial cus	Homo sapiens mr.NA for NAADOT protein, partiel ods	ÌÌ		Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

					Gillio	5 10011	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8861	1 22436		4.33	2.0E-55	2.0E-55 Al002836.1	EST_HUMAN	am98h05.s1 Stratagene scritzo brain S11 Homo saptens cDNA done IMAGE:1884185 3' similar to contains THR.b2 THR repetitive element;
9442	╗		0.67	2.0E-55	2.0E-55 BE007969.1	EST_HUMAN	QV0-BN0147-280400-213-gC6 BN0147 Homo septens cDNA
11192	П	37897	2.35	2.0E-55	2.0E-55 AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens ciDNA clone HEMBATUU3363 3
13177	_ 1		1.34	2.0E-55	4507798 NT	NT	Homo sepiens ubiquitin protain Igase E3A (human papilioma virus Eo-associateo protein, Artigentian syndrome) (UBE3A) mRNA
	Т	T	3	105.55	4505060 NT	N	Homo saplens mannose 6-phosphate receptor (cation dependent) (M6PR) mRNA
	13334	26361	40.5	1.0E-55	1.0E-65 U09823.1	Z	Oryctolegus cuniculus New Zealand white elongation factor 1 alpha (Rabeflaz) mRNA, complete cds
88	╗	٦	1.38	1.0E-65	.0E-65 Al026718.1	EST_HUMAN	ov85g09.x1 Soares_testis_NHT Homo septens cDNA clane IMAGE:1844160 3
1173			3.92	1.0E-55	.0E-55 AB020710.1	ZT	Homo septens mkNA for KIAAUSUS protein, paruai cus
2006		28251	2.33	1.0E-55	1.0E-55 BE277861.1	EST_HUMAN	601120110F1 NIT_MGC_at notice saparis CONA close IMACE-9987097 5
2006		28252	2.33	1.0E-55	1.0E-55 BE277861.1	EST_HUMAN	Spice of the circumstance
2401			4.65	1.0Ε-55	5803174 N I	2	Toring subjects owners (Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Started Starte
2415			1.44		.0E-55 AF000990.1	NT	
2586	Γ	Γ	19.68	Γ	1.0E-55 X1311p.1	2	Comp series mBNA for KIAAAAAA protein partial cds
2620	Γ			1.05-00	1.0E-55 ABUUT,666.2	12	Libera see mBNA for KIAAAAAA rectein partial cds
262	T	Γ			1.UE-35 ABOUT,000.Z	1 -	Homo saniens CI P mRNA perfiel cds
26/7	18/61	20914	33	T	1 DE SE ABORROAS 1	NT:	Homo sapiens mRNA for KIAA1219 protein, pertiel cds
3485	$\Box$				1.0E-55 W 28189.1	EST HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo saplens cDNA
4097	$\Box$				1.0E-55 AL 163 267.2	NT	Homo sepiens chromosome 21 segment HS21CU6/
4409	П	30536	1.1		1.0E-55 AL163210.2		Homo saplens chromosome 21 segment HSZ1CUTU
4853		j	0.94		1.0E-55 N77261.1	EST HUMAN	JV44gU3.TI Soares retailiver speech INTLO norma septema convolución improcuencione
4949		31054			1.0E-55 AB037163.1	NT	Homo sapiens DSCR5b mkNA, complete cas
4949	9 18079	31055			1.0E-55 AB037163.1	Z	Homo sapiens Dockson mkna, compieus cus
5614				Γ	AF1198	Z	Homo sepiens PRC1851 mRNA, complete cus
8401	1 19570	32832	7.26	1.0E-55		NT	Homo saprens necrooman and necrotal, minutes
6401	19570	32933				IN	Homo sapiens neci comein and neci 2 (nenvez), illinary
8178	8 21260	34782				Z	Homo sapiens discs, large (Dissophila) homologic (vinapo). 110) (DI G2) mRNA
8178	78 21260	34783	1.7			NI	Homo sapiens discs, large (Drosopina) Indirado a (criados) (1-1-0) (DECE) Indivent
8266	6 21348	34863	0.49		11421648 NT	NI	Homo saplens arver so nonrocular (arver in Civi), mixtos
8273	3 21365	34872	0.93		1.0E-65 AF224492.1	S	Homo sapiens prosprioripire scientilese i gene, complete code
8273	73 21355	5 34873	0.93		1.0E-55 AF224492.1	Z	Homo septens prosphorate scientificase i Beris, withhom cas

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Scurce	Top Hit Descriptor
11152	24223	37851	2.41	1.0E-55	1.0E-55 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11162			2.41			NT	Homo sapiens chromosome 21 segment HS21C010
11733	٦		1.86			NT	Human infant brain unknown product mRNA, complete cds
	$\neg$						seq1676 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft61 5' similar to similar
11755	23941	37567	1.34	1.0E-55	T10045.1	EST_HUMAN	to Chinese Hamster DHFR-coamplified protein mRNA
11789	$\neg$		2.67	1.0E-55	8822743 N	NT	Hamo sapiens hypothetical protein FLJ10891 (FLJ10891), mRNA
11876			1.78	1.0E-55	10567821 NT	,	Homo sapiens DNA-binding protein (LOC35242), mixNA
7522	20595		1.85		9.0E-56 BE378074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens CUNA Cione IMAGE:3009002 0
11545	П		1.34		8.0E-56 AL163209.2	NT	Homo sapiens chromosome 21 segment HSZ1C009
2793	15909	29017	7.08		7.0E-56 H19934.1	EST_HUMAN	yn62g03. In Soares adult orain Nzcomboot Indria septets cores cours indoor. Indeed a summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of summer of s
7818			1.93		7.0E-56 AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapions oUNA
7818		34372	1.93		7.0E-56 AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 C10252 Homo sapiens CUNA
1727		27868	2.7		AW997712.1	EST HUMAN	IXC3-BNUU053-17UZUU-U11-NUT DNUU05 moino sapirais cuivo
9362		35995	0.71		5.0E-58 AW015507.1	EST_HUMAN	OFFI Dipagnator-Colar NC CON Jour Turing appears CON Services of INA
10589	П		1.35	Γ	5.0E-56 W 28189.1	EST HUMAN	CHR 22003 Chromosome 22 evon Homo septens cDNA clone C22 56 5
12013	Т	Τ	14.2	Ī	4 OF ES AE141249 4	NT	Homo sapiens bete-tubulin mRNA, complete cds
2 8	13266	26269	8.64		4.0E-56 AF141349.1	Z	Homo sapiens beta-tubulin mRNA, complete cds
2773	7		3.61		37728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773			3.61	4.0E-56	4507728	NT	Homo sepiens tubulin, beta polypeptide (1088) mixiva
2873	13732	26756	922		4.0E-68 AF003528.1	NT .	Homo sapiens X-linked amilorolitic ectoderma dyspiesia protein gene (CLA), count a entermal report regions
6387	╗				4.0E-56 AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cos
6387	٦	32916	4.94		4.0E-56 AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BNU31 mNNA, complete cus
10724	23767	37364	1.68		4.0E-56 AF043348.1	ZT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allere, parual cus
11163	24234	37863	7.73		4.0E-56 A149806611	н	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens culva cicria imm6cE.x1a2046 3
11163	24234	37864			4.0E-56 A1498066 1	EST_HUMAN	tm65g12.X1 NCL CGAP_Brizo nomo capiens cuivo dura invece. 2 195940 0
1372	14527	27601				N-T	Homo sapiens hypothetical protein FRC1304 (FRC1304), mrvvx
1804	14953	28047	1.84			NT	Homo saplens 5-3 exoridonuclease 2 (ARNZ), ITINNA
2217	15351	28482	1.6		0912697 NT	N	Homo sapiens oncogene ( UZ1 ( I UZ1), MKNA
3195			1.67		3.0E-56 AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens culva o ena
3195	16370	29377			3.0E-56 AA325826.1	EST_HUMAN	KS126689 Cerebellum II nomo septems corvo o en d
3939	17098		281	Γ	3.0E-66 AF 05006.1	1	TOTIO addiction in 10 chave 1 region

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Table 4

Single Exon Probes Expressed in Placenta

		0.00-01 00 220-01	Γ	1.1.4	20220	4 24552	11484
Homo sapiens serine protease 17 (KLK4) gene, complete cds	NT	A 508/07 4	T			Т	1404
Homo saplens serine protesse 17 (KLK4) gene, complete cds	NT	9 0E-67 AF228497 1	T			Т	
QV0-OT0033-070300-152-h03 OT0033 Horno sapiens cDNA	EST HUMAN	9.0E-57 AW880836.1				Т	2
RC2-CT0163-220999-001-E02-C10163 Homo sapiens CUNA	EST_HUMAN	1.0E-56 AW845937.1			36886	┪	10254
Homo sapiens chromosome ZI segment To Zi Cook	NT	1.0E-56 AL 163203.2		0.69	3		10161
QV-B1077-130189-079 D1077 Tollio septemb convo	EST_HUMAN	1.0E-56 Al905162.1		1.42	31238		5145
12	EST HUMAN	1.0E-56 AW589833.1		1.84	29929	18926	3765
INGZGCTLXT NOT COAP GOO DOING septemb CDNA claims (WAGE: 29484523)	EST_HUMAN	1.0E-56 AW589833.1			29928	16926	3765
Macaca tascicularis protein vicesne prospinalese (Frich.) Illinois, complete cus	Z,	1.0E-56 AF190930.1		3.01			1003
Homo sepiens on I domain and mariner unisposase lesser generoles code	8 NT	5730038 NT		1.39	33767	20323	7239
AV/03164 AUG Homo Septems CUNN Giving NUBCH Give o	EST HUMAN	AV70318	Γ	1.26	29805	16788	3624
Homo sapiens gene for activit receptor type tip, complete was	3	2.0E-56 AB008691.1		0.84		16561	3391
Homo sapiens mixing for NAX14 14 protein, pared out	3	2.0E-56 AB037835.1		0.94	29249		3053
RC4-B10310-110-010-110-D10310 Horito explains convi	EST_HUMAN	2.0E-56 BE084386.1			26976	П	761
INCAR 10310-110300-010-110 D Total C Hamping Spirit	EST_HUMAN	2.0E-56 BE064386.1		1.18	26975	16021	751
zg62a08.91 Stratagene neuroepimellum (#80/231) monto septens contro della livroca. Ottoba	EST HUMAN	2.0E-56 AA199818.1		11.95		13730	637
Homo sapiens caveolin 3 (CAV3), mixiva	8 NT	11434876 NT				П	12377
Homo sapiens caveolin 3 (VAV3), ITINIA	BNT		Г	1.62	32075	25268	12377
Homo sapiens nuclear pore complex interacting protein (INFIF), in INVIC	3 NT						11594
Homo sapiens nuclear pore complex meracung protein (NFIF), minutes	NT		3.0E-56	4.64			11594
	TV	3.0E-56 AB042558.1	3.0E-56	2.62	37693	24069	10980
Homo saptens KIAAUST / gene product (NIAAUST / , IIIINAA	SNT	11434956 NT	3.0E-56	1.39	37336	23731	10698
Homo sapiens micro NAAO 140 protein, paren da	NT		3.0E-66 D63479.	0.9	36652	23056	10018
Homo sapiens bone morphogeneric protein a (pwir a), minux	NT	11418704 NT	3.0E-56	6.11	35635	22095	9016
Homo sapiens LIM binding domain 2 (LUDZ) INKINA	Z	4504970 NT	3.0E-56	2.07	34024	7	7476
Homo sapiens Lim binding domain 4 (LDD4) Inining	TNT	4504970 NT	3.0E-56	2.07	34023		7476
Homo sapiens lysosomai-essociated memorane protein z (Chier z), illinuro	N.	1:1421124 NT	3.0E-56	5.5	33571		7014
	NT	4759183 NT	3.0E-56	1.5	32294	18891	6801
Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA	NT	4759163 NT	3.0E-56	1.5	32283	18991	5801
Hamo sapiens superkiller virgiciaic activity a (G. cereviseo izulitate) "ilie (Characte)" ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) ilina (Characte) i	NT	5902085 NT	3.0E-58	2.4	30816	17830	4695
Homo sapiens chromosome 21 segment no2 (1900) septens chromosome 21 segment no2 (1900) in SKINO (1900) mBNA	NT	3.0E-56 AL163263.2	3.0E-56	4.42	30664	17682	4544
Homo sapiens Down syndrome candidate region 1 (USCK1), mKNA	NT	7657042 NT	3.0E-56	0.67	30634	17646	4507
	Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	NO:	SEQ ID
	Tao ∐:		Most Similar	-		E	p.

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Table 4

Single Exon Probes Expressed in Placenta

2768	2484	1362	827	3849	13185	3982	3982	3344	2698	2698	1246	12808	12791	12102	12041	11768	7827	7027	7607	6593	6593	6529	5355	1856	907	308	14	11811	Probe SEQ ID NO:
15883	15591	14516	14005	17009	26071	17139	17139	16517	15817	15817	14405	26528	25528	25082	25022	13252	20977	20977	20877	19753	19753	1988	26034	16005	14082	13524	13262	24801	SEQ ID
28992	28716		27062	30010		30144	30143			28932	27487	32007	32007	38789	38726	26252	34487	34486	34152	33139	33138	33086	31679	28112	Ž7147	26558	26252	38500	ORF SEQ
1.03	1.12	1247	0.64	6.03	3.99			0.81	0.97		88.0	1,94	1.67	1.53	1.74	3.51	1.54	1.54	0.62	12.82	12.82	0.61	1.92	1.45	7.49	2.03	1.02	2.2	Expression Signal
	Γ		4 3.0E-57		-			7.0E-57	7.0E-57			8.0E-57		8.0E-57	8.0E-57	8.0E-57			8.0E-57					Ι,			8.0E-57		Most Similar (Top) Hit BLAST E Value
3.0E-67 BE676622.1	3.0E-57 AA348335.1	3.0E-57 AA230279.1	4507798	4.0E-57 AB026898.1	6.0E-57 AJ271735.1	7.0E-67 AF012872.1	7.0E-57 AF012872.1	0005979 NT		  -  -	AJ003100	11545732 NT	11545732 NT	11431260 NT	11433356 NT		8.0E-57 AB020844.1	8.0E-57 AB020644.1	7682263 NT	8.0E-57 AB023177.1	8.0E-57 AB023177.1	8.0E-57 AB020705.1	11418185	8.0E-57 AA486109.1	8.0E-57 AW 264539.1	8.0E-57 AW816405.1	8923349 NT	9.0E-57 AB020981.1	Top Hit Acession
EST_HUMAN	EST HUMAN	EST_HUMAN	8 NT	Ŋ	2	2	Z	NT	NT	NT	NT	TNT	NT	NT	NT	NT	NT	N <sub>1</sub>	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	Top Hit Database Source
CE20263;	EC 1947 / O nippocarripus il nonto sapieto convo o circ	1 -	syndrome) (UBE3A) mRNA	complete cds)	Homo content NA DI FOY to ORCTI 4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	- 13	Homo sapiens phospheroylinositol 4-kinese 230 (pi4K-230) inRVA, complete cds	-	Homo sapiens and GUO-ADDOCIA IEU PAO IEIN (GWPC), IIINNA	Homo saplens sing GDS-ASSOCIATED PROTEIN (SMAP), ITINAN	Homo sapiens GYS2 gane, exon 14	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mixing	Homo saplens SH3-domain binding protein 1 (SH3BP1), mKNA	Homo sapians Ras suppressor protein 1 (NSUT), mixina	Homo sapiens ninein (LOC31189), mixiva	Homo saptens hypothetical protein FLJ203/1 (FLJ203/1), mixivis		Homo septens mRNA for KIAA0837 protein, partial cos	Homo sapians KIAA0/16 gene product (NAA0/10), mixiva	Home sapiens mRNA for KIAA0960 protein, partial cds	Homo septens mRNA for KIAA0960 protein, partial cds	Homo sapiens mRNA for KIAA0888 protein, partial cos	Homo saplens aconilase 2, mitochondrial (ACC2), mKVA	Z/51b12.r1 Soares_tests_NH   Homo sapiens CUNA CIONE IIVIAGE. 757 131 3	י חוי	QV4-S10234-181199-037-103 S10234 Homo septems CUNA	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mixtys	Homo saptens mRNA for cyclin bz, complete cus	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

					Most Similar	ن. ن. ن.	Tan Hii	
	Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Database Source	Top Hit Descriptor
								7/33br10.x1 NCI_CGAP_CLL1 Homo septens cDNA clone IMAGE:3286443 3' similer to WP:Y47H9C.2
	2768	Τ.	28993	1.03	3.0E-57	3.0E-57 BE676622.1	NT HOMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein t(Cin) gene, complete cds
	3788	10040	100	51.29	3.0E-67	_	THUMAN	RC3-CT0254-110300-027-d10 CT0254 Hamo sapiens cDNA
	6153	Т	32675	1.25	3.0E-57	5608	1	
	6251	$\neg$		3.25	3.0E-57	3.0E-57 BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo capians cUNA clone INAGE:3944302 3
	8338		34945	3.92	3.0E-67		EST_HUMAN	4276 Human retina cDNA randomly primed subjictary monto sapients colven
	8363	21444	34966	1.99	3.0E-57		N	Homo sapiens hypothetical protein FLJ 11000 (FLJ 11000), Tilinium
	8363	21444	34967	1.99	3.0E-57		N.T	Homo sapiens hypometical protein run 1900 (run 1900), finales
٠.	8476			0.78	3.0E-57	11427757 NT	Z	Homo sapiens NAANOGS genie product (NAANOGS) III NAA
	8624	21704	35240	514	3.0E-57	3.0E-57 AU117659.1	EST HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5
	9451	Т		0.60	3.0E-57	11545798 NT	- 1	Homo saplens hypothetical protein FLJ11656 (FLJ11656), mRNA
	9451	П		0.69	3.0E-57	1,1646798 NT	NT	Homo saplens hypothetical protein FLJ11656 (FLJ11656), mKNA
	11148	24220	37847	2.34	3.0E-57	3.0E-57 AW 248374.1	EST HUMAN	2820473.5pnm6 NIH_NIGC_/ Homo septens CDNA claric IMACE 308549.5
	12384	Г		6.37	3.0E-6/	3.0E-5/ W Z38/1.7	EST HUMAN	A innaede Selected chromosome 21 cDNA library Homo saplens cDNA clone MPIpI10-1L1
	7087	20040	37783	280	205-57	20E-57 AF246219 1	N	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
	1630		T	2.89	1	2.0E-57 AF246219.1	TV	Homo septens SNARE protein kinase SNAK mRNA, complete cds
						205 67 0 00 00 00 0	EST LIMAN	at02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cUNA cione IMAGE:1404747 3 strittar to contains Atu repetitive element;
	3525	16690		1.4		2.0E-57 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
	3641	П	29818			2.0E-57 R07702.1	EST_HUMAN	ye98h01.11 Soares fetal liver splean 1NFLS Homo sapiens CUNA Cione IMAGE:125800.5
	3641			0.72		2.0E-57 R07702.1	EST_HUMAN	yesenot. T Soares retailiver spicen (INTL) number spicilis colver close introductives of
	4304	17447				2.0E-67 AA018299.1	EST HUMAN	ZEPUCUS.TI CORTOS TEURIS NOCIONAS SERVIS CONO COMO COMO TRADOS TEURIS CONO COMO COMO COMO COMO COMO COMO COMO
	4304	T			Γ	2.0E-5/ AA018299.1	ESI_HUMAN	Homo seriens chromosome 21 segment HS21C083
	4632	2 1//68	30/49	74.1		7.0E-01 AL 100203.2		2631c05.r1 Soares retina N2b4HR Homo sepiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1
	6786	6 18977		1.48	T	2.0E-57 AA016131.1	EST_HUMAN	repetitive element; 7n80704 x1 NC  CGAP 0v18 Homo septens cDNA clone INAGE:3570966 3' clmiter to contains TAR1.H
	6158	8 19334	<del></del>	31.41		2.0E-67 BF115263.1	EST_HUMAN	MER22 repetitive element;
	6288	٦	32813	6.34	П	11431281		Homo septens small inducible cytokine subtamily A (Cys-Cys), member 22 (CC 1 A 22), manyer
	8832		35449	1.03		2.0E-57 AF045452.1	NT	Homo saptens cell-line KG1 transcriptional regulatory protein por finance, complete cas
	10051	23089	36691	1.08	Γ	2.0E-57 AF057722.1	2	Homo septems in recently discognized with a control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control

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Table 4
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Table 4
Single Exon Probes Expressed in Placenta

Holling Schelle C. D. COM deservation broket of C. D. S. A. H. B. A.	INI	17424069 NI	4.015-58	7.44	38366	4 24675	11624
	EST HUMAN	BE 4638			34557	5 21045	7995
Homo sapiens EGF-like repeats and discordin t-like uprilative of EDICO/, https://doi.org/10.100/		5031660 NT			29996	16994	3834
Human mKNA, Xq terminal portion	NT	D16470.		1.41	29587	2 16572	3402
Human beta-prime-adaptin (BAM22) gene, exon 3	NT	4.0E-58 U36251.1		212	28930	15816	2696
(F9) mRNA	8 NT	4503648 NT		1.24	27731	3 14649	1488
Homo sepiene interleukin 10 receptor, bela (IL10RB), mKNA	NT.	4504634 NT	4.0E-58	1.87		П	819
conferring protein) (ATP50) mRNA	2 NT		4.0E-58	1.71	26627	13592	384
Homo senions ATD symbols H+ transporting mitochondrial F1 complex. O subunit (oligonycin sensitivity	I V	INI 0740741	3,05-36	1.4/		28102	12850
Homo septens cat eye synorome or orrowne region, certamen i (CLCXX), illixxx	3 NT	11526293 NT	6.0F-68	4.5		П	12362
Homo sapiens mRNA for KIAA0611 protein, partial cos	Z,	5.0E-58 AB014511.1				П	10812
Homo capiens mRNA for KIAAU611 protein, partial cas	3	5.0E-58 AB014511.1		0.65	37254		10612
Homo sapiens chromosome 21 segment HSZTCVTV	4	5.0E-58 AL163218.2	5.0€-58	1.8	36973		10328
Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA	7 NT	11430847 NT	6.0E-58	0.96	П	П	10061
Homo sapiens mRNA for KIAA1617 protein, partial cds	NT	5.0E-58 AB046897.1	5.0E-58		П	7	8548
Homo sapiens hypothetical protein FLJ10826 (FLJ10828), mRNA	NT		5.0E-58				8158
Homo sapiens holocytochrome c synthese (cytochrome c heme-lyase) (HCCS) mKNA	UNT	4885400 NT	6.0E-58			7	7255
Homo sepiens nibrin (NBS) mRNA, complete cds	ZT	AF051334.1	5.0E-58			丁	6917
Homo sapiens nibrin (NBS) mRNA, complete cds	NT	5.0E-58 AF051334.1	5.0E-58	0.6	1	7	6917
Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA	NT	11421330 NT	5.0⊑-68	1.03		П	680
Homo sapiens chromosome 21 segment HS21C085	NT	5.0E-58 AL163285.2	5.0E-58	0.79		П	6524
ym51h07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5	EST_HUMAN	5.0E-58 H23072.1	5.0E-58	6.55	32834	I	6307
Homo sapiens placenta-specific 1 (PLAC1), mRNA	TN	11496282 NT	5.0E-58	1.9.1		╗	5748
P19984 PROFILIN II;	EST_HUMAN	5.0E-58 A1636745.1	5,0E-58	0.93	30486	17616	4373
G98e07.s1:NCI_CGAP_Lu5 Homo septens cDNA clone IMAGE:3338488 3' similar to SW-DRO2	EST_HUMAN	5.0E-58 AA988183.1	5.0E-58	4.09	29585	П	3400
CM3-LIM0043-240300-127-e07 UM0043 Homo sapiens cDNA	EST_HUMAN	5.0E-58 AW 797948.1	5.0E-58	2		П	1222
CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	EST_HUMAN	5.0E-58 AW 797948.1	5.0E-58	2		7	1222
CM3-UM0043-240300-127-eD7 UM0043 Homo sapiens cUNA	EST_HUMAN	5.0E-58 AW 797948.1	5.0E-58	2.9			1221
CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	EST_HUMAN	6.0E-58 AW 7979,48.1	6.0E-58	2.9		П	122
RC4-NT0057-160600-016-b05 NT0057 Homo sapiens CUNA	EST_HUMAN	5.0E-58 BE763984.1	5.0E-58	6,96		٦	728
Homo sapiens synaptojanin 1 (SYNJ1), mRNA		4507334 NT	5.0E-58	3.06	26560	13527	311
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E Vatue	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:
							]

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Table 4

Single Exon Probes Expressed in Placenta

noillo sabialis o protei receptor con Contraction and	1	5174444 N	1.0E-58	1.01	6 28322	2 15206	2892
	921		Ι.			15977	2863
Long series stord regulatory element hinding transcription factor 2 (SREBF2) mRNA	2	1.0E-58 AFZ1/014.1			Γ	16837	2719
Homo sepiens uncharacterized bone marrow protein BM038 mRNA, complete cds	1010000	.00-30 DE#00 102.1				Г	1697
hydriga x1 NCI CGAP GC6 Homo saplens cDNA clone IMAGE:3196935 3'	ECT LINAN	UE-08 AJZ30083.1			Τ	Т	1427
Homo sanims partial AF-4 dene. exons 2 to 7 and Alu repeat elements	EG L TOWN	1.0E-58 AW857 152.1			Γ	Г	1358
FST369252 MAGE reseguances, MAGD Homo sapiens cDNA		1.0E-30 AW307 102.1				Т	1358
Homo capiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (22/U, 522) (NDC 53), III NYS EST360762 MAGE reseguances, MAGD Homo septems cDNA	BOT LIMAN	8274649 NT	1.0E-58			1	1093
		,			1	$\neg$	
Human complement component C5 mKNA, 3 end	፭	1.0E-58 M65134.1	1.0E-58	1.06		П	746
hm25108.x1 NCI_CGAY_I ny4 nomo sapiens cona cione ilvinoci. so isori s	EST_HUMAN	2.0E-58 AW872641.1	2.0E-58	1.68	37913		11207
601890812F1 NIH _WGC _1/ Homo sapiens CDNA Grove INVACE: 3013871 3'	EST_HUMAN	2.0E-68 BF307745.1	2.0E-68	16.01	37692		10979
Homo septens endocytic receptor Endo lau (ENDO lau) III. NA, cultiplica de	NT	2.0E-58 AF134838.1	2.0E-58	2.79	33849		7307
	Z	2.0E-58 AF134838.1	2.0E-58	2.79	33848		7307
qm84c01.XT NCI_CGAP_Lub rigino sapiens cons cons invoce. 1030-7-7-7	EST HUMAN	2.0E-58 AI291407.1	2.0E-58	0.63	33533		7086
yq08h06,r1 Soares fetgi liver spiesh TNFL3 monto sapielis opino digita importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis importo socialis imp	EST_HUMAN	2.0E-68 R92587.1	2.0E-68	0.83	32806	$\Box$	6283
BINDING PROTEIN:	EST HUMAN	2.0E-58 A1124874.1	2.0E-58	2.16	32769	19423	6249
CE05065 UBIQUITIN CONJUGATING ENZYMEY, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM							
UI-H-BW1-ams-g-11-0-UI-ST NCI_CGAT_OUD/ Horro sapietis CONA cide invade-work to Wi	EST HUMAN	2.0E-58 BF513488.1	2.0E-58	1.7			6182
601499961F1 NIH_MGC_70 Homo sapiens CUNA cione IMAGE 307106	EST_HUMAN	2.0E-58 BE907186.1	2.0€-68	2.53		7	5473
	EST_HUMAN	2.0E-58 BE907186.1	2.0E-58	2.63	31662		5473
	EST_HUMAN	2.0E-58 AW074831.1	2.0E-58	0.94	31630	$\neg$	5451
protein (MOUSE);	EST_HUMAN	2.0E-58 BE208532.1	2.0E-58	7.88		14474	1318
ba08b07.y/ NIH_MGC_7 Homo septens cDNA clone two Citizazations o stimute to governor to be RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.muscullus mRNA for TAX responsive element binding							
Homo sapiens o-aminoievulinate syrunase c (ALAGE) Beila, complete cos	NT	20E-68 AF068624.1	20€-68	12,47	27197		963
AV712977 UCA Homo sapiens cuiva cione UCAAACOVA O	T HUMAN	3.0E-58 AV712977.1	3.0E-58	2.49			6778
HSC1TG081 normalized infant brain cDNA Homo septens CDNA cione C 1000	L	F07056.1	3.0E-58 F07056.1	1.1		- 1	6674
QV0-BT0702-170400-194-139 BT0702 Homo sapiens CUNA	EST_HUMAN	3.0E-58 BE089509.1	3.0≅-58	0.61	7	T	6390
602185789F1 NIH_MGC_45 Homo sapiens CUNA Cione IMAGE: 4509943 O	EST_HUMAN	3.0E-58 BF569848.1	3.0E-58	3.07		٦	3248
602185789F1 NIH_MGC_45 Homo sapiens CUNA cone IMAGE: 4300043 51	EST_HUMAN	3.0E-68 BF569848.1	3.0⊑-58	3.07		Т	3246
Homo sapiens peptide YY (PYY) mixing		4758981 NT	3.0E-58	2.6	27647	14574	1420
yg10e02r1 Soares Infant brain 1NIB Homo sapiens cUNA clone IMAGE:31093 5	HUMAN	₹17878.1	3.0E-58 R17878.	0.96		13556	345
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	(Top) Hit BLAST E	Expression Signal	ORF SEQ	SEQ ID	Probe SEQ ID NO:
		,	Most Cimiler				
	9.0	99					

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Table 4
Single Exon Probes Expressed in Placenta

					Single	EXON Ploues	Single Exon Floores Expressed in Flacetica
 Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signed	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
3827	16791	29809	0.93	1.0E-58	4758081 NT		Homo sapiens chandrottin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3627	П		0.83	1.05-58	4758081 NT		Homo sapiens transition protein 1 (during histone to proteinine replacement) (TNP1) mRNA
3814	Т	Γ	0.66	1.02-68	11 070/0C#	TUIMANI	0743h01 x1 Sogres NhHMPu S1 Homo sapiens cDNA clone IMAGE:1678129 31
5086	Т	Τ	7.13	1.05-58		EST HUMAN	
7002	20138	33556	0.87	1.0E-58	1.0E-58 11422031 NI	1	Homo sepiens hypothetical protein (LOC51260), mRNA
8305	П		0.49		1.0E-58 AW973537.1	EST_HUMAN	EST385637 MAGE resequences, MAGM Homo sapiens cUNA
 9070	22149	35695	0.62		4505314 NT		Homo septens myomesin (wr-proven) z (100xC) (wri Cwz), ilinxyn
9182	Г	Γ	0.77	1.0E-58	1.0E-58 AV751001.1	EST HUMAN	AV 3100 I NF C Fights NHT Homo sacions cDNA clone IMAGE:730497 5'
2828	22300	35025	0.04		1.0E-58 AA412397.1	EST HUMAN	
10389	П		0.65		11432994 NT	NT	Homo sepiens disce, large (Drosophila) homolog 2 (chapsyn-110) (ULGZ), mixWA
12074	25055		2.1	1.05-58		Z	H. Seplens immunogiopulin keppa ugiri chain variawe regioni - i r
12100	Г	Π	2.61		1.0E-68 D61405,1	2 7	Homo seniens TATA box binding protein (TBP) mRNA
2303	2000	33835	0.74	Ī	8.0E-59 AA382291.1	EST HUMAN	EST95883 Testis i Homo sapiens cDNA 5' end
6979	П	٦	0.74		8.0E-59 AA382291.1	EST_HUMAN	EST95683 Testis   Homo septens cDNA 5' end
8374	П	П	1.65		8.0E-59 AI761963.1	EST_HUMAN	wh50d06.x1 NCI_CGAP_Kid11 Home sapiets CDNA close IMA GE-3863086 5
182	16006		1.97		6.0E-59 BF035327.1	ESI_HOMAN	ou lacostir I win _MGC_Got Idailo septens con ex cismo image: 1553550 3' similar to TR:Q13732 Q13733
8015	21066	34579	0.62		6.0E-89 AA962431.1	EST HUMAN	SA GENE PRODUCT PRECURSOR.;
8440	21521	35050	0.69		6.0E-69 AI760970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo septems cDNA clone NHTBC_cn06h02 random
3197	16372	29379	7.75		5.0E-59 AJ807484.1	EST HUMAN	WI46011.X1 Coales WFL 1 GOO at Finding september reposit
4780	17915	30801	9.94		5.0E-59 X83497	2	gu66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains
7129	18555	31470			5.0E-59 AW162304.1	EST_HUMAN	element TAR1 repetitive element :
8008	3 22085	35628		Γ	11421778 NT	NT	Hamo sapiens polymerase (Puva) ill (Piva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Pa Coo), ill ale cool (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilected) (Puva dilect
9906	Г	Γ		Γ	AV/628	EU I TOMAN	Homo seplens hypothetical protein (LOC57143), mRNA
11148	Τ.	Γ			I NI OCHTENI I		Liumen mRNA for KIAA011RA gene partial cds
816	6 13995	2/050	8.F	Ī	4.00-39 000000.1	1	Home sapiens phosphatidylinositel-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated
1266	6 14423	3 27489	0.61	4.0E-59	4505818 NT	NT	products

Page 334 of 550 Table 4 Single Exon Probes Expressed in Placenta

					Guid	Culfie Lyon, 10000	י ראקו ליסטים וווי ו מסטי מע
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Velue	Top Hit Acession No	Top Hit Database Source	Top Hit Descriptor
1266	14423	27490	0.61	4.0€-59	4505818 NT	NT	Homo sepiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIPSKZB) mkna, and translated products
4912			1.14	4.0E-59	4506758 NT	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4912	٦	٦	1.14	4.0E-59	4506758 NT	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5654			0.95	4.0E-59	11034810 NT	TN	Homo sepiens catenin (cadherin-associated protein), delta 2 (neural piakophilin-related arm-repeat protein) (CTNND2); mRNA
12498	. ]		3.89	4.0E-59	4.0E-59 AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydroganase IV (HSD17B4) gens, promoter region and exon 1
1	П		6.74	3.0E- <del>5</del> 9	3.0E-59 AW 865524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cUNA
234	П	26481	3.88	3.0E-69		NT	Homo saplens KIAA0580 gene product (KIAA0580), mRNA
1748		27992	10.81	3.0E-59		NT	1.
1748	14897	27993	10.81	3.0E-59	4505860 NT	NT.	Homo septens plasminogen dedecut, usedo (r Cris) ili avo
2198	16333	28459	8.54	Γ	3.0E-59 AB029035.1	Z	Homo sapietis minina tor NAA i i iz protein, periol cyte
2198	15333	28460	9.52		3.0E-59 AB029035.1	Z	
3104	16280	Γ	0.67	3.0E-59	T18865.1	EST HUMAN	102017: Tacific 4 Homo septeme cDNA clone h02017 5' and
3104	Τ.	Τ	0.67	3.00-60	1 100001.1	NT TOWN	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
2100	1837	2020	4 27			Z-I	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3930	1	T	1.19			NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (2P2) mRNA
4808		30929	2.75		3.0E-59 AL163284.2	NT	
4965		31071	2.12	Γ	7427522 NT	N.T	Homo sapiens protein tyrosine prospinalase, receptur type, i (T i T \ ), iii \ \
5162		Γ	1.22	Γ	M95961	Z	Human pronormone convening encyline (1/10/2) years, www. 2
6350	19520	32877	2.4	3.0E-69		Z	Tionio sapiens nucleos recentos consenses ( NOOR1) mRNA
7516	Г	Γ	1.85	Γ	5454137		10000
8116	Γ	Γ			3.0E-59 X12556.1	12	Turisa Time to the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference of the conference
8116	Т	Ţ		Ţ	3.0E-59 X70284 3	2 7	H. sapiens CKII-albha gane
10250	23285	36881	1.04	7	3.0E-59 X70251.1	ZT	
12635	П		11.11		11417866 NT		Homo sapiens gamma-glutamytransferaso-like activity 1 (GG LA1), mktiva
6946		9	0.59		2.0E-69 AA470073.1	EST HUMAN	Z98d05.S1 Soares_lestis_INT I nomo sapiens cuina cione inviade
7216	6 20081	33494	0.59		2.0E-59 AF135187.1	Z	Homo sapiens interieron-induced piotein pro (MAT) galle, complete cas
9837	7 22877	7	4.84	Γ	2.0E-59 AA3097/4.1	EG HOMAN	COL 190933 CHINAL TODIS VIDOLO SUPPLIES COLLO COLLO
10745	ì			Γ	2.0E-69 BF365854.1	EST HUMAN	SOOTANI AND 17 Home saries cDNA close IMAGE: 2881654 5
11069	B 24144	3//80	2.18	Γ	2.0E-38 AVV410080.1	LO TOTAL	

7/7/2/10 OM

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Table 4
Single Exon Probes Expressed in Placenta

Dono sapteris illustration to receptor, see (12 to 12),	184	4504634 N	7.0E-60	1.47	27071		838
HOMO SEDENS WITH CIESS I region	Z	AF05506	Γ	25.11	4 27004		774
Homo sapiens MHO class 1 region	2	7.0E-60 AF055068.1			27004	13954	773
Homo position VIII Close 1 region	2	8.0E-60 AL 163204.2			37784	24146	11071
Lamb spices chromosome 21 segment HS21C004	2	8.0E-60 AL 163204.2		4.17	37783	24146	11071
Homo serviens chromosome 21 segment HS21C004	100	INI VERSION	Γ			23832	10799
Homo seriens RAN hinding protein 7 (RANBP7), mRNA	2 2 2		Γ		Γ	Г	9671
Lomo sepiena KIAAOA33 protein (KIAAOA33) mRNA	S N		8.0E-60		Γ	22633	9871
	NI		Γ			22218	9139
Human mrnA for integrin airina and nineal diand (arrestin) (SAG), mRNA	N	X17033.				П	8152
Homo sapiens prospinate cytolyguariste ase i, crioting composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in the composition in	1 NT	11420841 NT	Γ	0.89	34434	20928	7874
hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	Z	S83182.		0.89	33181	19792	6833
Homo sapiene mixiva for NIAA 100 i proteiri, parusi cus	NT	8.0E-60 AB029004.1	Γ	1.18	П	19283	8103
ΠÈ	6 NT	5174656 NT	Γ	4.76	28503	15374	2241
Homo sapiens differentiation-related gene 1 (nicker-specific induction protein) (RTP) mRNA	6NT		8.0E-60	4.78			2241
Homo sapiens small nuclear abonucleoprotein to polypoprote (low) (City Co) in Co.	NT		8.0E-60	3.21			1499
ES 1389849 MAGE resequences, MAGO Homo sepsens CUVA	EST HUMAN	AW9778		1.45		П	783
Homo saplens mKNA for transcription recor	NT T	1.0E-59 AJ130894.1		10,98		П	11094
Homo sapiens 3-hydroxy/sooutyry-Coenzyme A nydrozase (nibCn), iinniv	NT	1/1428849 NT		0.58		$\neg$	9804
Homo sapiens 3-hydroxylsocutyry-Coenzyme A nydrozase (nibon), illuvyn	NT	1 1428849 NT		0.58		7	989
Homo sapiens zinc finger protein 2/5 (2NF2/5), mixix	NT		1.0E-69	0.88	٦	П	988
601111951F1 NIH_MGC_16 Homo sepiens dunA cicrie imprecissozoez o	EST_HUMAN	1.0E-59 BE256814.1		1.3		20947	7895
601111951F1 NIH_MGC_10 Homo sapians CONA Citals in ACC 3050505 5	EST_HUMAN	1.0E-69 BE256814.1		1.3	34454	20947	7895
Homo sapiens mRNA for transcription factor	NT	1.0E-59 AJ130894.1	1.0E-59	1.14	34285	20796	7735
O856h11.81 NCI_CGAP_GCBI HOMO SEPISITIS CLIVA COLIE MIXAGE. 1999-20 9 3 11 11 11 11 11 11 11 11 11 11 11 11 1	EST_HUMAN	1.0E-59 AA748468.1	1.0E-59	2.65		15803	2683
S21348 HYPOTHETICAL PROTEIN 4 - ;	EST_HUMAN	1.0E-59 T92522.1	1.0E-59	1.04	27803	14722	1569
6011/6/5/F1 NIH_MGC_1/ Tigno septions color color invocations in 18768 5' smiler to SP:S21348	EST_HUMAN	1.0E-59 BE286411.1	1.05-59	5.65		13392	167
Homo capiens alpha-tabulin mxnx, complete cas	Z	2.0E-59 L11645.1	2.0E-59	3.87		26019	12983
086542 RTVL-H PROTEIN. contains LTR7.b1 LTR7 repetitive element;	EST_HUMAN	2.0E-59 AI631809.1	2.0E-59	4.28	32118	25238	12373
th07h04x1 NIH_MGC_17 Home septens convenience has GE-2300182 3' similar to TR:086542	EST_HUMAN	2.0E-59 AW410698.1	2.0E-59	2.19	37781	24144	11069
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	SEQ ID	Probe SEQ ID NO:
		03					

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Table 4
Single Exon Probes Expressed in Placenta

									_							_		_		_		_		_,	_	_	_,	
13053	8940	8783	8597	8597	7093	5767	5494	4579	1918	1907	1807	9326	7508	3037	2308	2308	86	86	8632	2248	11646	9607		4698	4295	2845	2197	Probe SEQ ID NO:
26068	22019	21862	21678	21678	18520	П	18693	17716	$\neg$	٦	15050		20582	16213	П		13321	╗	21712	15381	24725	22662		17833	17438	16969	15332	Exon D DES
	35560	35405	35216	35215	31513	32251	31709	30699		28162	28161		34055				26349	26348		28509	38417	36235		30818	30425	29068	28458	ORF SEQ ID NO:
1.55	3.84	0.6	4.59		1.07	2.21	0.59		2.81	4.98	4,98	0.65	0.78	1.45	1.83	1.83			8.04	1.16	1.73	4.21		0.91	2.4	0.98	1.82	Expression Signal
	4 3.0€-60		9 3.0E-60														П			Γ		1	٦		7.0E-60			Most Similar (Top) Hit BLAST E Value
3.0E-60 AA4862E6.1	5174644 NI	3.0E-60 AI040235.1	5174644 NI		3.0E-80 AI792814.1	3.0E-60 AW836196.1	3.0E-60 BF365143.1	3.0E-60 AJ271735.1	6031190 NT	3.0E-60 BE562611.1	3.0E-60 BE562611.1	4.0E-60 AL163278.2	4.0E-60 BF196068.1	4.0E-60 AA299037.1	4.0E-60 AW 503208.1	4.0E-60 AW 503208.1	5.0E-60 AI807917.1	5.0E-60 A1807917.1	6.0E-60 H52456.1	6.0E-60 BE984974.2	7.0E-80 H58041.1	7.0E-60 H58041.1	1	7.0E-60 AF264750.1	4505488 NT	7.0E-60 AB011153.1	7.0E-60 AF077188.1	Top Hit Acession No.
EST_HUMAN	1 N	EST_HUMAN	N	A NT	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	TNO	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		N	8 NT	NT	27	Top Hit Database Source
LTR10.rt LTR10 repetitive exament:	From Septemb profile deligate September (From September 2018 Alone IMACE-840151 5' similar to contains	SW:FORM_MOUSE Q05860 FORMIN;	nome sapiets promite deligategorismo (promite occasio) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (1. 1997) (	Homo septens proline denyologenese (proline oxidese) (PRODH) mRNA	P52624 URIDINE PHOSPHORNASE:	RC3-L10023-200100-012-801 L10023 Forms septems cONA clane INAGE: 1534053 5' similar to SW-UDP MOUSE	QV4-NN1149-2000-420-101 INN 149 Forms serious CDNA	Homo sapiens Xq pseudoautosomai region; segiment i/2	Homo sapiens prohibitin (PHB) mRNA	601336446F1 NIH _MGC_44 Homo septens CUNA claim IMAGE. Joeguse C	601336446FT NIH_MGC_44 Homo Septems CDINA Gathe IMAGE. 3600306 8	Homo sapiens chromosome 21 segment nozitovio	(261085 GTP-RHO BINDING PROTEIN 1:	ESTITABLE CIBRUS HOMO SEPTENS COVEN OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE TO SEPTENS OF CITA STITUTE STITUTE STITUTE TO SEPTENS OF CITA STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE STITUTE S	UI-HF-BNO-aki-g-O/-0-UI-TI NIH_MGC_30 Homo septens colve crain a live of colored or	UI-HF-BNO-axi-g-07-0-UI-1 NIH MGC OU Homo septens CUIVA Gord IWA GE-3078348 5	W/62c07.x1 Soares NHL I GEC S1 Homo septens curix cigno IMACE: 2078248 5	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens CUIVA Cigne IMAGE.235624.23	OFR repetitive element:	001008/01K I NITI_MGC_08 Hollo schools contains cDNA cons IMAGE:201953 6' similar to contains	LTR6 repetitive element:	LTR5 repetitive element;	yr12704,r1 Soeres fetal liver spison 1NFLS Homo sapiens cDNA clone IMAGE:20508/ 5 Smiler to contains	Homo sapiens ALR-like protein mRNA, partial cos	Homo sapiens ornithine decarboxylase 1 (OUC1) mruva	Homo sapiens miRNA for KIAAUSS1 protein, partial cas	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds	Top Hit Descriptor

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Table 4
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		ı			9.19		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession	Top Hit Databese Source	Top Hit Descriptor
3	13269	26273	1.7	2.0E-60	2.0E-60 AY008285.1	NT	Homo saptens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1458	Т	I	3.99	2,0E-60	2.0E-60 Z11694.1	NT	H. sepiens 41kDa protein kinase related to rat ERK2
1759	П		2.2	2.0E-80	2.0E-80 M24803.1	NT	Human ber protein mRNA, 5' end
3669	7				4757867 NT	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4025	7				2.0E-60 AF231919.1	NT	Homo sepiens chromosome 21 unknown mRNA
	$\neg$					TOT LI MAN	m01f12.y5 NCI_CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1070493 3 similar to contains inclusions.
6430	T	T		200.00	COE-00 AFRO 1877 1	N.7	Homo saplens pro-alpha 2/1) collagen (COL1A2) gene, complete cds
6621	19/81	33748	108		2.0E-60 AF157476.1	N	Homo sapians DNA polymerase zela catalytic subunit (REV3) mRNA, complete cds
6869	Т	T			4503044 NT	NT	Homo saplens corticotropin releasing hormons receptor 2 (CRHR2) mRNA
6989	T				4503044 NT	1 1	Homo sapiens controtropin releasing hormone receptor 2 (CRHR2) mRNA
7259			8.18		2.0E-60 AA311159.1	1,-	EST181949 JURKet 1-cells V Homo sapiens CDNA o end similar to similar to promy income whose
7259		33794	8.18		2.0E-60 AA311159.1	EST_HUMAN	ES [181949 JURKet 1-cells V Homo sapiens CLIVA o end similar to similar to produyincom, expres
7810	П		6.0		2.0E-60 BF512808.1		UI-H-BW1-emu-c-02-0-181 NCI_CGAP_Sub7 none septems colver claim introduction (2.10.0)
8194	4 21276	34799	1.33		2.0E-60 X85597.1	EST_HUMAN	HOTODEO! numan adult resus none septent (SDE1b) mRNA complete cds
8908	22147	30694	3.12		Z0E-00 L30033.1	1	
10183	3 23220	36813	1.83	2.0Ε-60	11991659 NT	NI NI	(SEMA6A), mRNA Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
10183	3 23220	36814	1.83	2.0E-60	11991659 NT	Z,	(SEMA6A), mRNA
11769	П	37672	1.7			NT	Homo sapiens ribosomel protein S6 kinase, 80kD, polypepude 5 (RPSorAS), rinking
12672	2 25448		236		11418192 NT	S	Homo sapiens non-historie Chromosome protein & (3. cerevisiae/plane region and perfiel ode
12829	9 25985	Ĭ.	1.47		2.0E-60 AF068757.1	Z	Homo sapiens somatostatin receptor subtype 3 (33 i N3) gerio, 3 italianing region and partial occupions
12848	8 25564		1.5		AB011369.1	N <sub>1</sub>	Homo sabiens gene for Arte, complete dos
535	5 13728	26752			1.0E-60 BE178588.1	EST_HUMAN	PNS-H 10003-270200-00 1-0000 Floring Squares Scotter
4011	1 17168			Γ	1.0E-60 AU143389.1	EST_HUMAN	15
6070	0 18198	31172		Γ	1.0E-60 AL163285.2	NT	Homo sepiens choinescribe 1 seguirem index reviews child
8134	4 21216	34737	1.39	Τ	1.0E-60 BE064410.1	EO L'IONNA	nc04e12rl NCI_CGAP_Pri Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.11 L1
8955	5 22034	-	2.84	Γ	1.0E-60 AA244041.1	EST_HUMAN	repetitive element :
8982	2 22061	1 . 35601	1.35		1.0E-60 AV754081.1	EST HUMAN	T GALLOO
12606	Π			Γ	1.0E-60 AJ252313.1	TOT LINAN	A) 1419344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5
1123	14288	27343	8.4		9.UE-01 AUT 18344.1	EO LOMPIN	NO I CONTINUE TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF T

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Table 4

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Linea contraction for interest project FI 11026 (FI 11026) mRNA	EO I TOWAIN	AFTOUTE	Ī			8 21698	8616
A 5150100 Himson mRNA from cd34+ stem cells Homo sepiens cDNA clone CBDAGB04	EST HOMAN	4.0E-61 AV731140.1				9 26252	12349
TIONE SEPRETS UNTIL TOWNS CONTROL CONTROL TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEACHERS TO THE TEAC	7661637 NT			0.71	2 32435	6 19122	5936
AU140307 PERCEZ DOINS SECIES COUNT COUNT DESCRIBED 23 MRNA	EST_HUMAN	AU14030			7 28039		1798
Homo septens I -cell lymphome investion and inecesses I ( 1977) 1777	Z	4507500		0.75	9 26612		5118
Homo sapiens 959 kb contig between AMC1 and Cont of Citation Series 2 (422, 229, 221)	NT	AJ22904				П	4090
Homo sapiens amyloid beta (A4) precursor protein (protesse nexin-II, Alzheimer disease) (APP), mRNA	4502166 NT			1.82	29462	8 16442	3268
Homo sapiens chromosome 21 seguinairi 1921/2019	NT.	5.0E-61 AL163279.2		219	7 29291		. 3101
	4506008 NT			2.84			1713
	4507500 NT		6.0E-61	0.7		$\sqcap$	370
Home septens hypometical protein ruli 1919 (ruli 1919), illinovo	8922990 NT					П	226
Homo sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein regulation (regulation), in the sapiens hypometrical protein	8922990 NT	8922	5.0E-61	2.64		╗	226
Human breakpoint cluster region (BCR) gene, complete cos	NT	6.0E-61 U07000.1				Т	13167
601300938F1 NIH_MIGC_Z1 Hamb septems curve Live all	EST_HUMAN	6.0E-61 BE409310.1				$\neg$	12564
Homo sapiens general transcription factor 24 (GTP2) minner, complete cos	NT	6.0E-61 AF035737.1			$\exists$	7	7785
Human autosomal dominant polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry disease property (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc wontry (1707) Polycysuc w	NT	6.0E-61 U24498.1			٦	٦	7497
ig-beta/828=CD78b (elternatively spilose) (numeri, o cells, ilinive) Fariar, ording	NT	6.0E-61 S79249.1	6.0E-61			╗	6155
AU 130689 N I 24P3 Homo capiens CUNA Cione N I 27F 300 1203 3	EST_HUMAN	6.0E-61 AU130689.1	6.0E-61			٦	3381
mbshuy.si NCJ_CGAF_Lati numi saharis com ourio maroni recessore	EST_HUMAN	6.0E-61 AA596033.1	6.0E-61	2.91		$\neg$	1878
601109238F1 NIH _MGC_16 Homo sapiens GUNA Gure IMPGE-10888973	EST_HUMAN	6.0E-61 BE257400.1		1.04			1659
	NT	6.0E-61 AF119860.1		12.72	١	- 1	1352
601300938F1 NIH MGC 21 Homo Eaplens CUIVA CICITE IMPLOIT. 3000-700 C	EST_HUMAN	6.0E-61 BE409310.1	6.0E-61	6.49		T	83 42
	EST_HUMAN	6.0E-61 BE409310.1		3.06		╗	276
Homo sapiens PXRZb protein (PXRZb), mr. IVA	7706870 NT	7706		0.79		╗	<u>1</u> 8
Homo sapiens PXR2b protein (PXR2b), mxNA	7706670 NT	7708	7.0E-61	0.79	1	╗	18
nn59g06.s1 NCI_CGAP_LerI Homo sapiens cuiva cione invade: 10002.1000	EST_HUMAN	8.0E-61 AA583968.1	8.0E-61	1.03	34679	П	8079
Human endogenous retrovirus PHE. 1 (ERVV)	NT	8.0E-61 X57147.1	8.0E-61	2.63		$\neg$	3016
W105b10.XT NCI_CGAP_Co3 Homo septents cultiva cities invision. 20000000	EST_HUMAN	8.0E-61 AW006478.1	8.0E-61	1.41	٦	7	2736
	EST_HUMAN	8.0E-61 AW006478.1	8.0E-61	1.41		П	2735
Tomo sapiens into miger protein a (intra control mayor of sapiens 3)	4885546 NT	4886	9.0⊑-61	0.63		21987	8908
Homo saplens PHD linger protein 2 (PHF2) mixiva	4885546 NT	4885	9.0E-61	0.63	35526	21987	8908
	Source		Value	<b>4</b>	5	Ņ.	N O
Top Hit Descriptor		Top Hit Acession	Most Similar (Top) Hit	Expression	0	SEQ ID	Probe .
	 - 						]

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Table 4
Single Exon Probes Expressed in Placenta

			ſ		2000	1240	/341
Homo sagiens hypothetical protein FLJ20128 (FLJ20128), mRNA	NT				T	7	100
Homo sepiens SC35-interacting protein 1 (SRRP129), mRNA	1 NT	4759171 NT				T	1
Human P40 1-cell and mast call grown ractor (nr 40) gells, cultiples cus	3	1.0E-61 M30135.1				Т	7041
Homo sapiens survival of motor neuron i, sapinario (caritar), mastro	NT	11416891 NT	1.0E-61	1.32			6004
TOTAL SALIBITIS PARAMETERS AT INCIDENT (SAMAT) INRIVA	32			1.07	32301	6 18996	5806
The particular candidates of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con	2	M76423.1		0.71	8 31723	9 18708	5509
U contents carbonic anhydrase VII (CA VII) gane, exons 4.5.6, and 7, and complete cds	2	1.0E-61 AL163210.2	Γ			5 18203	5076
United the property of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control o	EST HOMAN	1.0E-61/AW298181.1	Γ		Γ	18110	4981
III L BWIG all bons of III st NCI CGAP Sub6 Homo sablens cDNA clone IMAGE:2732871 3'	EST HUMAN	1.0E-61 AW298181.1			Г	П	4981
HOMO SEMENS TIVE TRAILING CICAP Suba Homo sepiens cDNA clone IMAGE 2732871 3'	S N	4759249 N I	Γ			1 17699	4561
Homo serviens TRAF family member-associated NFKB activator (TANK) mRNA	2 2		Γ			1 17699	4561
Homo services TRAE family member associated NFKB activator (TANK) mRNA	2	M68840.				П	4374
QVZ-H10977-140300-077-good F10977 Finance explored codes	EST_HUMAN	1.0E-61 BE174455.1				16986	3826
Homo sapiens NAXOCOC Belle product (NAXOCOC), III NO.	3	7662319		0.85	0 29650	3 16630	3463
CIAAABB COO EXCHANGE WAS ARREST (KIAAABBA) MRNA	EST HUMAN	1.0E-61 BE386363.1	Γ.		5 29093		2896
MSR1 repetitive element;		1.0E-61 AW827281.1	1.0E-61	1.54	3 28531	15403	2270
xn11b09:y1 NCI_CGAP_Li5 Home sapiens cDNA clone IMAGE:2693368 5' similar to contains element					20100	10048	1800
Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA	NT	6005983 NT	1.05-61			T	1000
Human polymorphic trinuclectide repeat in X-linked retinits pigmentosa (Kr.3) gene region	NT	.0E-61 U32657.1	1.0E-61		1	T	
Homo sapiens chromosome 21 segment HS21CUU3	NT	1.0E-61 AL 163203.2	1.0E-61		1	┑	143
Homo sapiens origin recognition complies, subulition (years in interest from the compliance)	NT	5453829	1.0E-61	126	3 27026	7	797
Homo sapiens chiomosome 21 segment noze 10000	Z	1.0E-61 AL163203.2	1.0E-61	1.37	4	7	<b>\$</b>
QV0-BN0042-170300-162-110 BN0042 Floring Sapients CONS	EST_HUMAN	2.0E-61 AW 995328.1	2.0E-61	1.45	31850	П	13144
Homo sapiens neoscina promin Law (Nr.Cary), 111 NAV	1	11419729 NT	2.0E-61	4	U1	П	11123
19	TN	11421778 NT	2.0E-61	2.84	37101	$\neg$	10466
OI-TIT-BING-EXC-1- (2-0-OI.) INTO DA directed) (36KD) (RPC39) mRNA	EST_HUMAN	2.0E-61 AW 500256.1	2.0E-61	1.34	36763		10126
Homo sapiens mixivy for avvivoso protein, per les constants anno la figure IMA GE:3076774 5	Z	2.0E-61 AB011108.1	2.0E-61	0.98		٦	9762
	EST_HUMAN	2.0E-61 AV694317.1	2.0E-61	1.67		22295	9217
1A (110/116kD) (ATP6N1A), mRNA	1	11426166 NT	2.0E-61	0.88	33094	19718	6556
WOSTITUTI Soares measures at the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of t	EST HUMAN	2.0E-61 N39397.1	2.0E-61	1.72			2706
gb.1.25444 60S RIBOSOMAL PROTEIN LSSA (HUMAN)	EST_HUMAN	2.0E-61 N63039.1	2.0∈-61	1.36	27938	14851	1699
QV3-H10513-060400-147-001 m 10513 nome septems colved clone IMAGE: 246453 3' similar to	EST_HUMAN	2.0E-61 BE168410.1	2.0E-61	5.33	27461	14398	1239
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:
			Name of Street				7
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Table 4

Single Exon Probes Expressed in Placenta

TOTAL COMPLICATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP	121	3.UE-02 AJZ/1/33.1	Γ	0.76	5 28730	15605	2478
Home series to resulte theorie region: segment 1/2		0.0E-06/AJA/1/03.1	T				2478
Homo saplens Xq pseudoautosomal region; segment 1/2	ZT	A 1271735 1	Ī		T	Т	22.4
WX51807 X1 NCT_CGAY_L028 Home Septents cover come was contained to contain the contained was contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the contained to contain the con	EST HUMAN	5 0F-82 A 1950528 1					3
IMR3-6 10203-130100-025-9808-0 10203 Floring septems Convo	EST_HUMAN	6.0E-62 AW814393.1		3.67	9 36189	22619	9554
Homo sapiens Coi-18 protein (LOCalous), mixture		11431138		1.52	3 35063	21633	8462
OFHT-BPOP-BI-G-US-C-UITT NIT MGC_31 DOTTO SAPIETIS CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CIONE INFOCE SEL ESCO CONTA CONTA CIONE INFOCE SEL ESCO CONTA CONTA CIONE INFOCE SEL ESCO CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA CONTA	EST_HUMAN	AW501		0.66	] [		8277
wi04d02x1 NCI_CGAP_CLL1 Homo saplens conva clone IMA clone IMA GE-2079893 5	EST_HUMAN	6.0E-62 AI762801.1		3.47			. 7803
wi04d02,X1 NCI_CGAP_CILT Homo sapiens conva cione inva del 23ee221 3		6.0E-62 AI762801.1	6.0E-62	3.47	34351		7803
Homo sapiens CGI-56 protein (CGI-56), MIXIVA		11418255		5.37	3		3471
Human zinc finger protein ZNF131 mkNA, perual cos	NT	6.0E-62 U09410.1		1.56			3063
1 9	EST_HUMAN	7.0E-62 AI208681.1			38403	24712	11632
Homo sapiens hypothetical protein ()	Z	11427965	7.0E-62	0.97	32544	19221	6038
(AUTOANTIGEN NOR-90)	SWISSPROT	P17480	7.0E-62			16759	3595
NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)	1000	7.00-04.0004.1	70-10.7	1.12	2/301	14290	1131
AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'	FST HUMAN	۵۱/714934 1	705.83		T	T	
Co88111.s1 NCI_CGAP_GC81 Homo sapiens curva cidre invase. 1991/20 3 silling word. Or_merrica P31795 POL POLYPROTEIN;	EST_HUMAN	8.0E-62 AA830420.1	8.0E-62	58.0	30798	17808	4673
RC4-B10310-110300-015-110 B10310 Homo septens conv	EST HUMAN	BE064386.1	9.0E-62	1.06	37206		10565
Homo sapiens GTP binding protein 1 (GTPBP1), mKNA		11418127	1.0E-61	10.94		$\neg$	13026
Hamo saplens low density lipoprotein-related protein 2 (LKF2), mKIVA	NT	1,1430460	1.0E-61	4		П	12286
Homo sepiens low density lipoprotein-related protein 2 (LKP2), mKNA	NT	1,1430460	1.0E-61	4	31677		12286
Home sapiens gene for AF-6, complete cas	NT	1.0E-61 AB011399.1	1.0E-61	21.57	٦	П	12242
Home saplens mRNA for CSR2, complete cds	NT	1.0E-61 AB007830.1	1.0E-61	1.44		╗	11325
Homo sapiens PIOKol. 19 mRNA for ubiquitin-conjyugating enzyme EZ, complete cos	NT	1.0E-61 AB044550.1	1.0E-61	1.72		Т	11178
Homo septens actinin, alpha 4 (ACTN4), mRNA	NT	1425578 NT	1.0E-61	5.61		П	10871
Homo sapiens KIAA0971 protein (KIAA0971), mKNA	NT	11428892 NT	1.0E-61	4.8		7	10235
Homo septens cadherin 18 (CDH18), mRNA	NT	11416280	1.0E-61	0.68	36193	П	9557
MR0-BN0070-040400-010-h01 BN0070 Homo sapiens CUNA	EST_HUMAN	1.0E-61 AW889726.1	1.0Ё-61	2.78		7	9482
(UBE2D3) genes, complete cds	NT	1.0E-61 AF224669.1	1.0E-61	3.34	35123	21589	8508
Homo sepiens mannosidase, beta A, lysosomai (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3						Т	
Homo sapiens growth hormone releasing hormone (GHRH), mKNA	N,	11034840 NT	1.0E-61	2.69		Т	2338
Homo sepiens hypothetical protein FLJ20128 (FLJ20128), mRNA	NT	8923130 NT	1.0E-61	1.39	33884	20421	7341
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
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			4.00-02	1.00	8	68697	1249/
Homo saplens non-historie chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA	JUL		T		30300	Т	1225
Homo sapiens putative nuclear protein (HRIHFB2122), mRNA	A VI	11418086 NT	T		I	1	11900
thyroid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4]	3	4 0F-62 S70584.1	T	63.7	Τ	Т	1200
H. sepiens flow-sorted chromosome 6 Hindill fragment, SC6pA16D3	ZŢ	4.0E-62 Z78766.1			T	Т	
H. sepiens flow-sorted chromosome 6 Hindill fragment, SCopA15U3	NT	Z78768.1				7	11263
Homo sapiens mRNA for KIAA1263 protein, parual cos	NT	4.0E-62 AB033089.1					8047
Homo sepiens 265 proteasonne associated paut indicately (Contr.), im sec	S NT	11429973 NT	4.0E-62	1.12	34988	-	8364
Homo sapiens eukeryogo gensiauon iniuauon lavior zo, subulin z (ucar, sono) (En EDE), militario e	ZNT						7812
Homo sapiens eukaryoud transiation intitation too, seroning a form 3000 (FIEDRO) mRNA	7NT	7657057 NT	4.0E-62	2.21	7 34361	20867	7812
Homo sabiens prosphoriosy pyrophosphale symmetric ( the Sch.) (FIFSH2) mRNA	NT			1.75	33866	20404	7322
Homo sepiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USPBX), mRNA	N		4.0E-62	. 281	32960	19594	6426
mRNA	N	4506978 NT	4.0E-62	1.71	32553	19229	6046
Homo sapietis kerauri to (NN 10) in No.	N	4557887	4.0E-62	9.09		16654	3486
AN);	EST_HUMAN	4.0E-62 AI827900.1	4.0E-82		28779		2529
H2B.2 (HUMAN);	EST_HUMAN	4.0E-62 AI827900.1	4.0E-62	1.9	28778	15654	2529
ATP SYNTHASE COLLING FACTOR 6, MITOCHONDRIAL PREGINGSOR (HUMAN);  ATP SYNTHASE COLLING FACTOR 6, MITOCHONDRIAL PREGINGSOR (HUMAN);	EST_HUMAN	4.0E-62 AW161479.1	4.0E-62	1.32	27103	14040	864
ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECINGSOR (HUMAN);  ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECINGSOR (HUMAN);	EST_HUMAN	4.0E-62 AW161479.1	4.0E-62	1.32	27102	14040	864
ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PREIGHT AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND	EST_HUMAN	4.0E-62 AW161479.1		2.17	27103	14040	883
ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HIMAN);  ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	EST_HUMAN	4.0E-62 AW161479.1	4.0E-62	2.17	27102	14040	88
Homo saplens muscle specific gene (Ma), mining	NT	11425574 NT	6.0E-62	2.38		$\neg$	11543
Homo sapiens muscle specific gene (M9), mKNA	NT	11425574 NT	5,0E-62	2.38		П	11543
tho7g09x1 NIH_MGC_17 Home sapisms cuiva ciona image: 250 io io o	EST_HUMAN	5.0E-62 AW 410687.1	5.0E-62	12.91		П	9717
Homo sapiens ryanodine receptor 3 (KYR3) mKNA	1	4506758 NT	5.0E-62	0.74			8746
5	EST_HUMAN	5.0E-62 AA431093.1	5.0E-62	1.75	30568	17587	4447
Homo sepiens ryanodine receptor 3 (RYR3) mRNA	T	4506758 NT	5.0E-62	2.55	29683	16673	3506
Top Hit Descriptor	. Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	NO: OI DES	Probe SEQ ID NO:
		9.19					

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Single Exon Probes Expressed in Placenta

	22335 35886		22335 35885	8957 22036 35677 0.54	20377 33835	2007	20977	20367 33820	6418 19587 32850 2.02			17784 30767	16167 29176	1842 14988 28088 1.64	1575 14728 27809 18.41		24973	11462		8974 22053 35596 5.59	8974 22053 35595 5.59	1259 14417 27482 2.71	8737 21816 35351 3.74		16950 29956	16287	16287 29301	13312	26693 31965	25653		12946 25657 31955 1.66	NO: ID NO: Signal	E constant	
1.0E-02/01/0000	X15533	1.0E-62 7662289 NT	1.0E-62 7662289 NT	1.0E-62 AA2800E0.1	1.UE-02 AA ( 220/0.1	0 € 63 00 722878 1	1.0E-62 AA722878.1	1.0E-62 AA490060.1	1.0E-62 U52111.2			1.0E-62 8923201	1.0E-62 AL039044.1	1.0E-62 AA625207.1	1.0E-62 L78810.1	٤		OF 62 BE330678 4	2 0F-62 AF224669.1	2.0E-62 BF32891,1.1						3.0E-62 AB040909.1	3.0E-62 AB040909.1			4.0E-62 11417862 NT	4.0E-62 11417862 NT	4.0E-62 11418322 NT	BLASTE No.	Most Similar Ton Hit Acession	Gingin
2	L	NT	NT	EST HOWAN	TOT LINE	EST HIMAN	EST HUMAN	EST_HUMAN	N				EST_HUMAN	EST_HUMAN	2		Ĺ	II MAN	Z	EST HOMAN	L	L	T HUMAN		NT	NT	NT						Database Source	Top Hit	Citigle Exert 10500
		Homo sepiens KIAA0763 gene product (KIAA0763), mRNA	Homo saptens KIAAU/03 gene product (NIAAU/03), ITINVA	TI MANAGE SOCIETION OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL O	TEGERAT A NCI CGAR GCR1 Homo saplens cDNA clone IMAGE:705060 5	2080f10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:409771.3	zg89f10.s1 Sceres_fetal_heart_NbHH19W Homo sapiens cDNA done IMAGE:409771 3	ab05c02 s1 Stratagene fetal retina 837202 Homo sapiens cUNA cione IMAGE 33990 3	CDM protein (CDM), adrenoleukodystrophy protein >	protein L18a (RPL18a), Ca2+/Celmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal	Homo saplens hypothetical protein FLJ20212 (FLJ20212), mRNA	DKFZp566F104_f1 566 (synonym: hfkd2) Homo capiens cuna ciene unrappor ios o	CE03463;	Promo septems AUT In It cannot be proved (AMT - 2) young company (AMT - 2) similar to WP:K01H12.1	ADDITION OF THE CANAL CANT 2) Land complete rds	Homo saniens intersectin 2 (SH3D1B) mRNA, complete cds	OV4-BT0257-081199-017-603 BT0257 Homo saplens cDNA	Homo sapiens mannosidase, ped A, lysosonila (woxxon) golio, alic doctrini co (peganile origini a complete cds	KCU-DINOZOM-DUDUU-US I-BUS DINOZOM I IMINOSOMBA) dana and ubiquitin-conjugating enzyme E2D 3	RCG-DIVIZOR-2000000-03 Feb DIVIZOR FOR SERIORS CON .	Homo sapiens chigmosumo 2 i segiment i seciment china	THR repetitive element;	wg33f04_x1 NCI_CGAP_Kid11 Homo saptens cDNA clone IMAGE:2299903 3' similar to contains THR.12	Human cyclophilin-related processed pseudogene	Homo sapiens mRNA for KIAAT476 protein, partial cus	Homo sapiens mRNA for KIAA 1476 protein, partiel cos	Homo sapiens neurofibromin 2 (bilateral acoustio neuroma) (NF2) mK/NA	Hamo sepiens low density ipoprotein-related protein 2 (LRY2), INNA	Homo saptens calcineurin binding protein 1 (KIAAU330), mKIVA	Homo septems calcineting protein i (NANOSON), illustra	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CCLON I), IIINNO	i op Hit Descriptor		LAND AND THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOT

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Table 4

Single Exon Probes Expressed in Placenta

6603	2882	2840	1989	11397	11397	6575	6576	3910	3910	3398	9075	5455	952	4381	3550	3550	2448	2420	11296	8521	8009	7332	5582	6358	4152	4152	2421	348	13042	12809	11648	Probe SEQ ID NO:
19763	14425	15954	16131	24458	24458		19737	17069	17069	16568	22154	18655	14125	17524	16715	16715	15574	15549	24362	21602	21059	20413	18777	18484	17304			13559	25684	25540	24727	Exan SEQ ID NO:
33151	27493	29061	28235	38122	38121	33117	33116	30067	30066	29584	35698			30505	29728	29727	28703	28677	38003	35139	34571	33875	31822	38824	30298	30297		26587	31962		38419	ORF SEQ ID NO:
33.93	11.84	1.49	15.19	2.02	2.02	2.6	2.6	1.08	1.08	0.88	0.62	70.59	3.38	4.36	4.26	4.26	2.58	3.05	1.3	1.18	1.77	3.78	1.44	4.69	8.77	8.77	2.17	2.27	3.15	4.63	2.28	Expression Signal
3.0E-63	3.0E-63										5.0E-63	6.0E-63						8.0E-63			9.0E-63		9.0E-63	9.0E-63	9.0⊑-63	9.0E-63			1.0E-62	1.0E-62	1.0E-62	Most Similar (Top) Hit BLAST E Value
11545810 NT	6005963 NT	3.0E-63 J00310.1	3.0E-63 AB018280.1	4.0E-63 AW 134709.1	4.0E-63 AW 134709.1	4.0E-63 AW 750372.1	4.0E-63 AW 750372.1	4.0E-63 AB014607.1	4.0E-63 AB014607.1	4.0E-63 AL163278.2	11626464 NT	6.0E-63 AA420803.1	7.0E-63 AI872137.1	8.0E-63 AL163238.2	AF198349.1	8.0E-63 AF198349.1	5031810 NT	4557734 NT	9.0E-63 BF203406.1	11421160 NT		11426985 NT	Y15056.1	11418185	9.0E-63 AB002348.2	9.0E-63 AB002348.2	9.0E-63 C18159.1	9.0E-63 AW 818405.1	11430460	11418322 NT	Z78698.1	Top Hit Acession
NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	Z	NT	NT	NT	NT	EST_HUMAN	NT	NT	NT	TN	5 NT	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	TN	Top Hit Database Source
Homo saplens hepatocellular carcinoma antigen gene 620 (LOC83928), mRNA	Homo saplens zinc finger protein 144 (Mel-18) (ZNF144), mRNA		Homo sapiens mRNA for KIAA0717 protein, partial cds	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo capiens cDNA clone IMAGE:27124823'	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 31	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA	CM3-BT0595-190100-072-a09 BT0595 Homo saplens cDNA	Homo sapiens mRNA for KIAA0707 protein, partial cds	Homo saplens mRNA for KIAA0707 protein, partial cds	Homo sapiens chromosome 21 segment HS21C078	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA	nc63f02r1 NGL_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S (RIBOSOMAL PROTEIN (HUMAN);	wm55g11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'	Homo sapiens chromosome 21 segment HS21C068	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Gellus gallus Dech2 protein (Dech2) mRNA, complete cds	Homo sapiens iL2-inducible T-cell kinase (ITK), mRNA	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA	601865828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098487 5	Homo saplens Ras association (RaIGDS/AF-8) domain family 2 (RASSF2), mRNA	Homo saplens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA	Homo sapiens nucleoporin 88kD (NUP88), mRNA	Homo sapiens mRNA for PkB kinase	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for KIAA0350 protein, partial cds	Homo saplens mRNA for KIAA0350 protein, partial cds	C18159 Human placenta cDNA (TFujiwara) Homo saplens cDNA clone GEN-558C10 5"	QV4-ST0234-181199-037-105 ST0234 Homo sepiens cDNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	H.sapiens flow-sorted chromosome 6 HindIII fragment, SCSpA14D8	Top Hil Descriptor

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Single Exon Probes Expressed in Placenta

Τ	7	7222 20	7222 20	6887 20	6887 20	Г		6315 18	6315 19	6005 18	6005 18	5376 20	4988 18	4014 1	3357 10	3225 16	2148 1	1806 1		1597 1	849 1	510 1:	203 1	196	9907 2	9907 2	Probe E) SEQ ID SE(
			20086 33		20039 33			19487 32		19190 32	19180 32	25802 31	18117 31	17171 30	16529 29	16389 29	15282 28	14956 28			14027 27	3704	13426 26	13419 26	22947 36	22947 36	SEQ ID ORF SEQ
35346	34517	33503	33502	33449	33448	33403		32843	32842	32510	32509	31447	31098	30179	29544	29411	28407	28049	27835	27834	27087		26457	26449	36534	36533	
4 29	88.0	1.72	1.72	0.72	0.72	1.43		1.07	1.07	2.41	2.41	0.95	1.28	3.19	2.4	1.94	1.05	2.02	1.54	1.54	3.07	1.19	1.65	1.69	0.83	0.83	Expression Signal
20E-83	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0€-63	2.05-63		2.0Ε-63	2.0E-63	20E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0Ε-63	2.0€-63	2.0Ε-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	3.0€-63	3.0E-63	Most Similar (Top) Hit BLAST E Value
20E-63 AL 1632 10.2	2.0E-63 AB046844.1	8910365 NT	9910365 NT	2.0E-63 AB032359.1	2.0E-63 AB032389.1	2.05-63   U68058,1		11421940 NT	11421940 NT	20E-63 BF373541.1	2.0E-63 BF373541.1	11419429 NT	2.0E-63 AF111187.2	2.0E-63 L39891/1	2.0E-63 AF1097,18.1	4502166 NT	AI863961.1	2.0E-63 BE410739.1	2.0E-63 AB030388.1	2.0E-63 AB030388.1	7657042 NT	4557624 NT	4885226 NT	1.÷0870U	3.0E-63 BE876;58.1	3.0E-63 BE876;58.1	Top HI: Acession
3	S	NT	NT	NT	NT	NT		NT	NT	EST_HUMAN	EST_HUMAN	T	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	TN	NΤ	NT	NAMUH_TSE	EST_HUMAN	Top Hit Database Source
Homo sapiens chromosome 21 segment HS21C010	Homo sapiens mRNA for KIAA1624 protein, partial cds	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens MIST mRNA, partial odc	Homo sapiens MIST mRNA, partial cds	TCRBV13S9/13S>	Human gamiline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T,	Homo sepiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA	QV1-FT0170-040700-265-c05 FT0170 Homo septens cDNA	Homo septens similar to ectonuclectide pyrophosphatase/phosphodiesterase 3 (H. septens) (LOC63214), mRNA	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	Homo sepiens polycystic kicney disease-associated protein (PKD1) gene, complete cds	Homo sepiens chromosome 3 subtelomeric region	Homo sapiens emyloid beta (A4) precursor protein (protease nexin-II, Alzheimer discaso) (APP), mRNA	wj54b02.x1 NCI_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2406803 3" similar to gb:M57609 GLI3 PROTEIN (HUMAN);	601301627F1 NIH_MGC_21 Homo septens cDNA clone IMAGE:3836103 5'	Homo sepiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds	Homo saplens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	Homo sapiens glutamats-cystelne ligase (gamma-glutamylcystelne synthetase), catalytic (72.8kD) (GLCLC) mRNA	Homo sepiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA	Human DNA topoisomerase I mRNA, partial cds	601485656F1 NIH_MGC_69 Homo saplens cDNA clone IMAGE:3888253 5'	601485656F1 NIH_MGC_69 Homo septens cDNA clone IMAGE:3888253 5'	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

17	1760	10239	4854	48	38	12243	12187	6268	1071	8051	6089	13121	8668	6521	85	6890	2	4	2	7	7	13172	13101	12380	11012	11012	10985	10143	83	92	Prabe SEQ ID NO:
1760 14909	14909	39 23274	64 17087	4854 17987	3618 16782			Γ	71 14237	51 21134		21 26047	68 21748	21 19688	21 19888	90 19078	5468 18668	li	4461 17601	786 13965		72 25760	01 25717	80 25929	12 24091	12 24091	185 24084	43 23181	9254 22331	9254 22331	Exen ID SEQ ID
09 28003	09 · 28002	74 36865	87 30975	30974	82	85	6	42 32791	37	34654	70 32598	47	48	33059	33058	78 32388	38 31647	30580	01 30579	65 27017		50 31930	17 31940	29 31759	en 37729	91 37728	84 37699	81 36778	31 35880	31 35879	ORF SEQ
3 5.73	2 6.73	5 2.62	5.34	6.34	0.74	3.68	2.79	3.61	3.46	4 5.57		8.88	2.97	89.0	0.68	1.38	7 1.73		9 3.31			1.37		9 3.64		8 2.89	9 10.73	8 1.2	0.94	0.94	Expression Signal
			4 7.0E-64	4 7.0E-64																		7 2.0E-63		4 2.0E-63					4 2.0E-63	4 2.0E-63	Most Similar (Top) Hit BLAST E Value
6.0E-64 A165199:2.1	6.0E-64 AI651992.1	7.0E-64 Y07848,1	4507490 NT	4507490 NT	7.0E-64 BE394321.1	8.0E-64 T60651.1	11418177	8.0E-64 BE885755.1	8.0E-64 BE280796.1	9.0E-64 AI478186.1	9.0E-64 AW 401433.1	1.0E-63 AL163207.2	1.0E-83 AL163247.2	1.0E-63 AW 451950.1	1.0E-63 AW 451950.1	1.0E-83 AW 582286.1	1.0E-63 AJ271736.1	1.0E-63 F08485.1	1.0E-63 F08485/1		7106446 NT	AB011399.1		11418185 NT	2.0E-63 AF099810.1	2.0E-63 AF0998,10.1	2.0E-63 N78945.1	2.0E-63 AL163218.2	11420949 NT	11420849 NT	Top Hij Acession
EST_HUMAN	EST_HUMAN	NT	)O NT	TNO	EST_HUMAN	EST_HUMAN	77 NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	EST_HUMAN	EST_HUMAN	NT	NT	N	57 NT	35 NT	NT	TN	EST_HUMAN	Ŋ	19 NT	TN 63	Top Hit Database Source
wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);	wb51e07.x1 NCI_CGAP_GC6 Homo septens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);	Homo sapiens EWS, gar22, rrp22 and barn22 genes	Homo sepiens thimet oligopeptidase 1 (THOP1) mRNA	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA	801311455F1 NIH_MGC_44 Home sapiens cDNA clone IMAGE:3633204 5'	y698b02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'	Homo saplens Ran GTPase activating protein 1 (RANGAP1), mRNA	601508958F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'	tm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:21616263'	UI-HF-BK0-aad-b-09-0-UI r1 NIH MGC 36 Homo sapiens cDNA clone IMAGE:3053153 5'	Homo septens chromosome 21 segment HS21C007	Homo sapiens chromosome 21 segment HS21C047	UI-H-Bi3-alt-h-02-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068783 3'	UI-H-BI3-alt-h-02-0-UI.s1 NCI_CGAP_Sub5 Homo saplens cDNA clone IMAGE:3058763 3	QV0-ST0215-060100-083-b09 ST0215 Homo sepiens cDNA	Homo sepiens Xq pseudoautosomal region; segment 2/2	HSCZVD111 normalized Infant brain cDNA Homo saplens cDNA clone c-zvd11	HSCZVD111 normalized Infant brain cDNA Homo sapiens cDNA clone c-zvd11	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA	Mus musculus wingless-related MMTV Integration site 3A (Wnt3a), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sepiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA1), mRNA	Homo saplens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens neurexin III-alpha gene, partial cds	Homo sapiens neuredn III-alpha gene, partial cds	2b18b05.s1 Soares_fetai_lung_NbHL19W Homo septens cDNA clone IMAGE:3023853' similar to gb:X17208 40S RIBOSOMAL PROTEIN S4 (HUMAN);	Homo sepiens chromosome 21 segment HS21C018	Homo sapiens kinesh family member 3B (KIF3B), mRNA	Homo sepiens kinesin family member 3B (KIF3B), mRNA	Top Hit Descriptor

7L7LS/I0 OM

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Table 4
Single Exon Probes Expressed in Placenta

IDNO:   Signal   BLASTE   No.   Databass   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Source   Source   Value   Value   Value   Value   Source   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value   Value	Probe SEQ ID	D Exam	0	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit	
18397   28372   3.91   6.0E-44   AW028445.1   EST_HUMAN     18397   28373   3.91   6.0E-44   AW028445.1   EST_HUMAN     18392   32230   2.95   6.0E-44   Y18933.1   NIT     18392   32252   5.32   6.0E-44   Y18933.1   NIT     19137   32452   6.32   6.0E-44   Y18933.1   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32453   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.74   6.0E-64   71422189   NIT     19137   32452   0.75   6.0E-64   71422189   NIT     19137   32452   0.76   6.0E-64   71422189   NIT     19137   32452   0.76   6.0E-64   71422189   NIT     19137   32452   0.77   4.88   6.0E-64   71420197   NIT     19137   32452   0.76   4.18   6.0E-64   AW026445.1   EST_HUMAN   RIT     19137   32453   0.76   4.18   6.0E-64   AW026445.1   EST_HUMAN   RIT     19137   32452   0.71   4.18   6.0E-64   AW026445.1   EST_HUMAN   RIT     19137   32452   0.71   4.18   6.0E-64   AW087733.1   NIT   7142018   RIT     19137   32452   0.71   4.18   6.0E-64   AW087333.1   NIT   7142018   RIT     19137   32452   0.71   4.18   6.0E-64   AW087333.1   RIT   AW1873783.1   EST_HUMAN   RIT     19137   32452   0.71   4.0E-64   AW087373.1   EST_HUMAN   RIT     19137   32652   0.71   4.0E-64   AW087373.1   EST_HUMAN   RIT     19137   32652   0.71   3.0E-64   G18851.1   EST_HUMAN   RIT     19137   32652   0.71   3.0E-64   G18851.1   EST_HUMAN   RIT     19137   32654   0.82   3.0E-64   G18851.1   EST_HUMAN   RIT     19137   32654   0.82   3.0E-64   AV08733.1   EST_HUMAN   RIT     19137   32654   0.82   3.0E-64   AV08733.1   EST_HUMAN   RIT     19137   32654   0.82   3.0E-64   AV08733.1   EST_HUMAN   RIT	N.			Signal	BLAST E Value	N <sub>p</sub>	Database Source	Top Hit Descriptor
16387   28373   3.91   6.0E-64   AW028445.1   EST_HUMAN   18832   32230   2.95   6.0E-64   Y18933.1   NT	318			3.91	6.0⋶-64	AW026445.1	EST HUMAN	WASHIS MINICI COAD BIRS LIVE
18932   32230   2.95   6.0E.44   Y1893.1   NT	31			3.91	6.0E-64	AW028445.1	EST HUMAN	wydaeda yd NOI COAD Bross Homo sapiens CL
18932 3231 2.95 6.0E.84   Y1893.1   NT     18950 32252 5.32 6.0E.84   Y1893.1   NT     18950 32250 0.68 8.0E.84   E912491   NT     19137 32452 0.74 8.0E.84   1122189   NT     19137 32452 0.74 8.0E.84   1122189   NT     19137 32452 0.74 8.0E.84   1122897   NT     19137 32452 0.74 8.0E.84   1122897   NT     20462 33925 2.54 8.0E.84   1122897   NT     22593 38194 7.39 6.0E.84   1122857   NT     22699 39546 2.16 8.0E.84   X78475.1   NT     22699 39546 2.16 8.0E.84   X78475.1   NT     22699 39546 2.16 8.0E.84   XW02845.1   EST_HUMAN     22699 39546 2.16 8.0E.84   XW02845.1   EST_HUMAN     18967 29372 1.73 6.0E.84   XW02845.1   EST_HUMAN     18967 29373 1.73 6.0E.84   XF231919.1   NT     14021 27079 4.18 5.0E.84   XF231919.1   NT     14038 27685 1.15 5.0E.84   XF231919.1   NT     14068 27685 1.15 5.0E.84   XF231919.1   NT     14683 2774 4.43 5.0E.84   XF231919.1   NT     14698 27685 1.15 5.0E.84   XF231919.1   NT     14724 30231 7.25 5.0E.84   XF231919.1   NT     14898 27789 4 1.54 5.0E.84   XF231919.1   NT     14998 27784 4.43 5.0E.84   XF231919.1   NT     14998 27784 4.43 5.0E.84   XF231919.1   NT     14998 27784 2.34 4.0E.84   XF231919.1   NT     14998 27784 2.34 4.0E.84   XF231978.1   EST_HUMAN     24128 37784 2.34 4.0E.84   XF231973.1   EST_HUMAN     15404 28532 8.77 3.0E.84   XF231919.1   EST_HUMAN     15694 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23191.1   EST_HUMAN     16894 28704 1.83 3.0E.84   XF23	ยู			2.95		Y18933.1	l,	The series NOB 1 225 and 1 tomo septens of
Basic   1895   32262   6.32   6.0E-64   M13975.1   NT     1895   32260   0.68   6.0E-64   6.912461   NT     19137   32452   0.74   6.0E-64   11422189   NT     19137   32452   0.74   6.0E-64   11422189   NT     19137   32453   0.74   6.0E-64   11422189   NT     20462   33925   2.54   6.0E-64   11422189   NT     22593   36164   7.39   6.0E-64   11422189   NT     22593   36164   7.39   6.0E-64   71420555   NT     22594   36266   2.16   6.0E-64   776475.1   NT     22595   36546   2.16   6.0E-64   776475.1   NT     22595   36546   2.16   6.0E-64   776475.1   NT     22697   37724   4.88   6.0E-64   71420197   NT     22698   37725   4.68   6.0E-64   AW026445.1   EST_HUMAN   16367   29372   1.73   6.0E-64   AW026445.1   EST_HUMAN   16367   29373   1.73   6.0E-64   AW026445.1   EST_HUMAN   16367   29373   1.73   6.0E-64   AW026445.1   EST_HUMAN   16367   29373   1.73   6.0E-64   AW026445.1   EST_HUMAN   14524   27698   1.02   5.0E-64   AW026445.1   EST_HUMAN   14608   27685   1.15   5.0E-64   AW02645.1   NT   14608   27685   1.15   5.0E-64   AW0333.1   NT   14608   27685   1.15   5.0E-64   AW0333.1   NT   14608   27686   1.15   5.0E-64   AW0333.1   NT   14608   27686   1.15   5.0E-64   AW0333.1   NT   14608   27686   27686   1.15   5.0E-64   AW0333.1   NT   14608   27686   3.774   4.43   5.0E-64   AW0333.1   NT   14608   27685   0.71   4.6E-64   E794607.1   EST_HUMAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   RESTONAN   R	97		П	2.95		Y18933.1	Z	Homo conione MCP-1 gens and enhancer region
18959   32260   0.68   6.0E-64   691249   NT     19137   32452   0.74   6.0E-64   11422189   NT     19137   32453   0.74   6.0E-64   11422189   NT     22462   33928   2.54   6.0E-64   11525879   NT     22563   36164   7.39   0.0E-64   11525879   NT     22589   36546   2.16   6.0E-64   4F274753.1   NT     22687   37724   4.68   6.0E-64   AV026445.1   EST_HUMAN     24087   27775   4.28   6.0E-64   AV026445.1   EST_HUMAN     16367   29373   1.73   6.0E-64   AV026445.1   EST_HUMAN     16367   29373   1.73   6.0E-64   AV026445.1   EST_HUMAN     14524   27688   1.02   5.0E-64   AV026445.1   EST_HUMAN     14608   27685   1.15   5.0E-64   AV02633.1   NT     14608   27686   1.15   5.0E-64   AV0333.1   NT     14608   27686   1.15   5.0E-64   AV0333.1   NT     14608   27686   1.15   5.0E-64   AV0333.1   NT     14608   27686   1.15   5.0E-64   AV0333.1   NT     14608   27686   1.15   5.0E-64   AV0333.1   NT     14608   27746   4.43   5.0E-64   AF3193.1   EST_HUMAN     14608   27686   0.71   4.0E-64   BF39450.1   EST_HUMAN     14608   27747   4.43   5.0E-64   AF3193.1   EST_HUMAN     24128   37763   2.34   4.0E-64   BF39450.1   EST_HUMAN     15404   28532   8.77   3.0E-64   AV081373.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV081373.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV081373.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV081373.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV07174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV71174.1   EST_HUMAN     16694	97	Т	T	6.32			NT.	Homo sapiens protein kinase C beta-II type (PRI
1   19137   32452   0.74   6.0E-64   11422189   IT   19137   32453   0.74   6.0E-64   11422189   IT   19137   32453   0.74   6.0E-64   11422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   1422189   IT   IT   1422189   IT   IT   IT   IT   IT   IT   IT   I	576			0.68	6.0E-64	6912461		
19137 32453 0.74 6.0E-64 1142789 NT	593	Г		0.74	8.0E-64	11422189		serios adoptine interacting protein 1;
4 20462 33925 2.54 6.0E-64 11528878 NT 4 20462 33926 2.54 6.0E-64 11528878 NT 8 22593 36164 7.39 6.0E-64 11420555 NT 22595 36326 1.75 6.0E-64 776476.1 NT 9 22595 36546 2.16 6.0E-64 776476.1 NT 9 16397 29372 1.73 6.0E-64 AF224763.1 NT 9 16397 29373 1.73 6.0E-64 AF224919.1 NT 14021 27078 4.18 5.0E-64 AF224919.1 NT 14021 27078 4.18 5.0E-64 AF224919.1 NT 14524 27698 1.02 5.0E-64 AB020710.1 NT 14608 27685 1.15 5.0E-64 AB020710.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 1.15 5.0E-64 AF234918.1 NT 14608 27686 5.0E-64 AF234918.1 NT 14608 27686 5.0E-64 AF234918.1 NT 14608 27686 1.55 5.0E-64 AF234918.1 NT 14608 27786 4.43 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27786 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1 NT 14608 27746 5.0E-64 AF234918.1	595	П	П	0.74	6.0E-64	11422189		como sapiens calcitanin receptor (CALCR), mr
4 20462 33926 2.54 6.0E-64 11528979 INT   8 22563 36164 7.39 6.0E-64 11528979 INT   9 22756 39326 1.75 6.0E-64 AF274753.1 NT   9 22989 36546 2.16 6.0E-64 71420197 INT   9 24087 37724 4.68 6.0E-64 AV026445.1 EST HUMAN   9 16367 28972 1.73 6.0E-64 AV026445.1 EST HUMAN   9 16367 28973 1.73 6.0E-64 AV026445.1 EST HUMAN   9 16367 28973 1.73 6.0E-64 AV026445.1 INT   14021 27078 4.18 5.0E-64 AF231919.1 INT   14021 27078 4.18 5.0E-64 AF231919.1 INT   14608 27688 1.02 5.0E-64 AB020710.1 INT   14608 27686 1.15 5.0E-64 AB020710.1 INT   14608 27686 1.15 5.0E-64 L40933.1 INT   14608 27768 1.15 5.0E-64 L40933.1 INT   14608 27769 4.43 5.0E-64 L40933.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27768 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 4.43 5.0E-64 AF231919.1 INT   14608 27769 5.0F-64 AF231919.1 INT   14608 27769 6.44 5.0F-64 AF231919.1 INT   14608 27769 6.44 5.0F-64 AF231919.1 INT   14608 27769 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.43 5.0F-64 AF231919.1 INT   14608 2774 6.43 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1 INT   14608 2774 6.44 5.0F-64 AF231919.1	738			2.54	6.0E-64	11828870		folio sapiens calcitonin receptor (CALCR), m
22563 36164   7.39   6.0E-64   11420555 NT   32786 36326   1.75   6.0E-64   AF274753.1   NT   22989 36546   2.16   6.0E-64   576475.1   NT   37724   4.88   6.0E-64   AF274753.1   NT   37725   4.48   6.0E-64   AF27476.1   EST_HUMAN   325260 32081   2.96   6.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27078   4.18   5.0E-64   AF231979.1   NT   14021 27079   4.18   5.0E-64   AF231979.1   NT   14021 27079   4.18   5.0E-64   A6020770.1   NT   14021 27079   4.15   5.0E-64   A6020770.1   NT   14021 27079   4.43   5.0E-64   A6033.1   NT   14021 27049   4.43   5.0E-64   A6033.1   NT   14021 27049   4.43   5.0E-64   A6033.1   NT   14021 27049   4.43   5.0E-64   A60743.1   NT   14021 27049   3.443   5.0E-64   A60743.1   NT   14021 27049   3.443   5.0E-64   A60743.1   NT   14021 27049   3.443   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   5.0E-64   A60743.1   NT   14021 27049   3.458   3.0E-64   A60743.1   NT   14021 27049   3.0E-64   A60743.1   NT   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084   A6084	738	П	П	2.54	6.0E-64	11525879		omo seniens mesenchyme homeo box 1 (M
3 22766 39326 1.75 6.0E-84 AF274733.1 NT 3 22989 36548 2.16 6.0E-64 S76476.1 NT 3 24087 37724 4.68 6.0E-64 11420197 NT 3 24087 37725 4.68 6.0E-64 AW026445.1 EST HUMAN 3 16367 28372 1.73 6.0E-64 AW026445.1 EST HUMAN 3 16367 28373 1.73 6.0E-64 AW026445.1 NT 4 14021 27078 4.18 5.0E-64 AF231979.1 NT 4 14021 27078 4.18 5.0E-64 AF231979.1 NT 4 14021 27078 4.18 5.0E-64 AF231979.1 NT 4 14021 27078 4.18 5.0E-64 AF231979.1 NT 4 14038 27769 1.15 5.0E-64 AB020770.1 NT 4 14038 27769 1.15 5.0E-64 L40933.1 NT 4 14608 27689 1.15 5.0E-64 L40933.1 NT 4 14608 27689 1.15 5.0E-64 L40933.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF231979.1 NT 4 14608 27769 1.54 5.0E-64 AF2319	952	Г		7.39	6.0⋶-64	11420555		omo naniena acetta-CoA synthetica (1 COE
22999   36546   2.16   6.0E-64   S76476.1   NT	970	Т		1.75	6.0E-84			fomo sapiens progressive ankylosic-like prot
24087   37724   4.68   6.0E-64   11420197   NT	ree	Т		2.16	6.0E-64			rkC [human, brain, mRNA, 2715 mt]
19867   29372   1.73   6.0E-64   11420187   NT     19867   29373   1.73   6.0E-64   AW0.26445.1   EST_HUMAN     18367   29373   1.73   6.0E-64   AW0.26445.1   EST_HUMAN     18367   29373   1.73   6.0E-64   AW0.26445.1   EST_HUMAN     18367   29373   1.73   6.0E-64   AW0.26445.1   EST_HUMAN     14021   27078   4.18   5.0E-64   AF231619.1   NT     14021   27078   4.18   5.0E-64   AE231619.1   NT     14022   27698   1.02   5.0E-64   AE231619.1   NT     14036   27685   1.15   5.0E-64   L40933.1   NT     14036   27686   1.15   5.0E-64   L40933.1   NT     14698   277994   1.54   5.0E-64   L40933.1   NT     14698   27746   4.43   5.0E-64   AE017433.1   NT     14698   27747   4.43   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   EST_HUMAN     24128   31763   2.34   4.0E-64   AW813783.1   EST_HUMAN     15404   28532   8.77   3.0E-64   AW813783.1   EST_HUMAN     15500   28518   0.82   3.0E-64   AV711714.1   EST_HUMAN     16694   28704   1.83   3.0E-64   AV711714.1   EST_HUMAN	1 2	Т	Τ	4.68	6.0E-64	11420197		lomo sapiens stromal antigen 3 (STAG3), mi
15367   29373   1.73   6.0E-64   AW028445.1   EST_HUMAN     15367   29373   1.73   6.0E-64   AW028445.1   EST_HUMAN     25280   32081   2.98   6.0E-64   AF231919.1   NIT     14021   27078   4.18   5.0E-64   AF231919.1   NIT     14021   27079   4.18   6.0E-64   AF231919.1   NIT     14524   27688   1.02   5.0E-64   AB020710.1   NIT     14608   27685   1.15   5.0E-64   L40933.1   NIT     14608   27686   1.15   5.0E-64   L40933.1   NIT     14608   27746   4.43   5.0E-64   U80368.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF017433.1   NIT     14608   27747   4.43   5.0E-64   AF01743	1100	Т	3//25	4,68	6.0E-64	11420187		iomo sapiens stromal antigen 3 (STAG3), mf
25280   32881   2.88   6.0E-64  AF231618.1   NT   14021   27078   4.18   5.0E-64  AF231618.1   NT   14021   27079   4.18   6.0E-64  AF231618.1   NT   14624   27698   1.02   5.0E-64  A6020710.1   NT   14608   27685   1.15   5.0E-64  L40933.1   NT   14608   27686   1.15   5.0E-64  L40933.1   NT   14698   27747   4.43   5.0E-64  L40933.1   NT   14698   27747   4.43   5.0E-64  A601743.1   NT   14698   27747   4.43   5.0E-64  A601743.1   NT   14698   27747   4.43   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   17224   30231   7.25   5.0E-64  A601743.1   NT   NANN  A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6018   A6	1126	Т	29373	173	6.0E-64			v/13e03_x1 NCI_CGAP_Bm23 Homo saplens
14021 27078 4.18 5.0E-64 AF2319(3.1 NT 14021) 27079 4.18 6.0E-64 AF2319(3.1 NT 14524 27698 1.02 5.0E-64 AF2319(3.1 NT 14608 27685 1.15 5.0E-64 L40933.1 NT 14608 277686 1.15 5.0E-64 L40933.1 NT 14608 277694 1.54 5.0E-64 L40933.1 NT 14608 277994 1.54 5.0E-64 L40933.1 NT 14608 277994 1.54 5.0E-64 L76093.1 NT 14608 277994 1.54 5.0E-64 L76093.1 NT 14608 277994 1.54 5.0E-64 L76093.1 NT 14608 277994 1.54 5.0E-64 AF017433.1 NT 14608 27794 1.54 5.0E-64 AF017433.1 NT 176050 34563 0.71 4.0E-64 BE794607.1 EST HUMAN 15404 28532 8.77 3.0E-64 AW813783.1 EST HUMAN 15500 28518 0.82 3.0E-64 BE794391.1 EST HUMAN 16500 28518 0.82 3.0E-64 BE794391.1 EST HUMAN 16500 28518 0.82 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1 EST HUMAN 16504 28704 1.83 3.0E-64 AV711714.1	12400	П	32081	2.98	6.05-64	200	HOMAN	V13e03x1 NCI_CGAP_Brn23 Homo sapiens
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14608   27685   1.15   5.0E-64   L40933.1   NT     14606   27686   1.15   5.0E-64   L40933.1   NT     14608   277894   1.54   5.0E-64   L889368.1   NT     14608   27746   4.43   5.0E-64   L889368.1   NT     14603   27747   4.43   5.0E-64   KF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   NT     17224   30231   7.25   5.0E-64   AF017433.1   EST HUMAN     18500   34563   0.71   4.0E-64   AW813783.1   EST HUMAN     15404   28532   8.77   3.0E-64   AW813783.1   EST HUMAN     15500   28518   0.82   3.0E-64   BE794381.1   EST HUMAN     16594   28704   1.83   3.0E-64   AV711714.1   EST HUMAN	136	Г	27598	1.02	5.0E-64/			omo saniene mRNA for KIAAOON3 protein n
1.4905   27886   1.15   5.0E-64   L40933.1   NT     1.4808   277994   1.54   5.0E-64   U880368.1   NT     1.4808   27746   4.43   5.0E-64   U880368.1   NT     1.4933   27747   4.43   5.0E-64   AF017433.1   NT     1.7224   30231   7.25   5.0E-64   AF017433.1   NT     1.7224   30231   7.25   5.0E-64   AF017433.1   NT     1.7224   30231   7.25   5.0E-64   AF017433.1   NT     1.7224   30231   7.25   5.0E-64   AF017433.1   NT     1.7224   30231   7.25   5.0E-64   AF017437.1   EST_HUMAN     24128   31763   2.34   4.0E-64   AW813783.1   EST_HUMAN     15404   28532   8.77   3.0E-64   AW813783.1   EST_HUMAN     15500   28518   0.82   3.0E-64   BE794381.1   EST_HUMAN     16594   28704   1.83   3.0E-64   AV711714.1   EST_HUMAN     16594   28704   1.83   3.0E-64   AV711714.1   EST_HUMAN     16595   28704   1.83   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   3.0E-64   AV711714.1     17500   28518   0.82   0.82   0.82   0.82     17500   0.82   0.82   0.82   0.82   0.82     17500   0.82   0.82   0.82   0.82   0.82     17500   0.82	140	Т	27685	1.15	5.0E-64 L			omo sapiens phosphoglucomutase-related n
1.64   5.0E-04   U880368;   NT     1.4683   27746   4.43   5.0E-04   U880368;   NT     1.4683   27747   4.45   5.0E-04   7682205   NT     1.7224   30231   7.25   5.0E-04   AF01743; 1   NT     1.7224   30231   7.25   5.0E-04   AF01743; 1   NT     2.1050   3.4563   0.71   4.0E-04   AF01743; 1   EST HUMAN     2.4128   3.7763   2.34   4.0E-04   AW813783; 1   EST HUMAN     1.5404   2.8532   8.77   3.0E-04   AW813783; 1   EST HUMAN     1.6506   2.8518   0.82   3.0E-04   BE794381; 1   EST HUMAN     1.6507   2.8518   0.82   3.0E-04   AV711714; 1   EST HUMAN     1.6508   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   1.83   3.0E-04   AV711714; 1   EST HUMAN     1.6509   2.8704   2.8704   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.8704   2.8704     1.6509   2.8704   2.870		Π.	2/686	1.15	5.0E-64			omo sapiens phosphoglucomutase related r
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24128         37763         2.34         4.0E-64 AWB13783.1         EST_HUMAN           24128         37764         2.34         4.0E-64 AWB13733.1         EST_HUMAN           15404         28532         8.77         3.0E-64 C18895.1         EST_HUMAN           16500         28518         0.82         3.0E-64 BE794391.1         EST_HUMAN           16694         28704         1.83         3.0E-84 AV711714.1         EST_HUMAN	800	Т	34563	0.71	4.0E-64 B		T HUMAN	11690382F1 NIH MGC 7 Homo seriese CD
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22505	710.47	21947	21040	19993	19881	19774	19541	19308	17046	17046	15721	15721	16717	14582	14277	24975	24571	24571	22779	22779	22682	22682	21772	21772	21741	21741	19782	19638	19381	16694	SEQ ID
36071	38481	35480	34662	33402	33272	33165	32900	32649	30046	30045	28841	28840		27655	27334	38679	38249	38248	36350	36349	36252	36251	35304	35303	35282	35281	33170	32997	32731	29705	ORF SEQ
1.08	1 08	1.08	0.67	2.96	1.3	5.04	1.23	2.28	0.98	0.98	24	24	1.28	3.2	1.1	2.16	1.54	1.54	0.66	0.66	1.12	1.12	1.48	1.48	1.86	1.86	3.2	. 0.68	1.31	1.83	Expression Signal
20E-64	205.64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64	2.0E-64								3.0E-64	3.0E-64							Most Similar (Top) Hit BLAST E Value
20E-64 411432570 1 EG	11/3/00	11434008 NT	11431054 NT	2.0E-64 M77185.1	2.0E-64 AI078387.1	2.0E-64 BF668537.1	2.0E-64 AF113708.1	2.0E-64 AU124387.1	2.0E-64 AW958145.1	2.0E-64 AW958145.1	2.0E-84 AL183248.2	2.0E-64 AL 163245.2	2.0E-64 Al927030.1	4757701 NT	2.0E-64 AA609940.1	3.0E-64 AL163227.2	3.0E-64 AL163248.2	3.0E-64 AL163248.2	3.0E-64 AW977384.1	3.0E-84 AW977384.1	3.0E-64 AL163246.2	3.0E-84 AL163246.2	3.0E-64 BE206521.1	3.0E-64 BE206521.1	3.0E-64 AF248953.1	3.0E-64 AF248953.1	3.0E-64 BF370000.1	3.0E-64 AW 600361.1	3.0E-64 Z26273 1	3.0E-64 AV7117,14.1	Top Hil Acession
EST HIMAN	217	8 NT	NT NT	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	NI	EST_HUMAN	ΝT	NT	Ŋ	EST_HUMAN	EST_HUMAN	Z	NT	EST_HUMAN	EST_HUMAN	NT	N	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	Top Hit Database Source
AU132570 NT2RP4 Homo seriems cDNA clone NT2RP4400100 5'			Homo sepiens atexin 2-binding protein 1 (A2BP1), mRNA	H. saplens dopamine receptor D5 pseudogene 1, partial eds	oz29b03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE::1876717 3'	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'	Homo sapiens angiopoletin 4 (ANG4) mRNA, partial cds	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5	EST370216 MAGE resequences, MAGE Homo septens cDNA	EST370215 MAGE resequences, MAGE Homo sapiens cDNA	Homo sepiens chromosome 21 segment HS21C046	Homo saplens chromosome 21 segment HS21C048	we87b01x1 NCL_CGAP_Kid11 Home sepiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;	Homo sapiens elF4E-like cap-binding protein (4EHP) mRNA	af09d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'	Homo sapiens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	EST389493 MAGE resequences, MAGO Hamo sapiens cDNA	EST389493 MAGE resequences, MAGO Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	b572h12 y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:1.08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);	b572h12 y1 NIH_MGC_12 Homo septens cDNA clone IMAGE:3047975 5' stmilar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	Homo sapiens golgi mairix protein GM130 (GOLGA2) mRNA, complete cds	RC8-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA	UI-HF-BP0p-aix-c-05-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073161 6'	H.saplens Isoform 1 gene for L-type calcium channel, exon 28	AV711714 DCA Homo sapiens cDNA clone DCAAMCO1 5	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

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	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
0184	23221	36815	0.5	2.0E-64	T06397.1	EST HUMAN	EST04286 Fetal brain, Stratagene (ca拼936206) Homo sapiens cDNA clone HFRDSB8
0184	23221	36816	0.5	2.0E-64	T06397.1	EST HUMAN	EST04286 Fetal brain, Stratagene (catt936206) Homo saplens cDNA clone HFBDS88
000	24079	37714	221	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE: 4180556 5'
1308	24371	38012	4.28	2.0E-64	AI922911.1	EST_HUMAN	
1306	24371	38013	4.28	2.0E-64	AI922911.1	EST_HUMAN	wn81b06x1 NCI_CGAP_Utf Homo sapiens cDNA clone IMAGE:2452211 3
1509	24567	38244	1.46	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo saplens cDNA
2804	25537		3.59	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sepiens cDNA clone C22 132.5'
268	13487	26517	1.39	1.0E-64	.1	NT	Homo sapiens chromosome 21 unknown mRNA
1820	14969	28061	24.22	1.0E-64	Al929419.1	EST HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519138 3' similar to
076	16252	29274	0.8	1.0E-64	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
							Homo saplens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,
J601	16765	29761	5.47	1.0E-64		Y	JIM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel as
675	16838	29848	1.14	1.0E-64		NT	Homo saplens TRIAD3 mRNA, partial cds
675	16838	29849	1.14	1.0E-64		TN	Homo sapiens TRIAD3 mRNA, partial cds
8	17165	30173	0.88	1.0E-64	2829	T	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
28	23304	36901	1.17	1.0E-64	L	EST_HUMAN	2k53f08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486567 31
291	25216		4.56	1.0E-64		NT	Homo sapiens chromosome 21 segment HS21C046
350	15481	28613	1.87	9.0E-65		NT :	H. sapiens DNA for endogenous retroviral like element
350	15481	28614	1.87	9.0E-65		NT	H.sapiens DNA for endogenous retroviral like element
82	24815		19.08	9.0E-65		EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
799	24789	38486	7 24	8.05-65		_	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:25190053' similar to
358	23393	37004	2.16	7.0E-65 I		_	QV2-BT0635-240400-162-c02 BT0635 Homo septens cDNA
89	26076	38782	2.88	7.0E-85		EST_HUMAN	HSAAAEAWO TEST1, Human adult Testis tissue Homo saniens cDNA clone cem testi46 (h)
183	14247	27304	0.81	6.0E-65		EST_HUMAN	AV721898 HTB Homo sapiens cDNA clane HTBBZC06 5'
974	15117		20.04	6.0E-65		EST HUMAN	nj86d10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA cione IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN):
88	19857	33247	0.8	6.0E-65/		EST_HUMAN	nh37b07.s1 NCI_CGAP_Pr5 Homo sapiens cDNA cione IMAGE:954517
946	22024	35564	2.45	6.0E-65/			xx07b09x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q83306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORES: CONTAINING 1 A NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO. 14 NO.
213	22291	35833	4.63	6.0E-65/	Ш	Ц	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
			Exon SEQ ID OR NO: ID ID ID ID ID ID ID ID ID ID ID ID ID	Exon SEQ ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign 23221 38815 23221 38816 23221 38816 24477 38012 24371 38013 24567 38244 25537 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 18252 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 28274 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Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rate No: Signal Rat	Exon SEQ ID NO:         ORF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Value         Top Hit Acession (Top) Hit Value           23221         36815         0.5         2.0E-64         T08397.1           23221         36816         0.5         2.0E-64         T08397.1           24978         37714         2.21         2.0E-64         T08397.1           24371         38012         4.28         2.0E-64         Al922911.1           24371         38013         4.28         2.0E-64         Al922911.1           24567         38244         1.46         2.0E-64         Al922911.1           24587         38013         4.28         2.0E-64         Al922911.1           24587         38244         1.46         2.0E-64         Al922919.1           14969         28061         24.22         1.0E-64         AF188779.1           16838         28484         1.14         1.0E-64         AF228527.1           16838         28484         1.14         1.0E-64         AF228527.1           16838         28484         1.14         1.0E-64         AF228527.1           16838         28613         1.9E-64         AA042875.1           285216	Exon   ORF SEQ   Expression   Clop   Hit   SEQ   ID   ID NO:   Signal   BLAST E   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.  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9213 SEQ ID 20785 20785 21043 20447 19457 20317 20349 18457 13946 20144 15357 16643 16543 16501 200 ORF SEQ 34273 34274 34555 33910 32808 33760 27751 28670 28671 27614 28487 29519 29520 33563 37324 26452 33801 32807 26991 27613 38001 38475 26859 Expression Signal 0.65 5.04 0.66 1.02 4.96 102 1.44 23 138 8 23 . 192 1.89 4.0E-65 AB033083.1 4.0E-65 AB033083.1 7-C-65 AY008372.1 (Top) Hit BLAST E Most Similar 4.0E-65 U403721 4.0E-65 U403721 4.0E-65 4.0E-65 AI266438.1 4.0E-65 BE221469.1 4.0E-65 AB033093.1 5.0E-65 4.0E-65 BE221469.1 4.0E-65 AL120419.1 5.0E-65 5.0E-65 AB033768.1 6.0E-65 AL 163210.2 6.0E-65 BE667816.1 5.0E-65 AF064504.1 5.0E-65 AF009668.1 6.0E-65 AID85314.1 AI2664638.1 Top Hit Acession ş 4507848 4507848 7661951 3333 Z LN EST\_HUMAN EST HUMAN ፯ IN EST\_HUMAN EST\_HUMAN ξ EST\_HUMAN EST HUMAN ST HUMAN Top Hit Database Source HUMAN HUMAN Human MAP kinase kinase 6 (MKK6) mRNA, complete cds Homo saplens hypothetical protein FLJ22087 (FLJ22087), mRNA
Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds Humen clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats hu25e64.x1 NCI\_CGAP\_Mel15 Homo capiens cDNA clone IMAGE:3171102 3 Homo saptens mRNA for KIAA1267 protein, partial cds qm46e01x1 Scares\_placenta\_8to9weeks\_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3 DKFZp761G108\_r1 761 (synonym: hamy2) Homo saplens cDNA clone DKFZp761G108 5 Homo sepiens nel (chicken)-like 2 (NELL2), mRNA Homo saplens nel (chicken)-like 2 (NELL2), mRNA qm46e01.x1 Soares\_placenta\_8to9weeks\_2NbHP8to9W Homo saplens cDNA done IMAGE:1891800 3 Homo sepiens KIAA0156 gene product (KIAA0156), mRNA Homo sepiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds Homo sapiens chromosome 21 segment H321C010
Homo sapiens KE03 protein mRNA, partial cds
Homo sapiens KIAA0156 gene product (KIAA0156), mRNA qf18h05x1 NCI\_CGAP\_Brn25 Homo sepiens cDNA clane IMAGE:1750425 3' Homo saptens mRNA for KIAA1267 protein, partial cds hu25e04.x1 NCI\_CGAP\_Me116 Homo sapiens cDNA clone IMAGE:3177102 3 Multiple scierosis associated retrovirus polyprotein (pol) mRNA, partial cdc Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA Homo saplens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA 602037721F1 NCI\_CGAP\_Bm64 Homo saplens cDNA clone IMAGE:4185677 5 gf18h05.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:1750425 3' 601340485F1 NIH\_MGC\_53 Homo sapiens cDNA clone IMAGE:3682677 6' Homo saplens ribosomal protein L34 (RPL34) mRNA domo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA Homo eapiens interferon-related developmental regulator 1 (IFRD1), mRNA zw53b06.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sepiens cDNA clone IMAGE:7737473 kinase 2 (a protein tyrosine kinase) (JAK2), mRNA Top Hit Descriptor

Single Exon Probes Expressed in Placenta Page 349 of 550 Table 4

SEQ ID

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Single Exon Probes Expressed in Placenta	

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Table 4

Single Exon Probes Expressed in Placenta

Novel human gene mapping to chomosome 22	NT	8.0E-66[AL16031,1.1	8.0E-66/A	8.0	20000	10010	
			a.∪⊏-00 A	0.8	10001	3 3	3 2
Homo septens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA		10322	1.05		28224	13910	73
Limitation protest CG12-1 (CG12-1), TRIVA		14440333	105.85	3 77	32078	25276	12391
Torro seniens TNE indirethie postolo CC43 4 (CC43 4) TOWAIV,		18041	1.0E-65	2.38		25217	12292
1878606.x1 NCI_CGAP_GCS Homo saplens cDNA clone IMAGE:2237170 3' similar to gb:L15533_ma1	NAMUH TSE	AI621017.1	1.0E-65 A	2.58	38217	24545	11486
602126239F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4283313 5	EST_HUMAN	1.0E-65 BF698707.1	1.0E-65 E	1.9	38118	24456	11395
Homo sapiens ribosomal protein L7a (RPL7A) mRNA	NT	08880	1.0E-65	9.39	37734	24095	11016
Human platelet factor 4 varation 1 (PF4var1) gene, complete cds	TN		1.0E-65 M2616711	1.91	37599	23969	1080
Homo sepiens mRNA for KIAA1411 protein, parttal cds		2.1	1.0E-65 /	1.23	37453	23829	10/96
275a04.r1 Scares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 6			1.0E-65 /	0.65	37155	23544	10509
AU153783 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'	$\Box$	1.0E-65 AU153793.1	1.0E-65 /	1.32	36730	23127	10089
qd56a02x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN):contains MER19 H MFR19 condition closurer!	EST_HUMAN	1.0E-65 AI191716.1	1.0E-65	5.5	3 <del>6</del> 210	22640	9678
Homo sepiens KIAA0656 gene product (KIAA0656), mRNA		7662227 NT	1.0E-65	0.55	35837	22385	9309
Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (TTPR1) mRNA		11431894 NT	1.0E-65	2.79		22308	9231
AU129040 NT2RP2 Homo saplens cDNA clone NT2RP2004714 5		1.0E-65 AU129040.1	1.0E-65	1.33	35844	22300	9222
AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5	┙	1.0E-65 AU128040.1	1.0E-65	1.33	35843	22300	9222
602126239F1 NIH MGC 56 Homp sapiens cDNA clore IMAGE: 42923412 51		1.0E-65 BF698707.1	1.0E-65	1.01	35682	22120	9041
AU141295 THYRO1 Homo saplens cDNA clone THYRO1000330 3		1.0E-65 AU141295.1	1.0E-65	2.04	35130	21595	8514
AU141295 THYRO1 Homo septens clove clove THYRO1000356 5		1.0E-65 AU141295.1	1.0E-65	2.04	35129	21595	8514
601568124F1 NIH MOC 21 Homo septems controlled invitor 3041012 3	Ŀ	1.0E-65 BE732118.1	1.0E-65	0.66	35089	21556	8476
601566124F1 NIH MGC 21 Homo seriene cDNA disco IVACE courses		1.0E-65 BE732118.1	1.0E-65	0.66	35088	21556	8475
OV2-ST0208-140200-042-12-ST0208-Homo septens CDNA		1.0E-65 AW820481.1	1.0E-65	1.5	35058		8448
12 ST0208 Homo contons		1.0E-85 AW820481.1	1.0E-65	1.5	35057	21529	8448
qh88h07.x1 Soeres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823	EST HUMAN	1.0E-65 AI243738.1	1.0E-65	0.58	31837		5594
QV0-BT0702-170400-194-f09 BT0702 Hamo sapiens cDNA	EST_HUMAN	1.0E-65 BE089509.1	1.0E-65	0.86	31573	18602	5400
QV0-BT0702-170400-194-109 BT0702 Home saniens cDNA	EST_HUMAN	1.0E-65 BE089509.1	1.0E-65	0.86	31572	Т	5400 0400
xx20c01.x1 NCI CGAP HN10 Home sapiens cDNA close IMAGE: 3730806 3	EST HUMAN	1.0E-65 AW238282.1	1.0E-65	1.57	31236	18266	5143
xx20c01.x1 NCI CGAP HN10 Homo saniens con constitute CE-3740eas at	EST. HUMAN	1.0E-65 AW238282.1	1.0E-65	1.57	31235	18266	5143
wx09c09x1 NCI CGAP Gas4 Homo sanians cDNA chos IMAGE: 25431523	EST HUMAN	1.0E-65 AW023340.1	1.0E-65	253	30452	17468	4323
WXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	EST HUMAN	AW0283	1.0E-65	2.53	30451	17466	4323
Homo septens alvoicen 4 (GPC4) mRNA	NT	4504082 NT	1.0E-65	2.07	30260	17259	4105
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:
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Homo saplens mRNA for KIAA0998 protein, partial cds	NT	4.0E-66 AB023276.1	4.0E-86	1.63	38430	24739	11660
UI-H-BW 1-amr-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'	EST_HUMAN	4.0E-66 BF507493.1	4.0E-66	1.49	37612	1	10896
Humen endogenous retrovirus pHE.1 (ERV9)	NT	4.0E-66 X57147.1	4.0E-66	0.7	34936		8327
Homo sepiens hypothetical protein FLJ20116 (FLJ20116), mRNA	NT	11421638 NT	4.0E-66	6.14	34867	21351	8269
Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA	NT	11428643 NT	4.0E-66	0.83	32147	18862	7807
Homo sepiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds	NT	4.0E-86 U78168.1	4.0E-66	7.88	33817	20364	7281
EST377546 MAGE resequences, MAGI Homo sapiens cDNA	EST_HUMAN	4.0E-66 AW965473.1	4.0E-66	4.91	31506	18514	6995
QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA	EST_HUMAN	4.0E-66 AW939119.1	4.0E-66	0.87	32368	19051	6861
Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA	NT	11428643 NT	4.0E-86	3.67	32147	18862	5668
Human endogenous retrovirus, complete genome	3	9635487 NT	4.0E-66	5.02		18035	4905
Homo sapiens germ-line DNA upstream of Jkappa locus	3	4.0E-66 AJ223364.1	4.0E-86	3.15		15688	2543
H.sapiens DNA for endogenous retroviral like element	NT	4.0E-66 X89211.1	4.0E-66	5.3	28618	15488	2356
RC1-NN0063-100500-022-a02 NN0063 Homo sapiens cDNA	EST_HUMAN	4.0E-66 AW897798.1	4.0E-66	0.97	28018		1775
Mus musculus fragile X mental reterdation syndrome 1 homotog (Fmr1), mRNA	NT	6879816 NT	4.0E-66	1.8	27046		813
Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA	NT	11420557 NT	6.0E-66	8.4	36113	22551	9494
RC4-BT0311-141199-011-h06-BT0311 Homo saplens cDNA	EST_HUMAN	5.0E-66 BE0644 10.1	5.0E-66	2.45	27827	14552	1398
H.sapiens mRNA for ribosomal protein L31	NT	6.0E-66 X69181.1	6.0E-66	3.22	38152		11427
PM2-HT0604-030300-001-506 HT0604 Homo sapiens cDNA	EST_HUMAN	6.0E-66 BE178663.1	6.0E-66	0.46		П	8629
CE18595;	EST_HUMAN	6.0E-66 AI924653.1	6.0E-66	1.16	30607	17625	4485
wn57h07 x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE 2449597 3' similar to WP:F15G9.4A						٦	
wn57h07x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;	EST_HUMAN	Al924653.1	6.0E-66	1.16	30606	17625	4485
CE18595;	EST_HUMAN	6.0E-66 AI924653.1	6.0E-66	1.16	30605	17625	4485
RC4-BT0311-141199-011-h06-BT0311 Homo sapiens cDNA	EST_HUMAN	7.0E-66 BE0644 10.1	7.0E-68	1.6		24708	11628
Human caldum-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	1_	9.0E-65 M72393.1	9.0E-66	0.66	30172	17164	4007
Human caldium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	NT	9.0E-66 M72393.1	9.0E-66	0.66	30171	17184	4007
Human transposon-like element, partial	NT	9.0E-66 MB7299.1	9.0E-66	5.83		14666	1513
Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA		5031980 NT	9.05-88	1.53	27616	14540	1385
Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA	NT	5031980 NT	9.0E-88	1.53	27615	14540	1385
Top Hit Descriptor	Top Hit Database Source	Tap Hit Acessian No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Prabe SEQ ID NO:
		99					

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	Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hi? Accession No.	Top Hit Database Source	Top Hit Descriptor
	1458	14611	27692	14.83	3.0E-66	4502098 NT	NT	Homo sepiene solute carrier family 25 (mitochondrial cernier; edenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
	1458	14611	27693	14.83	3.0E-66	4502098 NT	NT	Homo sapiens solute carrier (amily 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
	2039	15180	28290	1.04	3.0E-66	3.0E-66 N56323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclarosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H281_TIGCA P35063 HISTONE H28.1/H28.2. [2] PIR:B55612;
	2039	15180	28291	1.04	3.0E-66	3.0E-66 N55323.1	EST_HUMAN	
·	2039	15180	28292	- - - -	3.0166	3.0E-66 N55323:1	EST_HUMAN	
_	2772	15887	28997	3.44	3.0E-66	11141880 NT		
_	3188	16361	29367	7.29	3.0E-66	7662223 NT	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
_	5583	18778	31823	0.85	3.0E-66	2	NT ·	Homo capiene mRNA for KIAA0892 protein, partial cds
_	2695	1888	32180	0.65	3.0E-66	3.0E-66 M13975.1		Homo saplens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
_	500	Toper	32381	1.72	3.0E-66	11417948 NT		Homo saplens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
_	7585	20657	34134	1.74	3.0E-66 X92211.1			H. saplens germline immunociobulin heavy chain variable region. (15-1)
_	9725	22790	38361	0.59	3.0E-66	3.0E-66 AK024453.1		Homo saplens mRNA for FLJ00045 protein, partial cds
	9920	22960	36547	0.52	3.0⊱-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
_	10278	23313	36911	0.86	3.0E-66	7019480 NT		Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
_	10741	23774	37386	0.95	3.0E-66	3.0E-66 AF155659.1	TV	Hamo saplens molybdenum cofactor biosysthesis protein E (MCBPE) mRNA, complete cds
r —	11800	24790	38487	4.55	3.0E-66	5453949 NT		المراقعة Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
_	25	13291	26304	1.48	2.0E-66	7657334 NT		
_	52	13291	28305	1.48	2.0E-66	7657334 NT		Homo sapiens Misshapen/NiK-related kinase (MINK), mRNA
	435	13235	28235	0.87	2.05-66	4505524 NT		Homo septens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
	435	13235	26236	0.87	2.0E-66	4505524 NT		Homo saplens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
	1873	15017	28126	2.02	20E-66	1.2	NT	Hamo sapieno chromosame 21 segment HS21C101
	3030	16215	29236	1.07	2.0E-66 X65859.		NT	H.sepiens pseudogene for the low affinity IL-8 receptor
_	3809	16773	29788	0.85	2.0E-66	8923290 NT		Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
_	3861	17021	30019	0.78	2.0Ε-66			Novel human gene mapping to chomosome 1
_	4176	17326	30317	0.69	2.05-68	2.0E-66 AF108389.1	NT	Homo sepiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds

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Single Exon Probes Expressed in Placenta

	т-	_	_	_			<del>,                                     </del>	т-	r	_				_	_	_		_	_		_	_			_	_		_	<del>,</del>
2871	2089	2089	1585	1685	1413	391	5034	12398	11185	10582	10582	9626	8652	7078	5900	6900	5497	4604	4504	2959	2959	1717	12637	9048	5937	5937	4778	4778	Probe SEQ ID NO:
13628	15229	15229	14737	14737	14567	13628	18162	25278	24254	23817	23617	22681	21732	20131	19089	19089	18696	16136	16136	16136	16136	14867	26147	22127	19123	19123	17913	17913	Exon SEQ ID NO:
26665	28351	28350	27818	27817	27641	28665			37889	37224	37223	36250	36271	33548	32403	32402	31712	29154	29153	29164	29153			35671	32437	32436	30899	30898	ORF SEQ ID NO:
1.36	1.94	1.94	1.39	1.39	2.66	1.63	0.91	1.62	2.24	0.93	0,53	0.64	1.2	1.53	0.67	0.67	6.97	4.18	4.18	1.47	1.47	1.14	2.84	3.57	0.82	0.82	13.88	13.88	Expression Signal
7.0E-67	7.0E-67	7.0E-67	7.0E-67		7.0E-67	7.0E-67	8.0E-87	9.0E-87																					Most Similar (Top) Hit BLAST E Value
7.0E-67 AW 162232.1	7667243 NT	7657243 NT	7.0E-67 W85947∵1	7.0E-67 W85847.1	7.0E-67 AA383416.1	7.0E-67 AW 162:332.1	8.0E-67 M78158.1	11418177	1.0E-66 AF111187.2	1.0E-66 AV748749.1	1.0E-66 AV748749.1	1.0E-66 AA018828.1	1.0E-66 AA668858.1	1.0E-66 BF32B623.1	1.0E-66 BE765232.1	1.0E-86 BE765232.1	1.0E-66 BF673088.1	1.0E-66 AV717817.1	1.0E-66 AV717317.1	1.0E-66 AV717817.1	1.0E-66 AV717317.1	1.0E-66 BE887173.1	11418318 NT	2.0E-66 N45480.1	2.0E-68 AW988854.1	2.0E-66 AW958854.1	2.0E-66 AJ133267.2	2.0E-66 AJ133267.2	Top Hit Acessian No.
EST_HUMAN	3 NT	' '	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	7 NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	- 1	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	NT .	Top Hit Database Source
7 - 1		Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA cione IMAGE:416049 5'	zh56b05.r/ Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5	EST98812 Testis I Homo sepiens cDNA 5 and similar to c. elegans hypothetical protein, cosmid 2K353	eu75d02:x1 Schneider fetal brain 00004 Homo saplens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	EST01750 Subtracted Hippocampus, Stratagene (cat. #336205) Homo sapiens cDNA done HHCPN31 if	Homo saplens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens jun dimertzation protein geno, partial cds; cfos gene, complete cds, and unknown gene	AV748749 NPC Homo sapisns cDNA clone NPCBVA05 5'	AV748749 NPC Homo saplens cDNA clone NPCBVA05 5'	ze57e12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363118 6	aa80e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clore IMAGE:827282 3	RC5-BN0193-010900-034-G09 BN0183 Homo sepiens cDNA	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	IL2+NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	602152898F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4294151 5	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	AV717817 DCB Homo sepiens cDNA clone DCBADC07 5'	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	AV717817 DCB Homo septens cDNA clone DCBADC07 5'		Homo saplens G-2 and S-phase expressed 1 (GTSE1), mRNA	yy59c02.r1 Soares_multiple_solerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277826 5	EST380930 MAGE resequences, MAGJ Homo capione cDNA	EST380930 MAGE resequences, MAGJ Homo sapiens cDNA	Homo sapiens HLA-B gene for human leucocyte antigen B	Homo sapiens HLA-B gene for human leucocyte antigen B	Top Hit Descriptor

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RC0-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA	EST HUMAN	4.0E-67 BF357321.1	4.0E-67	1.48		7,0917	85/6
o/26c05.x6 NCI_CGAP_Kid3 Homo saptens cDNA clone IMAGE:1493288 3' similar to SW:Z33A_HUMAN_ Q06730 ZINC FINGER PROTEIN 33A ;			4.0E-67	0.8	34813	21293	8211
yn02d11.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 51	EST_HUMAN	4.0E-67 R9081911	4.0E-67	1.13	27588	14514	1359
PM3-BN0176-100400-001-g04 BN0176 Homo septens cDNA	EST_HUMAN	9.1	5.0E-67	2.17		24289	11230
Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	TN		5.0E-67	2.26	29486	16467	3283
	T	1	6.0E-67 X68968.	2.74	26788	13765	13224
		7657020 NT	6.0E-67	2.22	30948	17860	4827
Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA		7657020 NT	6.0E-67	2.22	30947	17960	4827
Homo sapiens chromosome 21 segment HS21C001	NT	AL163201.2	6.0E-67	0.92	30376	17389	4243
Homo sapiens chromosome 21 segment HS21C001	NT .	6.0E-67 AL163201.2	6.0E-67	0.92	30375	17389	4243
Homo sapiens Synapsin III (SYN3) mRNA, and translated products		4507332 NT	6.0E-67	1.32	29699	16889	3524
Homo caplens Synapsin III (SYN3) mRNA, and translated products		4607332 NT	6.0E-67	1,32	29698	16689	3524
Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA		4508434 NT	6.0E-67	1.39	29426	16411	3237
Homo saplens PMP69 gene, exons 3,4,5,6 & 7	NT	Y14320.1	6.0E-67	1.07	27524	14458	1302
Homo sapiens mRNA for transmebrane receptor protein	TN	1	6.0E-67	2.4	27051	13997	818
H.sapiens mRNA for acetyl-CoA carboxylase	NT	1	6.0E-67 X68968.	1.09	26788	13765	573
Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA		11421527 NT	7.0E-67	1.74		25721	13106
- 1	NT	7.0E-67 AB011389.1	7.0E-67	1.92	32053	25441	12664
$\overline{}$		11430460 NT	7.0E-67	4.05	38830	25131	12168
Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA		11430460 NT	7.0E-67	4.05	38829	26131	12168
Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds	TI	U82486.1	7.0E-87 U82486	2.02	3860	24958	11973
Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA		11434579 NT	7.0E-67	2.42		24620	11565
Homo saplens retinaldehyde dahydrogenase 2 (RALDH2), mRNA		1	7.0E-67	0.68	35756	22211	9132
Homo sepiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	·		7.0E-67	0.7	35134	21599	8518
Homo saplens phosphodiesterase línucleotide pyrophosphatase 3 (PDNP3) mRNA		4826895 NT	7.0⊑-87	0.52	34857	21340	8258
Homo saplens mitochondrial carrier family protein (LOC55972), mRNA		11418212 NT	7.0E-67	0.89	34359	20864	7809
Homo sepiens mitochondrial carrier family protein (LOC55972), mRNA	•	11419212 NT	7.0E-67	0.89	34358	20864	7809
Homo sapiens ATPase, H+ transporting, lyacocomal (vacualar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA		4885084 NT	7.0E-67	1.12	33425	20015	6863
٠.,		11425572 NT	7.0E-67	1.67	32831	19569	6400
Homo saplens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	NT	11426672 NT	7.0E-67	1.67	32830		6400
Homo seplens zinc finger protein 304 (ZNF304), mRNA	NT	10190695 NT	7.0E-67	0.88	32730	Г	6205
Top Hit Descriptor	Top Hit Database Source	Top Hit Acessian No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
							1

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]					On Grid		EXPERIENCE EXPERSION II I INCOING
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
11318	24381		1.76	4 0E-67	4.0E-67 AA714294 1	NAWITH TOT	nw05e01.51 NCI_CGAP_SS1 Homo sepiens cDNA clone IMAGE:1238472 3' similer to TR:O10385 O10385 PRO-POI -DI ITPASE POI YEROTEIN :
2874		26862	2.03	3.0E-67	3.0E-67 AA3337,68.1	EST_HUMAN	EST37903 Embryo, 9 week Homo saplens cDNA 5' end
3542	16707	29718	2.05	3.0E-67	3.0E-67 BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo saplens cDNA
4816	17949	30934	2.96	3.0E-67	3.0E-87 AW 869 159.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
4846	17978		1.38	3.0E-67	3.0E-67 AL163279.2	TN	Homo sapiens chromosome 21 segment HS21C079
8375	21458	34980	1.37	3.0€-67	3.0E-67 BF196088.1	EST HUMAN	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA cione IMAGE:3134913 3' similar to SW:RHOP_MOUSE 061085 GTP-RHO BINDING PROTEIN 1;
11537	24593		15.42	3.0E-67		EST_HUMAN	om18b07.s1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1541365 3'
183	13416	26445	0.59	2.0E-67	2.0E-67 BE348354.1	EST_HUMAN	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9 CE09617 ;
888	14044	27109	6.29	2.0E-67	2.0E-67 AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo saplens cDNA
1128	14294		2.48	2.0E-67	2.0E-67 AF167460.1	NT	Homo sapiens double stranded RNA activated protein ktnase (PKR) gene, exons 2a, 2, 3, and 4
1833	15076	28179	1.23	2.0E-67	2.0E-67 BE303037.1	EST_HUMAN	ba/2g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 O54892 KIAA0798 PROTEIN. ;
1933	15076	28180	1.23	2.0E-67	2.0E-67 BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo septens cDNA done IMAGE:2805976 5' similar to TR:094892 084892 KIAA0798 PROTEIN. ;
2458	16685	28713	1.18	2.0E-67	2.0E-67 AF309581.1	NT	Homo saplens KRAB zinc finger protein ZFQR mRNA, complete cds
2502	15629	28749	1.37	2.0∈-67	4758795 NT	NT	
3557	16722	29737	3.76	2.0E-67	2.0E-67 AA625755.1	EST_HUMAN	
4109	17263	30263	3.13	2.0E-67		NT	Homo sapiens chromosome 21 segment HS21C100
6197	19372	32723	0.83	2.0E-67		TN	Novel human gene mapping to chemosome 13
6252	19428	32772	4.95	2.0E-67		EST_HUMAN	601875351F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4091893 5'
642g	19593	32958	1.74	2.0E-67		NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6425	19593	32959	1.74	2.0Ε-67		NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6779	18834	33330	0.64	2.0Ε-67		EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo saplens cDNA clone DKFZp761A229 5'
8755	21834	35374	1.09	2.0€-67		EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8755	21834	35375	1.09	2.0E-67		EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
9197	22275	35812	1.31	2.0E-67		EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9197	22275	35813	1.31	2.0E-87		EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9766	22763	36332	0.55	205-67	20E-67 AV731333.1	EST_HUMAN	AV731333 HTF Hamo sepiens cDNA clone HTFARD03 5'
9910	22960	36536	0.99	2.0E-87		EST_HUMAN	UI-H-BI2-ehn-o-10-0-UI.s1 NCI_CGAP_Sub4 Homo sepiens cDNA clone IMAGE:2727283 3'
10848	23881	37501	0.53	2.0Ε-87		_	on86b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
11141	24213	37840	1.75	2.0E-67	2.0E-67 BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5

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Table 4
Single Exon Probes Expressed in Placenta

г	г	_	т-	Τ-	_	_	Τ	_	_		_	_	,	_	r	_			· ·		_	_		_		_	_	_		
7859	6912	6912	6085	5090	2594	2594	4297	3216	842	842	825	825	13165	12868	11417	10686	8293	3973	3973	2245	12105	11268	4833	726	263	12527	11743	11504	11310	Probe SEQ ID NO:
20913	20227	20227	19267	18218	15719	15719	17440	16390	14020	14020	16986	16988	25756	25579	2447B	23700	21375	17130	17130	15378	25085	24337	17986	13908	13482	25988	23929	24562	26230	SEQ ID
34418	33660	33659	32596		28837	28836		29401	27077	27076	27060	27059	31927		38143	37310	34895	30134	30133	28506			30954	26948	26514	31770	37655	38240		ORF SEQ ID NO:
0.84	6.03	6.03	0.69	7.11		1	0.64	2.99	4.93	4.93	2	2	1.45	2.84	1.31	6.43	0.56	6.76	6.75	8.3	3.44	1.47	0.73	0.95	2.37	2.47	244	205	2.66	Expression Signal
4.0E-68	4.0Ε-68	4.0E-68	4.0E-68	4.0E-68 P04406	4.0Ε-68	4.0E-68	5.0E-68	5.0E-68	5.0E-68	5.0E-68	5.0≝-88				6.0E-68										1.0E-87	2.0Ε-67			2.0E-67	Most Similar (Top) Hit BLAST E Value
7661683 NT	1,1055991 NT	1,1065991 NT	4.0E-68 AF157063.1		1/1421388 NT	11421388 NT	4826967 NT	5.0E-68 AB0378521	5.0E-68 AF231919.1	5.0E-68 AF231919.1	5.0E-68 AF231919.1	5.0E-68 AF231919.1	6.0E-68 BF310675.1	6.0E-68 BE612554.1	6.0E-68 AF133901.1	11422086	7.0E-68 AI810505.1	8.0E-68 AA209458.1	8.0E-68 AAZ09456.1	8.0E-68 BE870732.1	4506090	1.0E-67 BE010038.1	1.0E-87 BF439247.1	AA70278	4502166 NT	11418189 NT	2.0E-87 BF377169.1	2.0E-67 BE295714.1	11436448 NT	Top Hit Acessian
NT.	S	TN	NT	SWISSPROT	TN	T	T	T	T	FN	NT	N T	EST HUMAN	EST HUMAN	NT .	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Z	EST HUMAN	EST_HUMAN	EST HUMAN	ST T	TNE	EST_HUMAN	EST HUMAN	BUT	Top Hit Database Source
Homo saplens DKFZP586L0724 protein (DKFZP586L0724), mRNA	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1) mBNA	Homo saplens serine carboxypeptidase 1 precursor protein (HSCP1) mRNA	Homo sapiens sedlin (SEDL) gene, exan 4	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE LIVER	Homo sapiens transcription factor NRF (NRF) mRNA	Homo septens transcription factor NRF (NRF), mRNA	Homo sapiens rettrioblastoma-binding protein 2 (RBBP2) mRNA	Homo sepiens mRNA for KIAA1431 protein, pertial cds	Homo saplens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	601894635F2 NIH MGC 19 Homo sablens cDNA cone IMAGE: 4124144 5	501452067F1 NIH MGC 66 Homo saplens cDNA chop IMAGE:3855761 5	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds	Homo sepiens brefeldin A-inhibited guanine nucleotide exchange protein 2 (BIG2), mRNA	wb89e03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE :2312860 3	zzi82h10.r1 Stratagene hNT neuron (#337z33) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. :	হা82h10.r1 Stratageno hNT neuron (#937233) Homo sepiens cDNA clone IMAGE:648163 5' similer to SW:SAV_SULAC Q07590 SAV PROTEIN.;	601448558F1 NIH MGC 65 Homo sapiens cDNA clone IMAGE 3852254 5	Homo sapiens mitogen-activated protein kinasa 6 (MAPKR) mRNA	PM3-BN0176-100400-001-g04 BN0176 Homo septens c7NA	nab6108.x1 Soares NSF F8 9W OT PA P S1 Homo saniers colvin close invoces of	290b04.s1 Spares feltal liver spiece 1NFI S S1 Homo services (DNA close MACE: 44004E S	2 1	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA	601175762F1 NIH MGC 17 Homo saplens cDNA clone IMAGE 3531038 5	Homo saplens KIAA0985 protein (KIAA0985), mRNA	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

Г	Γ	Ţ	Г	Γ	Γ	Т	Γ	Г	<u> </u>	Г	Т	Т	Γ	<u> </u>	Т	Г	Г		Γ	Г	Г			_		Γ	_	Τ-	ī	<u>ω_</u>
827	397	9115	67 <u>64</u>	6764	5966	5881	<b>633</b>	9174	8047	8047	648 <u>2</u>	3473	11128	4266	4246	1053	1063	23	22	13164	13100	12849	11963	11963	11580	11580	11468	11142	11089	Probe SEQ ID NO:
13812	13634	22194	19920	19920	19162	25812	13726	22252	21130	21130	19849	16840	24200	17411	17392	14218	14218	13260	13260	25755	26092	13316	24948	24948	24634	24634	24527	24214	24163	Exen SEQ ID NO:
26834	26672	35739	33316	33315	32467	32378		35795	34650	34649	33011			30397	30380	27276	27275	26261	28260		31661	26344	38664	38653	38314	38313	38200	37841	37800	ORF SEQ ID NO:
2.78	5.24	0.55	3.17	3.17	4.62	1.53	1.18	1.06	1.85	1.85	4.44	1.28	7.86	0.89	0.6	0.89	0.89	2.42	2.42	1.88	3.05	2.53	1.81	1.81	2.83	283	1.7	281	218	Expression Signal
3.0E-69	3.0E-69	4.0E-69	4.0E-69	4.0E-69	4.0E-€9					6.0E-69	7.0E-69			9.0E-69	9.0E-69	9.0E-69											1.0E-68	1.0E-68	1.0E-68	Most Similar (Top) Hit BLAST E Value
3.0E-69 AF221712.1	BE2580·12.1	4.0E-69 AU119634.1	4557732 NT	4557732 NT	A1764973.1	4.0E-69 BE661053.1	4.0E-69 AI873630.1	5.0E-69 AA825039.1	6.0E-69 AI192764.1	6.0E-69 AI192764.1	9966912 NT	AJ2377.44.1	9.0E-69 AU117241.1	4504010 NT	4757867 NT									11418431 NT	1.0E-68 U50319.1	GLE09N	11433277 NT	L76416.1	11418869 NT	Top Hit Acession No.
NT	EST_HUMAN	EST_HUMAN	32 NT	32 NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	12 NT		EST_HUMAN	10 NT	67 NT	NT OB	NT OB	70 NT	76 NT	13 NT	8 NT	22 NT	31 NT	31 NT	TN	TN	77 NT	NT	69 NT	Top Hit Database Source
Homo sapiens Smad- and Oif-interacting zinc finger protein mRNA, partial cds	601110371F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3351352.5	AU118634 HEMBA1 Hemp sepiens cDNA clone HEMBA1006283 5'	Homo sepiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Homo seplens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA		601344705F1 NIH_MGC_8 Homo sapiens cDNA done IMAGE:3677641 5	wm26h11.x1 NCI_CGAP_Ut4 Homo sepiens cDNA clone IMAGE:2437125 3*	cd60a03.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1372300 3	qe62/h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);	qe52h01x1 Soares_fetzl_lung_NbHL19W Homo saplens cDNA clone IMAGE:1743601 3' similar to the gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA	Homo sapiens RIBIIR gene (partial), exon 12	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5	Homo septens glutamate-cysteine ligase (gamma-glutamy/cysteine synthetase), regulatory (30.8kD) (GLOLR) mRNA	Hemo saplens v-raf murine sarcoma viral gnoogene homolog B1 (BRAF) mRNA	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA	Homo septens 26S proceasome associated pad1 homolog (POH1) mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA			Homo seplens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	Homo sapiens CGI-76 protein (LOC51632), mRNA	Homo sapiens CGI-76 proteh (LOC51832), mRNA	Human protein kinase C substrate 60KH (PRKCSH) gene, expn 4-5	Human protein kinase C substrate 80K-H (PRKCSH) gene, exen 4-5	Hamo saplens myosin IC (MYO1C), mRNA	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA	Top Hit Descriptor

	200		1.02-08	1.22	33709	2058	3
L	TARTORS NT	AW SES	T		94 33285	38 19894	6738
_1_	EST HIMAN	1.0E-69 BE902501.1			51 32698	П	6175
1	EGT LIMAN	1.0E-69 BE902501.1			51 32697	٦	6176
$\perp$	TOT HIMAN	1.0E-69 BE408CB4.1		0.63	30		5137
	HOT HIMAN	1.0E-69 AFUSO 00.1	Ι		38 27980	39 14888	1739
1	2 1	1.0E-09 DF-300127.1	Ī			14832	1680
$\perp$	FST HUMAN	2.0E-69 AA114270.1	T	0.95	35368	21830	8761
-1	FST HUMAN	S AMAST 107.1	Ī			16084	2906
_1	FST HUMAN	2.0E-69 BE237637.1			7 28181	4 15077	1834
- 1	EST HUMAN	Z.UE-09 AF 100Z.JZ. 1	Τ			7 13612	417
Homo sapiens KIAA0553 protein gene, complete cds, and apprain perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior, perior,	NT	NOT ON ACTIONS 1	1		١	Г	417
Homo sapiens KIAA0553 protein gene, complete cds; and alphalib protein gene, partial cds	Z	2.0E-09 AF 1004-32-1	Τ			Γ.	131
Homo sapiens KIAA0553 protein gene, complete cds; and alphalib protein gene, parual cus	27	20E-69 AF160202.	Γ			П	131
Homo sapiens KIAA0663 protein gene, complete cds; and alphalib protein gene, put us cos	ZT .	11600			Г	5 25223	12305
Homo sepiens HGC6.2 protein (HGC6.2), mRNA	77 N	3.0E-09/AD011041.1	T		2 38786		12112
Homo sapiens mRNA for MEGF8, pertial cds	Z	3.0E-09/ABO 1071.	Γ		Г	2 25092	12112
Homo sapiens mRNA for MEGF8, partial cds		3.0E-08 000011841 1	T				11080
EST88807 HSC172 cells II Homo septens cDNA 5 and similar to situate to incomme processing processing the second processing the second processing processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processing the second processin	EST HUMAN	2763	T	2/4	2 37590	Г	10877
Homo saptens ribosomal protein S18 (N-S19A), ribosomal protein S18	NT		T		Ī	Г	10034
Homo sepiens SEC10 (S. cerevisiae)-like i (SEC10L1), 13 VVV	36 NT	5730036 NT	T		T	T	9733
(MIF)-related protein	Z	3.0E-69 X06233.1					<u> </u>
Human mRNA for calcium-binding protein in macrophages (MIXF-14) illacity and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon		100	T	1./4	36238	22668	9613
H. sapiens mRNA for N-acetyglucosemido-(beta 1-4)-gatacus yuurinaraan minration inhibitory facto		9 DE 60 X1323	T	0.74		Г	8907
EST88807 HSC1/2 cells II nomo sapieria curro o mo empreso de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la co	EST HUMAN	3 0F-49 AA376389.1	58-30 E	77.0	30100	Т	866/
UI-H-BI1-ecw-g-01-0-UI.s1 NCI_CGAT_Subs runis september to similar to ribosomel protein S18	EST_HUMAN	3.0E-69 AW 1386.46.1	3.0⊑-69	1 33	T	Т	7724
Homo sapiens (Not Coulon & Promo Service Homo sapiens cDNA clone MAGE:2715840 3	NT.	3.0E-69 AF268075.1	3.0⊱-69	84	T	Ţ	10,0
TOUTION SELECTION TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE	Z	3,0E-69 U52351.1	3.0E-69	1.74		7	7
encoding mitochondrial protein, complete ods	깈	3.0E-69 AF095703.1	3.0E-69	0.76	34076	20802	7520
		114100101411	3.05-69	1.37	38823	18483	5357
_	N N	11/18/18	0.01	2.10			2449
	EST_HUMAN	3.0E-60 T80514.1	3.05-69	1.12		14738	1586
TO CO. AABRA			Value			70	Z.
Top Hit Descriptor	Top Hit Database Source	Top Hit Agession No.	Most Similar (Top) Hit BLAST E	Expression   Signal	ORF SEQ	SEQ ID	Probe SEQ ID

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Table 4
Single Exon Probes Expressed in Placenta

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Table 4
Single Exon Probes Expressed in Placenta

		Ţ	7.05.70	8	02 34618	9660 21102	8
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Homo saplens karyopherin beta 25, ransporun (17045), mRNA	11525964 NT	11525	T		-	9635 21078	98
Homo septens phospholipis screinbless ( general CTON) mRNA	I	7 0E 70 AF153715.1				9358 22433	8
Human PBX3 mKNA	N	7 0F-70 X59841.1	T			9358 22433	8
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Human displacement protein (CCAAT) mRNA	2	7.0E-70 M74099.1				Т	8
Human displacement protein (CCAAT) mRNA	17.	7.0E-70 AB03//10.1			35243	П	8626
Homo saplens mRNA for KIAA1294 protein, partial cds		7.0E-70 AB03//13.1		2.55		П	8626
Homo sepiens mRNA for KIAA1294 protein, partial ccs	NT.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			5 34506	7	7945
Homo sepiens titin immunoglobulin domain protein (myouling) ( ) 10 / 10 / 10 / 10 / 10 / 10 / 10 / 10		Moder	T		7 33531	34 20117	7084
Homo sapiens gene encoding splicing factor or 1, example (TTID) mRNA	ZI	A 1000050 1			Γ	0 18795	5600
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Imagin xi NCI CGAP Brn25 Homo sapiens cUNA dione inviger.	ECT LI MAN	8.0E-/UL//000:1	8.05-70	1.64	30615	٦	4483
Homo sapiens DGS-I mRNA, 3' end	Z	0.05-701-77500	0.05-70	1.56	28667	16061	2409
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DNA for KIAA1147 protein, partial cds	N	1.0E-69 AB032973.1	1.0E-69]A	2.91	22521	1	
Homo sapiens mRNA for KIAA1147 protein, partial cds	12	1 N C07700/	1.0E-69	1.22	33710	20271	8363
Homo sapiens KIAA0716 gene product (KIAA0718), mRNA		100000	_	_	_		
	Source	N.	BLAST E		D NO:	NO:	SEQ ID
Top Hit Descriptor	Top Hit Database	Top Hit Acession		Expression	ORF SEQ		Probe
			1				
	Citigate Lycus second	Sitto					

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Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	SEQ ID	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9857	22897	36480	0.53	7.0E-70	4557824 NT	TN	Homo sepiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.5kD) (GLCLC) mRNA
10505		37149	0.85	7.0E-70	7.0E-70 AB036429.1	TN	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10505		37150	0.85	7.0E-70	7.0E-70 AB036429.1	. TN	Homo septens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complets cds
11329	24392	38039	1.77	7.0E-70	11429885 NT	TN	Homo saplens spastic pareplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11329	24392	38040	1.77	7.0E-70	11429685 NT	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant, spastin) (SPG4), mRNA
11897	24885	38583	237	7.0⊑-70	11526319 NT	TN	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11897	24885	38584	237	7.0∈-70	11526319 NT	TN	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
894	14070	27135	. 251	6.0E-70	4502166 NT	TN	Homo sapiens amyloid beta (A4) precursor protein (protease nextn-ll, Alzhelmer discase) (APP), mRNA
2205	П	28468	2.29		6.0E-70 M30938.1	TN	Human Ku (p70/p80) subunit mRNA, complete cds
4629	17765	30747	0.7	6.0⊑-70	6.0E-70 AF154121.1	NT	Homo sepiens sodium-dependent high-affinity dicerboxylate transporter (NADC3) mRNA, complete cds
2618	15066	28854	1.78	5.0E-70	7662307 NT	TN	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2618	16066	28855	1.78	5.0E-70	7662307	TN	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12247	25188		5	5.0E-70	5.0E-70 BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-e06 HT0487 Homo sapiens cDNA
6894	20045	33454	1.03	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA cione HFBDN25
6933	20248	33682	1.84	4.0E-70	4.0E-70 AW783226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo capiens cDNA
6933	20248	33683	1.84	4.0E-70	4.0E-70 AW793226.1	EST HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo septens cDNA
1619	14771	27853	1.71	3.0⋶-70	3.0E-70 BE071788.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1619	14771	27854	1.71	3.0Έ-70	3.0E-70 BE071798.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
6270	18389	31357	1.11	3.0E-70	3.0E-70 AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
5737	18930	32227	0.59	3.0≅-70	11430988 NT	T	Homo sapiens plakophilin 4 (PKP4), mRNA
6737	18930	32228	0.59	3.0E-70	11430988 NT		Homo sepiens piakophilin 4 (PKP4), mRNA
6066	19248	32575	_	3.0E-70	3.0E-70 Al831975.1	EST_HUMAN	wh90d03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388005 3
6503	19669	33033	1.69	3.0E-70	3.0E-70 BF685233.1	EST_HUMAN	802141581F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 6'
6503	18669	33034	1.69	3.0E-70	3.0E-70 BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10314	23349	36965	0.62	3.0E-70	3.0E-70 BE502973.1	EST_HUMAN	hz81h02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419.3
39	13277	26283	1.03	2.0E-70	2.0E-70 AF012372.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds
707	13890	26923	15.24	2.0€-70	2.0E-70 N42161.1	EST HUMAN	yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR:
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	THE	1430460 NT		T	1.10	38628	24926	200	Ţ
1 4 4	Library seriens low density lipoprotein-related protein 2 (LKFZ), mixty	4503520 NT		T	178	38032	24387		Ţ
1 1	There enternotic translation initiation factor 3, subtrain o (1904) (1904)	8923420 NT		T	200	38031	24387		7
į g	Library saniens hypothetical protein FLJ20450 (FLJ20450), IIIN 10 (FLF3S6) mRNA	8923420 NT			3 30	38888	23377		_
T.	Homo satiens hypothetical protein FLUZUTOV (*	1	2.0E-70 AF123303.1	2.0E-70	1 26		12440	9370	_
<u> </u>	Homo septens calcium-binding transporter (FL 120450), mRNA	TINGO	1100002011	2.0Ε-70	1.14	36007	Syre Stars	Т	Τ
		- 1.	20E-10   11-10-0:	205-10	1.34		3	T	Γ
1-		EST HUMAN	11423599 NT	2.0€-70	0.66	35030	21498		
	storage disease type III) (AGL), mRNA				1.0	34/04	21185		1
L	Human guarrios amvio-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen vectorisme	NT	M21741	2.0E-70	3 84	31477	18562	7136 1	
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	ch threneferase 6 (N-acetyliacosaminide alpha 2.3-sialythansterase) (SM 10),	1	2.0E-70 AF 12007	2.01-70	10.35	33363	0308	EBOS 3	J.
<del></del>	Homo saplens Cytoplastics of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of t	NT N	2.0E-70 AF 120074 1	2.0€-70	10.35	33362	٦	Т	
	Homo sapiens cycles and Amein intermediate chain 1 mRNA, complete cos	2	AE422074 1	2.05.70	265	33321		Т	, ,
	Human mRNA for INF I process	3	20E-70 D12825.1	205-70	1.23	32862		Т	
_	Homo sapiens INALT I III Way	NT	AE310105.1	205-70	8.42	31902		T	
1		NT	2 05 70 X72662 1	200	8.42	31801		٦	<u></u>
	n. saprom for schwannomin (CS8)	NT	X72662.1	3 0E 70 X72662!1	100	30307	17311		4
_	ILL coniens gene for schwannomin (CS8)	Z	2.0E-70 M69181.1	2.0E-70	7 DO	300/6	Γ	3923 17	36
	S (MITTIN) III W.	12	2.0E-70 AL 133207.2	2.05-70 /	0.71		1	2394 15	23
	┸	EST HUMAN	2.0E-70 AA054010.1	2.0E-70 A	9.42		5		
					4.02	280Z3	4930		1781
L	A Coares retina N254HR Homo sapiens CUNA GIUID IIVA	Z	2.0E-70 AL 163202.2	20E-70 A	43	C78/7			1688
LIA	_\_	EST_HUMAN	2.0E-70 AA180003.1	2.0E-70 A	9	3		٦	
		EST HOWAIN	A180053.1	2.0E-70 AA180053.1	1.07	27824		8 14840	1688
	_						1	14391	1441
1	٦		1	2.0E-70 BE40/311	1.23	97669	1	T	 
		EST HUMAN		7.00-70	2.16	27433		T	
	Homo septems NUNCA Homo septems cDNA clone IMAGE:3212758 3	3	7681983 NT		2.16	27432		٦	3
	Homo sapus to Narios product (KIAA0193), mRNA	핔	7661983 NT	2027	1.36	27269		٦	26
	Horizo saporio III.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3923669 NT	305-70		26947		13905	723
L	Light carrians twoothetical protein FLJ20758 (FLJ20759), ""	EST HONOR		2.0E-70 AI24689911	a a	7007	Γ	13890	707
	SW:D3HI_KA I F23200 711101000 Septens cDNA clone IMAGE:2004813 3			2.0E-70 N42161.1	15.24	3			
1	yy07e10.r1 Soares melanocyte 2NDHW Homo Selbury DEHYDROGENASE PRECURSOR;							Š	Š
	colons con IMAGE:270522 5 similar to	300,00		Value -	Signal BL			SEQID	E G
	Top Hit Descriptor	Top Hit Database	Top Hit Acession		Mos Expression (To		ORF SEQ	EXON	Probe
				4	4	1			
		Single Exort 100	oignic	l					

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Table 4
Single Exon Probes Expressed in Placenta

7/7/S/10 OM

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Table 4

Single Exon Probes Expressed in Placenta

Π.	1	T	1	7	1	7	1	7	1				٦				<u> </u>	-		7	0	6		<u>.</u>			 دي	12		Probe SEQ ID
10476		8720	8720	7 2 2	7884	7678	7298	7060	8	82	4235	<b>2</b> 2	1014	8877	7633	10828	9270	200	3	7175	6065	6065		11175	0003	9480	3480	12662		
28511	23153	21800	21800	20063	20936	20744	20378	20113	18956	19187	17382	15416	24005	21966	20606	23861	22346	2000	302	20308	19247	18247		24244	23041	22537	16647	25439		Exon SEQ ID NO:
1 37124	1	T	٦	3 34471		34225		33528	6 . 33356	7 32506		28548		35491		37484		T		33751	32674	325/3		37877				32051		ORF SEQ ID NO:
				20.85		5 1.79				1.59	1.18	7.11	2.2	1.34	7.86	0.53	2.88		3.47	2.05	6.03	0.00	6	7.61	88.0	0.64	3.7%	2.42		Expression Signal
П		5.0E-71	5.0E-71		0.B 5.0E-71	Ţ						Γ						T				T					1.0E-70	2.01-70		Most Similar (Top) Hit BLAST E
5.0E-71 U70968.1	5.0E-71 X13467.1		1 5453777 NT	5.0E-71 AF072810.1	1 11626445 N	5.0E-71 M38106.1	1 11431580 NT				5.0E-71 AW816:105.1	5.0E-71 AF056322.1	7.0E-71 AL 1632 10.2	7.0E-71 AA705457.1	7.0E-71 AA442230.1	8.0E-71 AW273320.1	8.0E-71 AA171451.1		9.0E-71 AI554903.1	9.0E-71 A1654903.1	9.0E-71 AI143870.1	71100101	O OE 71 AH 43870 1	1.0E-70 AV738538.1	1.0E-70 AA442292.1	1.0E-70 W85795.1	4507476 NT	11430460 N		Top Hit Acession
NT	NT	5453777 NT	77 NT	Z	45 NT	Z	90 NT	09 N I	08 NT	NT	EST_HUMAN		ZT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	BNT	N.		Top Hit Database Source
Human errestin (SAG) gene exon o	disease of anywar promit provinces (minute)	Homo sapiens nuclear factor relation to kappa o official protein precursor (axon 2)	Protein (NERKR) mRNA	protein (NFRKB) mRNA	ngillo sapisila rancora procent witte mana complete eds	Turnan neuronologinawara Macari Sportsin Associated with Lins 2 (LOC51678), mRNA	Home sapiens pround in wheeler in the 1 mRNA 3' and of cds	Truing sapisio Notation of height (PRKCB1) mRNA	Turno sepietis reliaini, mai, carrier, (KIAA0623), mRNA	Homo sopieta Cycui Puepo Ident Primaro C (COTT)	UV 4-3 10254- 10 188-001-100 0 1020	DVI ST0224 181100 037 MS ST0234 Home sections CDNA	Hamo septens dural località A i seguina a completa completa cos	Zigi (800, 5) Coding John 21 comment HS21(2)10	ZYONDO 1 Scares fetal liver spieen 1NFLS S1 Homo sepiens cDNA clone IMAGE:462226 3'	OS4730 TRANSPLANT BLOOD SATISTICS OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA		2021d11.r1 Strategene neuroopithelium (#937231) Homo sapiens cDNA cione inviacie: o ivini o similia w	W65265XT NCI_CGAR_ GCG Paris Separa CDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.; CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;	CDU2, CDU1, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.: CDU2, CDU1, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.:	014045 PHOSPHOTRANSFERASE.;	geAf01 x1 Spares testis NHT Home sepiens cDNA done IMAGE:1738009 3' similar to TR:014045	Qe04f01.x1 Soeres_testis_NH1 Homo septents culva duris invaser. (1990) 014045 PHOSPHOTRANSFERASE;	AV738538 CB Homo sapiens culvin cione Condidio de la la la la la la la la la la la la la	2/64603.r1 Soares resus INTL nomo saprata con como como como como como como como	2)55g05,r1 Socroe Tetal liver spiece invito 3 of mails social section section and section section and section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section section	mRNA	Hemo sapians transplutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamytransferase) (TGM3)	Long sonions law density imported in-related protein 2 (LRP2), mRNA	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

	EST_HUMAN	2.0E-71 T85489.1	2.0E-71	4.88		26231	12318
	EST_HUMAN	2.0E-71 R55626:1	2.0E-71	2.05	38567	24870	11882
Tmul022 Human Epidermal Keratinocyte Subtraction Lii N similar to gi 6598881	EST_HUMAN	2.0E-71 BF149173.1	2.0E-71	1.46	38546	24848	11860
Tmul022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sepiens cDNA	EST_HUMAN	2.0E-71 BF149173.1	2.0E-71	1.46	38545	24848	11860
	EST_HUMAN	2.0E-71 BE018477.1	2.0E-71	4.37	37647	24015	10933
Homo sapiens short chain L-3-hydroxyacyi-CoA dehydr encoding mitochondrial protein, complete cds	NT	2.0E-71 AF095703.1	2.0€-71	2.12	37468	23846	10813
Homo saplens short chain L-3-hydroxyacyt-CoA dehydrocoding mitochondrial protein, complete cds	NT	2.0E-71 AF085703.1	2.0E-71	2.12	37467	23846	10813
	EST_HUMAN	2.0E-71 BF195585.1	2.0E-71	, 0.5	35826	22285	9207
	EST_HUMAN	2.0E-71 AL042439.1	2.0E-71	0.71	31489	18534	7107
Human mRNA for KIAA0272 gene partial cas	N N	2.0E-71 D87482.1	2.0€-71	723	31615	18635	6435
Human mRNA for KIAA0272 gene, partial cds	Z	2.0E-71 D87462.1	2.0E-71	7.23	31614	18635	5435
	N,	2.0E-71 AL163206.2	2.0E-71	4.54	27481	14416	1258
1	EST HUMAN	3.0E-71 AA557883.1	3.0E-71	3.32	37646	24013	10931
_	EST_HUMAN	3.0E-71 AU135/34.1	3.0E-71	1.13		21305	8223
Homo sapiens putative heme-binding protein (SOUI.) mRNA	22 NT	7657602 NT	4.0E-71	4.56	31200	18229	5101
Homo saplens SP100-HMG nuclear autoantigen (SP100) mRNA complete cds	3	4.0E-71 AF056322.1	4.0E-71	1.97	30667	17686	4548
Homo sapiens plasminogen (PLG) mRNA	80 NT	4505880 NT	4.0E-71	1.67	29141	16128	2951
Equus caballus divoeraidehyde-3-phosphata dehydrogenasa mRNA partial cda	N	4.0E-71 AF157626.1	4.0E-71	31.91	26602	13571	360
Equus caballus divoeraidehyde-3-phosphata dehydrograego mRNA portiol odg	N I	4.0E-71 AF157826.1	4.0E-71	31.91	26601	13571	360
Homo septens himor permais factor (ligand) curedantic	TNCC	4507592 NT	4.0E-71	1.84	26370	13342	106
Homo sociens similar to hypothetical protein FLJ20163	NT OF NT	11/100000 NT	5.05-71	1 76	8	25380	12558
tissue-activating peptide III, neutrophil-activating peptid	14 NT	11436514 NT	5.05-71	3.80	38100	2422	11467
Homo sapiens pro-platelet bacio protein (includes plats				3 00	27026	30676	11926
Homo septens similar to transcription factor CA 150 (H	12 NT	11417012 NT	5.0E-71	1.53	37661	24025	10943
Homo sapiens similar to trenscription factor CA150 (H.	12 NT	11417012 NT	5.0E-71	1.53	37660	24025	10943
Homo sapiens IGF-II mRNA-binding protein 3 (KOC1).	OO NT	5729900 NT	5.0E-71	1.45	37584	23955	10870
5 5	Top Hit On Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	SEQ ID	Probe SEQ ID NO:

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Single Exon Probes Expressed in Placenta

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		121	1.0E-71 AB011399.1		10.17	1	Т	Ţ
	Homo sapiens gane for AF-8, complete cds	217			9 3.2	24474 38139		<u> </u>
3 47	100	91 NT	ļ	Ţ		24474 36136	11413 24	<u> </u>
	u	91 NT		1		Τ	Γ	11121
	I Will GEFTS I WAS HAVE aminon entidase (LNPEP), mRNA	03 N I	11418903 NI	1.0E-71		T	Т	1100
	L	EQ. 1 Commun	1.0E-71 AV/6121/.1		2.49	3	Т	
	┙	COT LI MAN			0.97	92 37411	59 23792	10759
		- 1	17433142 NT	T				10273
RNA	L	EST HUMAN	1 0E-71 AV761217.1	1		T	Г	11/201
9	L	Z	1.0E-71 AY007643.1			T	Т	
	Homo segiens cytochrome c oxidase subunit VIIa-related protein gene, company care		1.0E-71 872380.1			03 36069	П	9429
persists cos	CSNK2A1=casein kinase II (CKII) subunit alpina li lullica i, Colonia	NT	2		4.63	21 35258	41 21721	8641
882 nt	Homo septens hypothesis in the first company (18862 nt)	N	8922811 NT	١		I	47 21/21	8641
	1.0098 (FLJ10998), mRNA	INI	8922811 NI	1.0E-71		1	Т	1
	Homo saplens hypothetical protein FLJ10998 (FLJ10998), mKNA	1			2.21	٦	П	23
,	Homo sapiens myomesin (M-protein) 2 (165kU) (MT CWZ), III WY	2	3,000			21 34946	21421	8340
	Homo saplens glypican-o (Groo) IIInivo, Campion month	N.T	AE4040A7 1	1			20539	7464
	Homo saprata Chock - DNA complete cds	N.	1 0F-71 U80753.1	1		T	Т	1233
	The second of the manual partiel cds	2	1.0E-71 AB011131.1	1.0E-71		I	Т	
	Home satiens mRNA for KIAA0559 protein, pertial cds	ZNI	11426182INI	1.0E-71	1.48	33443	20033	6881
	Homo sablens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN9L2), """	<u>-</u>				T	1	
DONE OF BRUA			1.0E-71 D284/6.1	1.0E-71	2.13	30712	T	4593
	Human mRNA for KIAA0045 gene, complete cus	21	1.00-71 70 21000	1.00-7	2.2	5 29997	5 16995	3835
		N,	AF218904.1	100 71		Γ	Γ.	3738
	Clone UZ 10 0 clinical sector (ATRN) nene exon 19	EST HUMAN	1.0E-71 BE122850.1	1.0E-71	0.8			
	A A F R similar to Homo sapiens chromosome 19					1	Т	
Italiscipis i miso orbini i	no 18 Human Enidermal Keratinocyte Subtraction Library- Opregulated Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest Interest	10101011	1,0E-71 BE122800.1	1.0E-71	0.9	9 29902	16899	3738
Topocointe Homo seplens cDNA	clone 02 15 5' similar to Homo sapiens chromosome is	DOT HIMAN						
	02_15 Human Epidermai Neraumovye Gubudasion Commo				999	28000	16848	3685
The Uprecrulated Transcripts Homo septens CUIVA	Turing salvers of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s	Z	1 0E-71 AF246219.1	1.0E-71	22.5	T	Т	900
	Lamo cardene SNARE protein kinase SNAK mRNA, complete cds	2	1.0E-71 AF246219.1	1.0E-71	6.57	1	Т	200
	Homo sepiens SNARE protein kinase SNAK mRNA, complete Cus		1.0E-/1 AF 118005.	1.05-71	1.56	29769	16764	3590
	Homo sapiens inorganic pyrophosphatase mKNA, complete cus	NT.	10005 4	1.7-30.1	6.08	28982	15874	2757
	Homo sapiens hairy/enhancer-or-spill related with the	NT	7857153 NT	200	1.00		15283	2147
L), mRNA	Homo sepiens riviozatio il ano, par un trapport mointlike (HEYL), mRNA	Z,	0€-71 AB017007.1	1 OE 71	3 1	T	Γ	214/
	Homo sapients i vicer to manual periol ods	NT	1.0E-71 AB017007.1	1.0E-71	183	T	1	13/1
	TOTAL BUILDING I A MANA nadial cds	N.	1.0E-71 AF012872.1	1.0E-71	11.13	J	T	
icte cas	Lorge seniens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cas	2	1.0E-71 AF205880.1	1.0E-71	13.07		Т	1124
	Harmo saniens disabled-2 gene, exons 2 through 15 and complete cas		7,70020	1.0E-/1	1.38	27198	٦	200
	Homo sapiens neuronal cell death-related protein (COCO 1010)	NT	10CONTT	1.05	1.00	26868	13841	655
	contains LOR1.b2 LOR1 repetitive element	EST HUMAN	A 0E-71 AI077927.1	A CE 71	1			
	oy15e03.s1 Soares_seriescent_fibroblasts_NbHSF Homo sapiens curvo curvo minimos				-			
clane IMAGE: 1665916 3' similar to				Value	•	i	ö	S O
		Source	N.	BLASTE	Signal	ō NO.	SEQ ID	SEQ ID
	Lob die Description	Database	Top Hit Acession		Expression	ORF SEQ	Exon	Probe
		Top Hit		Most Similar	~			
	Single Exon Probes Expressed in Flavoure	Exon Probes	Single					

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Table 4
Single Exon Probes Expressed in Placenta

			ſ		01140	/ Wose	/56/
Homo sapiens hect domain and RLD 2 (HERC2), mRNA	ZNT	4 0F-72 5729867 NT		2 28		Ţ	687
ydSte01.71 Sogres tetai liver spiedri INT DS Fruito septema Construction - HUMAN; SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN;	FOT LIMAN	T97047 4					
Homo sapiens zing linger protein zin 195 (zin 35) illinovit, allegan zin 19752 5' similar to	ZT	4.0E-72 AF170025.1		0.68	6 31821	7	558
nono salatria i y punicipa protei 750 ost /750cs) mRNA állernatívely spíced complete cds	4 N I	11034844 N		0.91	3		4943
UV I-B 10032-200806-312-417-B 10057-300-2 (D.11057B20.2), mRNA	EST HOMAN	6.0E-72 BE926845.1		246	6	0 23136	12390
Davogues, 9 1 All Linico L. 1988 April BT0632 Home septent cDNA	EST HUMAN	6.0E-72 BE208545.1			1 38634	5 24931	11945
bacogoo yi Niri NiGC 7 Hamo sapiens cDNA clone IMAGE:2823808 5	EST HUMAN	6.0E-72 BE208545.1	Γ		1 38633	5 24831	11945
INDEPOS A NILL MICE 7 Homo capiens cDNA clone IMAGE:2823808 5	HOMEN	5.0E-72 BF331571.1			5 38253	24676	11519
MRY-BIOSOS 10000-000 COS BIOSOS Homo sapiens CDNA	EST HUMAN	5.0E-72 BF331571.1	Γ		5 38252	24575	11519
AV / 2402 THIS HIGHER SEPARATION BETTA 508 Home septems CDNA	EST HUMAN	5.0E-72 AV724832.1		0.71	3 36797	23203	10166
au80c03.y1 Schneider fetal brain 00004 Homo sepiens cDNA clone iMAGE:2782564 5' similar to TR:089785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;	EST_HUMAN	5.0E-72 AW161274.1	5.0E-72	4.16	35598	22055	8976
AU 128364 N I ZAF Z Fidirio Safricia Contro Contro La Propertione	EST HUMAN	5.0E-72 AU128584.1	5.0E-72	1.62	33607	П	7089
Address applier would in a v., compose one	2	6.0E-72 L11645.1	5.0E-72	2.31	3		1162
Cro-Coord Classes and Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Coord Co	EST HOMAN	5.0E-72 BF333707.1	5.0E-72		26325	13302	65
QV0-CS0010-150800-399-611 CS0010 Homo septemb CDNA	EST_HOMAN	5.0E-72 BF333707.1	5.0E-72				65
CANCAGO 16-10600-300 544 CSO040 Homo septens CONA	EST HUMAN	5.0E-72 BF333707.1	5.0E-72	1.19	26325	13302	2
QV0-CS0010-100900-386-617 CS0010 Homo septiens CDNA	EST HUMAN	5.0E-72 BF333707.1	5.0E-72	1.19	28324		2
Homo sapiens circinosanie z i saginarii i oz rozna	NT	6.0E-72 AL163246.2	6.0E-72	5.7	Ť	7	8578
- 18	EST_HUMAN	7.0E-72 F26269.1	7.0E-72	1.53	<u> </u>		12857
(pseudogene) F 1 MPC 2-prouty itoeth cibre 1/1000051(CD2		\$41694.1	7.0E-72 S41694	. 3	33811	П	7274
Homo sapiens econitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA	NT	4501866 NT	7.0E-72	1.75	30363	17376	4228
Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding milocondrial protein, mRNA	NT	4501866 NT	7.0E-72	1.75	30382	17375	4228
Homo saplens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA	NT	4501866 NT	7.0E-72	1.75	30361	17375	4228
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3.0E-72 U80223.1 NI	3.0E-72 U16308.1 NT 3.0E-72 U80223.1 NT	3.0E-72 U16306.1 NT 3.0E-72 U16306.1 NT 3.0E-72 U80223.1 NT	4.0E-72   19823668 NT   4.0E-72   11434344 NT   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   4.0E-72   A765388.1   EST_HUMAN   A.0E-72   A7657857 NT   EST_HUMAN   A.0E-72   A7657057 NT   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7657057 NT   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.0E-72   A7673623.1   EST_HUMAN   A.
	3.0E-72 U16306:1 NT	3.0E-72 U16306.1 NT 3.0E-72 U16306.1 NT	4.0E-72   19823668 NT   4.0E-72   11434344 NT   4.0E-72   AW836230.1   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUM
3.0E-72 U16306.1 NT	3.0E-72 AA723823.1 EST_HUMAN anosavo.s I Soares resus_ 1		4.0E-72   8923668 NT   4.0E-72   4.0E-72   11434344 NT   4.0E-72   AW836230.1   EST_HUMAN   6.0E-72   AV836230.1   EST_HUMAN   6.0E-72   AA465388.1   EST_HUMAN   6.0E-72   AA465388.1   EST_HUMAN   6.0E-72   AA465388.1   EST_HUMAN   6.0E-72   AA465388.1   EST_HUMAN   6.0E-72   AA66538.1   EST_HUMAN   6.0E-72   AA66538.1   EST_HUMAN   6.0E-72   AA665388.1   EST_HUMAN   6.0E-72   AG65388.1   EST_HUMAN   6.0E-72   AG65388.1   EST_HUMAN   6.0E-72   AG65388.1   EST_HUMAN   6.0E-72   AG65388.1   EST_HUMAN   6.0E-72   AG65388.1   EST_HUMAN   6.0E-72   AG65388.1   EST_HUMAN   A.0E-72   AG65388.1   EST_HUMAN   A.0E-72   AG65388.1   EST_HUMAN   A.0E-72   AG65388.1   EST_HUMAN   A.0E-72   AG67057   NT   A.0E-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6-72   AU6
3.0E-72 AA723823.1 EST_HUMAN 3.0E-72 U16306.1 NT	3.0E-72 6031976 NT Homo sapiens pro-B-cell coorny-enhancing leaver (r. De-7) 3.0E-72 AA723823.1 EST_HUMAN ah63a06.s1 Soares_testis_NHT Homo sapiens cDNA clo	3.0E-72 5031976 NT Homo saplens pre-B-cell coony-enhancing lacus (1921)	0.87 4.0E-72 8823668 NT 0.57 4.0E-72 11434344 NT 0.54 4.0E-72 AW836230.1 EST_HUMAN 0.54 4.0E-72 AW836230.1 EST_HUMAN 0.54 4.0E-72 AW836230.1 EST_HUMAN 0.54 4.0E-72 AA465388.1 EST_HUMAN 0.54 4.0E-72 AA465388.1 EST_HUMAN 0.54 4.0E-72 AA465388.1 EST_HUMAN 0.54 4.0E-72 AA465388.1 EST_HUMAN 0.55 4.0E-72 AA465388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E-72 AA65388.1 EST_HUMAN 0.55 4.0E
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4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T89421.1 EST_HUMAN 4.0E-72 T89910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 AJ277546.2 NT 3.0E-72 AA723823.1 EST_HUMAN 3.0E-72 U168306.1 NT	4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T89421.1 EST_HUMAN 4.0E-72 T89910.1 EST_HUMAN 4.0E-72 T89910.1 EST_HUMAN 4.0E-72 AJ277546.2 NT 3.0E-72 AJ277546.2 NT 3.0E-72 AA723823.1 EST_HUMAN	4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T697057 NT 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 AJ277548.2 NT 3.0E-72 AJ277548.2 NT	0.87 4.0E-72 8823688 NT T T T T T T T T T T T T T T T T T
4.0E-72 AI248795.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T879421.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 AI277548.2 NT 3.0E-72 AA723823.1 EST_HUMAN 3.0E-72 U16306.1 NT	4.0E-72 AI248795.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN	4.0E-72 AI248795.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T8910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN	0.87 4.0E-72   8923668 NT   Homo septents injuduration promise (15EC101.1), m   0.57 4.0E-72   11454344 NT   Homo septents SEDIO (S. cerevisiae)-like 1 (SEC101.1), m   0.54 4.0E-72 AW836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septents cD1   0.54 4.0E-72 AW836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septents cD1
4.0E-72 AV485398.1 EST_HUMAN 4.0E-72 AA465398.1 EST_HUMAN 4.0E-72 AA465398.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 AA277548.2 NT 3.0E-72 AA2723823.1 EST_HUMAN 3.0E-72 INT 3.0E-72 AA2723823.1 EST_HUMAN	4.0E-72 AV465398.1 EST_HUMAN 4.0E-72 AA465398.1 EST_HUMAN 4.0E-72 AA465398.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 H79421.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 5.0E-72 AJ277548.2 NT 3.0E-72 AA723823.1 EST_HUMAN	4.0E-72 AV485388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 AA465388.1 EST_HUMAN 4.0E-72 T89421.1 EST_HUMAN 4.0E-72 T8910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN 4.0E-72 T81910.1 EST_HUMAN	0.877 4.0E-72   8923668   NT   Homo septents injuduration production   1 (SEC10L1), m   1494344   NT   Homo septents SICIO (S. cereptistae)-tilled 1 (SEC10L1), m   16031 T0023-200100-012-d11 LT0023 Homo septents CD
4.0E-72 AV835230.1 EST_HUMAN   F.   4.0E-72 AV835230.1 EST_HUMAN   F.   4.0E-72 AA465388.1 EST_HUMAN   F.   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 T781910.1 EST_HUMAN   4.0E-72 T81910.1 EST_HUMAN   4.0E-72 T81910.1 EST_HUMAN   5.0E-72 AA2723623.1 EST_HUMAN   8 A.0E-72 AA2723623.1 EST_HUMAN   9 3.0E-72 U16306.1 NT	4.0E-72 AW836230.1 EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN	4.0E-72 AW885230.1 EST_HUMAN   4.0E-72 AV885230.1 EST_HUMAN   4.0E-72 AL248798.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 AA465388.1 EST_HUMAN   4.0E-72 T69421.1 EST_HUMAN   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057 NT   4.0E-72 T697057	0.87 4.0E-72 8923668 NT Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), m
4.0E-72   11334344   N1  4.0E-72   AW836230.1   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HU	4.0E-72   AW836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AW836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AW836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV836230.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023-200100-012-d11 LT0023 Homo septens cDI   4.0E-72   AV465388.1   EST_HUMAN   RC3-LT0023	4.0E-72   11334344   N1 4.0E-72   AW836230.1   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HUMAN   EST_HU	

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Table 4
Single Exon Probes Expressed in Placenta

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Exan SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
Ģ			Value		Source	
5837 18831		1.12	3.0E-72	4759093	NT	Homo sapiens semaphorin W (SEWAW) mRNA
19281	32613	1.94	3.0E-72	AF073367.1	TN	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
19281	32614	1.94	3.0E-72	AF073367.1	T	
6295 19468	32822	4.53	3.0€-72	AB029004.1	NT	
6295 19468	32823	4.53	3.0E-72	AB029004.1	NT	Hemo eapiens mRNA for KIAA1081 protein, partial cds
19903	33296	4.1	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
20817	3.4307	s 2	200	10001	1	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
21450	3,4072	R 43	2001	E004000	1	Libert (half) and outstantinguist pount (ann) genes, compact das
23680	37290	109	3.05-72	XORORO 1	27	Homo senens S100412 case for Oddronilla ( 1905) n. member 3 (NATIOS), mixina.
25453	32018	2.18	3.0E-72	AB011399.1	N .	Homo sapiens gene for AF-6, complete cds
10261	32690	1.38	2.0⊑-72	11426071	T	Homo sepiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
22373	35923	0.64	2.0E-72	BF308580.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
22373	35924	0.64	2.0E-72	BF308580.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
24057	37691	5.46	2.0E-72	AA789277.1	EST HUMAN	e)28b09.s1 Soares_tests_NHT Home septens cDNA clone 1391609.3' similar to gb:X02067 H.saptens mRNA for 7SL RNA ossudociene (HUMAN):
26515	31699	3.39	2.0€-72	AF182714.1	NT	Rettus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
15273	28394	8.14	1.0E-72	AA846225.1	EST_HUMAN	ei83d02.s1 Soares_parathyrod_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395.31
18075	32384	3.54	1.0E-72	7657676		Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
19847	33237	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
19847	33238	1.22	1.0E-72	11321578	TN	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
26832	33319	1.29	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NPD Homo sapiens cDNA clone NPDAIE11 5
20870	34366	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo saplens cDNA
20870	34387	3.5	1.0E-72	BE175434.1	NAWUH_TSE	RC4-HT0578-170300-012-g02 HT0578 Homo saplens cDNA
22830	36408	7.37	1.0E-72	AF222742.1	NT	Homo sepiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
22830	36409	7.37	1.0E-72	\F222742.1	NT	
14641	27723	1.17	9.0E-73	AW374868.1	EST_HUMAN	MR0-CT0083-071099-002-h11 CT0083 Hamo saplens cDNA
19340	32687	0.92	9.0E-73	11525883		Homo sepiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
24262		24.49	9.0E-73	11424099		Homo saptens ribosomel protein L13a (RPL13A), mRNA
14228	27285	0.73	8.0E-73	W071755 1	EST HIMAN	ws55c06.x1 NCI_CGAP_Ern25 Homo eaplens cDNA clone IMAGE:2501098 3' similar to TR:Q59050
18892	32184	0.98	8.0E-73	4505798	NT	Homo sapiens phosphalidylinosital 3-kinase, class 2, alpha polypepiide (PIK3C2A) mRNA
	$\omega$	Exon SEQ ID NO: 18831 19281 19281 19488 19903 24057 22373 22373 22373 22373 18075 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 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19847 19847 19847 19847 19847 19847 19847 19847 19847 19847 19	EXON ORF SEQ Express SEQ ID NO: Signal 19281 32613 19281 32814 19281 32814 19281 32822 19468 32822 19468 32823 32266 228373 35924 22373 35924 226373 32381 22680 32281 19847 33238 19847 33238 18847 33238 22680 39499 15273 32394 18075 32384 18075 32384 18075 32384 18075 32384 18075 32384 18075 32384 18075 32384 226832 33319 226832 33319 226832 33499 14228 23830 38409 24367 34366 22830 38409 14228 23830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 22830 38409 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23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 23840 2384	Exon SEQ ID ORF SEQ Expression (T SEQ ID ID NO: Signal II 1.12 19281 32613 1.94 19281 32822 4.53 19903 32286 4.1 20817 34907 2.01 2.0817 34907 2.01 2.0817 34907 2.01 2.0817 34907 2.01 2.0817 34907 2.01 2.0817 34907 2.01 2.081 3.5923 0.64 2.2373 35922 0.64 2.2373 35922 0.64 2.2373 35924 0.64 2.2373 35924 0.64 2.2373 35924 0.64 2.2373 35924 0.64 2.2373 35924 0.64 2.2373 35924 0.64 19075 32384 3.54 19847 33238 1.22 19847 33238 1.22 19847 33238 1.22 19847 33238 1.22 19847 33238 1.22 19847 33238 1.22 19847 33238 1.22 19847 33238 1.25 1.26 2.2830 38408 7.37 1.26 2.2830 38408 7.37 1.28 2.2830 38408 7.37 1.28 1.2840 3.54 1.29 2.2830 38408 7.37 1.28 1.2840 3.54 1.29 2.2830 38408 7.37 1.28 1.2840 3.2887 0.92 2.2830 38408 7.37 1.17 1.1841 2.7723 2.117 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 38408 7.37 1.17 1.1841 2.7723 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.2830 3.2887 0.92 2.28807 0.92 2.28807 0.92 2.28807 0.92	Exon NO:         ORF SEQ ID NO:         Expression Signal         Most Similar (Top) Hit Value         Top Hit Top Hit Value           18831         32813         1.12         3.0E-72 19281         32813         1.94         3.0E-72 2.0E-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.0F-72 2.	Exon NC:         ORF SEQ ID NO:         Expression Signal         Most Simillar (Top) Hit Value         Top Hit Acession Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Database Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Database Value         Top Hit Acession Value         Top Hit Acession Database Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Database Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Hit Acession Value         Top Accession Value         Top Accession Value         Top Accession Value         Value Value         Value Value         Value Value         Value Value         Value Value         Value Value         Value Value         Value Value         V

Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA	Z	4502582 NT	Z.0E-/3	2.03	04487	10460	G4.70
Human beta globin region on chromosome 11	NT	2.0E-73 U01317:1	2.0E-73	1.49		15502	333
RC3-NN0066-270400-011-c04 NN0066 Homo septens cDNA	EST_HUMAN	2.0E-73 AW 898081.1	2.0Ε-73	9.67		15141	2000
Homo sapiens BASS1 (BASS1) mRNA, partial cds	NT	2.0E-73 AF139897.1	2.0Ε-73	1.57	27115	14050	874
RC3-NN0066-270400-011-c04 NN0066 Homo sepiens cDNA	EST_HUMAN	3.0E-73 AW 898081.1	3.0E-73	2.05		25732	13122
Homo sapiens chromosome 21 segment HS21C046	NT	3.0E-73 AL163246.2	3.0E-73	3.04		26730	13118
		3.0E-73 A1004040.1	3.0E-73	1.82		24897	11910
RC6+HT0678-290600-013-H10 HT0678 Homo saplens cDNA		3.0E-73 BE711238.1	3.0E-73	1.41	37971	24330	11281
RC6-HT0978-290600-013-H10 HT0978 Homo sepiens cDNA	EST_HUMAN	3.0E-73 BE711238.1	3.0E-73	1.41	37970	24330	11261
H.sapiens SH3GLP2 pseudogene, 5' end	NT	3.0E-73 X99660 1	3.0E-73	1.45		24010	10927
AV729428 HTC Homo saplens cDNA clone HTCAAF071 5'	EST_HUMAN	3.0E-73 AV728428.1	3.0E-73	0.73	35579	22037	8958
AV728428 HTC Homo saplens cDNA clone HTCAAF071 5'	EST_HUMAN	3.0E-73 AV729428.1	3.0E-73	0.73	35578	22037	8958
2n95604.s1 Stratageno fotal retina 937202 Homo sapiens cDNA done iMAGE:565950 3' similar to spical substance of the second stratageno fotal retina 937202 Homo sapiens cDNA done iMAGE:565950 3' similar to spical substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance of the second substance o	EST_HUMAN	3.0E-73 AA136403.1	3.0E-73	0.73	33398	19990	6837
Homo sapiens heme-binding protein (HEBP), mRNA	NT	11436913 NT	3.0E-73	1.34	28166	15054	1911
Homo saplens heme-binding protein (HEBP), mRNA	NT	11435913 NT	3.0E-73	1.34	28165	15054	1911
Homo septens HELG protein (FAM4A1), mRNA	NT	11422159	4.0E-73	2.05	31439	18571	5368
QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA	EST_HUMAN	6.0E-73 BE166574.1	6.0E-73	3.42	33867	20405	7323
Homo sapiens chromosome 21 segment HS21C018	NT	6.0E-73 AL163218.2	6.0E-73	3.04		13387	Ŕ
Homo sapiens chromosome 21 segment HS21C082	NT	7.0E-73 AL163282.2	7.0E-73	1.29		18187	5059
	NT	7.0E-73 AL 163206.2	7.0E-73	0.7	29559	16545	3373
Homo sepiens hypothetical protein FLJ20309 (FLJ20309), mRNA	NT	8923280 NT	7.0E-73	1.61	27376	14321	1157
Homo septens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	NT	11418189 NT	8.0E-73	4.66	31986	25560	12842
Homo sepiens DNA for Human P2XM, complete cds	Z	8.0E-73 AB002059.1	8.0E-73	1.2	32044	25403	12598
Homo sepiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds	NT	8.0E-73 AF084520.1	8.0E-73	1.49	38690	24986	12001
Homo seplens trensition protein 1 (during histone to protamine replacement) (TNP1) mRNA	N	4507628 NT	8.0∈-73	0.47	37490	23867	10834
	NT	8.0E-73 X91940.1	8.0E-73	0.51	36770	23172	10134
	TV		8.0E-73	1.76	36571	22980	9941
Homo sapiens interleukin 12 receptor, beta 1 (IL 12RB1), mRNA	NT.	11526037 NT	8.0E-73	1.76	36570	22980	9941
bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletel gamme-ectin mRNA, complete cds (MOUSE)	EST_HUMAN	8.0E-73 BE019300.1	8.0E-73	4.35	36188	22618	9553
Homo sepiens vecuolar ATPase Isoform VA68 mRNA, complete cds	TN	8.0E-73 AF113129.1	8.0E-73	2.1	34890	21369	8287
Homo sepiens lysozyme hamolog (LOC57151), mRNA	NT	11426469 NT	8.0E-73	6.29	33250	Г	6702
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:

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Table 4

Single Exon Probes Expressed in Placenta

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Table 4

Single Exon Probes Expressed in Placenta

12841	9444	3407	2004	6036	6036	769	12045	12045	11736	9699	6490	1824	12599	11339	11309	11309	10715	10715	10637	9732	9732	7984	6839	6839	6810	6567	6567	4665	3640		3640	Probe SEQ ID 1
25559	22560	16577	15144	19219	19219	13940	25026	25026	23922	22748	19656	14973	15141	24402	24374	24374	23748	23748	23671	22797	22797	21033	18992	19992	18770	19729	19729	17693	16804		16804	SEQ ID
31985	36123	29592	28249	32542	32541	26985	38732	38731	37647	36316	33019	28068		38051	38018	38017	37356	37355	37281	36371	36370	34546	33401	33400	33160	33107	33106		29817		29816	ORF SEQ ID NO:
4.73		1.83	4.96	1.73		4.83		1.34	3.74	1.22	1.19	3.52	4.32	1.44	2.91	. 2.91	85.1	1.38	1.31	0.54	0.54	1.01	1.87	1.87	5.46	0.69	0.59	1.31	0.68		0.68	Expression Signal
Γ					Γ		Γ					Γ		П	2.0Ε-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73				2.0E-73					2.05-73	20E-73		2.0∈-73	Most Similar (Top) Hit BLAST E Value
7.0E-74 BE266305.1	7.0E-74 BE967432.1	7.0E-74 AL163246.2	7.0E-74 AJ001889.1	8.0E-74 S83194.1	8.0E-74 S83194.1	4557428 NT	X77225.1	9.0E-74 X77225.1	1.0E-73 BE385477.1	1.0E-73 AI147427.1	1.0E-73 BE151283.1	1.0E-73 AU121585.1	2.0E-73 AW 898081.1	2.0E-73 AB028982.1	4557612 NT		11496980 NT			AF19834	2.0E-73 AF198349.1	2.0E-73 M94048.1	11431471		2.0E-73 AB046811.1	2.0E-73 AF086824.1	2.0E-73 AF086824.1	20E-73 AL163283.2	7659539 NT		7669539 NT	Top Hit Acession No.
EST HOMAN	EST HUMAN	N	Z	Z	Z	BNT	NT	Z	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	NT	NT	NT	NT	NT	NT	Z	NT	NT		NT	NT	Z	ZT	3	NT		NI	Top Hit Database Source
00 12 122 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1	IMAGE:3535855 5'	MAGE:3932997 5'	Homo septens NAGZU gene, excit to	I GOOD A VII GOOD	Ca2+/Calmodulin-dependent protein Minasa iv Minasa isoform fraits brain mRNA, 3429 of	riomo agrieris Cude-like 4 (Cude-4) ilimino. Il binese tenfera freta brein mRNA 3429 nti	H. SADIENS TIKNA TOT I FILE	H. Septens month out from	to House sabreils on the cities	MER22 repetitive element:	CWI-TI 0202-11 135-042-110 110-022-1-110 CDV done IMAGE:1839837 5 similar to contains element	AU121989 MAWIMA I Dollo depicia colar cicia matina colar	RCS-NNOUBB-Z/0400-011-004 NNV0000 FILLIO SELECTION	Homo saplens mRNA for KIAA 1009 protein, partials cos	Homo sapiens galactosyceramidase (Krappe disease) (GALC), ilinnya	Homo sapiens galactosyceramidase (Krabbe disease) (GALC), mixiwa	Homo sapiens supervilin (Svil.), transcript variant i, mrvva	Homo sapiens supervilin (SVIL), transcript variant 1, mixing	Homo sapiens giuratriche sylluterase (COO) il DNIA	Gailts Gailts Lacht protein (Cacht) IIININ, complete cas	Gallus gallus Dach2 protein (Dech2) mRNA, complete cos	Human peripheral myelin protein 22 minuw, complied cus	Homo sapiens inteneukin 4 receptor (IL4A), IIIVIVA	Homo sepiens interieurin + receptor (IL+A), IIINIVA	Homo septens mkny for knyy 1991 protein, perual cus	MUS musculus maracente acung count masse (count masses, comprose cos	Mus musculus morzeo niteracing cuton vinase (Crirk) mBNA complete ods	Homo capiens chromosome 21 segment no21 coop	mRNA	Homo saplens Parkinson disease (autosomal recessive, Juvenile) 2, parkin (PARK2), transcript variant 3,	Homo sepiens Perkinson disease (autosomai recessive, juvenile) 4, pervir ("Anna), uensonipi verenii vi mRNA	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

Homo sapiens rur gene	2	4.UE-/4[AJUU69/6.1	4.UE-/4	1.10	26/40	CZ0C1	2488
Homo sapiens mRNA for KIAA1168 protein, partial cds	ZT	ļ	4.DE-74	1.32	28463	15338	2201
Homo sapiens proteasome (prosome, macropain) subunit, bela type, 1 (PSMB1) mRNA	T	4506192 NT	4.0E-74	96'6	28391	15270	2134
Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA	NT	4506192 NT	4.0E-74	9.96	28390	15270	2134
Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, ecomplete cdc)	NT	4.0E-74 AB026898.1	4.0E-74	3.07	28263	15158	2018
Homo septens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	NT	4.0E-74 AB026898.1	4.0E-74	3.07	28262	15158	2018
Homo saplens mRNA for KIAA1019 protein, partial cds	NT	4.0E-74 AB028942.1	4.0E-74	10.3	27116	14051	875
Homo sapiens DNA for amyloid precursor protein, complete cds	NT	4.0E-74 D87675.1	4.0E-74	3.31	26542	13507	290
Homo sepiens cell adhesion molecule with homology to L1 CAM (close homologue of L1) (CHL1), mRNA	NT ·	5729766 NT	5.0E-74	1.36	37801	24184	11090
H.sapiens mRNA for HIP-I	TN	5.0E-74 Y09420.1	5.0E-74	1.67	37687	24053	10973
H.sapiens mRNA for HIP-I	TN	5.0E-74 Y09420.1 ·	5.0E-74	1.67	37686	24053	10973
Homo saplens hypothetical protein FLJ13222 (FLJ13222), mRNA	NT	11345483 NT	5.0E-74	2.33	34828	21308	8226
Homo septens KIAA0718 gene product (KIAA0718), mRNA	NT	7662263 NT	6.0E-74	3.59	33593	20171	7035
Homo sepiens interleukin 4 receptor (IL4R), mRNA	TN	11431471 NT	5.0E-74	2.94	32534	19213	6030
Horno sapiens interleukin 4 receptor (IL4R), mRNA	NT	11431471 NT	5.0E-74	2.94	32533	19213	6030
Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products	NT	4507866 NT	5.0E-74	8.1	32462	19147	5961
H.sapiens mRNA for TPCR16 protein	NT	5.0E-74 X89670.1	5.0E-74	12.5	32413	19099	5910
Homo sepiens phosphatidylinositol glycan, class L (PIGL), mRNA	TIN	11425417 NT	5.0E-74	1.92	31736	18720	6623
PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA	EST_HUMAN	5.0E-74 AW362756.1	5.0E-74	4.96		15882	2767
	EST_HUMAN	5.0E-74 AW020986.1	5.0E-74	1.93	27166	14103	928
Homo sapiens actin filament associated protein (AFAP), mRNA	TIN	11056013 NT	6.0E-74	3.49	31695	18680	5481
hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332.3'	EST_HUMAN	6.0E-74 BE048846.1	6.0E-74	1.22	29969	16965	3805
hr54e11.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:31323323'	EST_HUMAN	6.0E-74 BE048846.1	6.0E-74	1.22	28968	16965	3805
UHH-BIO-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'	EST_HUMAN	6.0E-74 AW01:1039.1	6.0E-74	0.97			2927
UHH-BI0-aah-h-03-0-UI,s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:27083653'	NAWOH_TS3	6.0E-74 AW01.1039.1	6.0E-74	0.97		16104	2927
601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'	NAMUH_TS3	6.0E-74 BE388260.1	6.0≅-74	16.52	28650	15521	2390
601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5*	NAWOH_TS3	6.0E-74 BE388260.1	6.0Ε-74	15.52	28649	15521	2390
xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700836 3'	NAMUH_TS3	6.0E-74 AW263177.1	6.0E-74	1.03	27893	14809	1656
Homo seplens S164 gens, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gens, partial cds	TN	6.0E-74 AF109907.1	6.0E-74	3.65	27368	14311	1146
Top Hit Descriptor	Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ID NO:	SEQ (	NO: SEQ ID
	Ton H		Most Similar			E Š	Probe
enigis enon i conce enprocessor in contra	1000	9.00					

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Table 4
Single Exon Probes Expressed in Placenta

		1,000	Γ		34/20	26 21208	8126
Homo sepiens mRNA for KiAA1395 protein, partiel cds	NT.	2 0E-74 AR037816 1		400		T	7252
601557524F1 NIH_MGC_58 Homo septens cuna cone intrace: 302/349 3	EST HUMAN	RF0307			1	Т	908/
	11439587 NT		7			Т	
Indino september 102-10 Indiana ( 100 30 )	11439587 NT		20E-74	8 2.78	I	Т	
	11439587 N		2.0E-74	1.77	92519	٦	6017
Home serions PDZ-73 nodeln (PDZ-73/NY-CO-38), mRNA	11439367 N	Ţ		8 1.77	6 32518	7 25816	6017
L	1	111/39	I		3 32419	9 25813	6919
1	EST HIMAN	2.0E-74 AL300UBZ.1	T		Γ	9 18245	5119
	1	2.0E-/4 AL3GOVAZ-1	T		Γ	9 18245	5119
	i k	AL OFFICE A	Ţ		Γ	8 15789	2668
PT2.1_15_G11.r tumor2 Homo septens cDNA 3	EST HUMAN	A155773	T		Ţ	Т	1625
	4885198 NT		2.0E-74	10 45			
homolog) (EGFR) mRNA	4885198 NT		2.0E-74	10.45	7 27861	5 14777	1625
	EST_HUMAN	2.0E-74 AI0505:28.1	2.0E-74	4.1	27501	3 14430	1273
wx51e07 x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN		2.0E-14 AF020082.1	2.02-74	1.83	4 27424	14364	1202
Human endogenous retrovirus HERV-X-T47D	T	10000			Ī	14163	980
Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (SAPU), mxvx	7669491 NT		١		T	Т	88
Homo sapiens glyceredemyde - priospirate deriyal syr according to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of	7669491 NT	76697			T	T	1
L	EST_HUMAN	3.0E-74 AA601493.1	3.0E-74		1	Т	105.45
	EST_HUMAN	3.0E-74 M78984.1	3.0E-74	2.32	36282	22714	9577
I Willy application and the second	1N 2169968		3.0E-74	0.62	36394		8773
Umno sanisms actin-related protein 3-beta (ARP3BETA),	EO LONOR	AA3003	3.0E-74	3.53		21828	8747
		45043	4.0E-74	1.12	31272	18307	6185
hydratase (trifunctional protein), beta subunit (HADHB) mRNA  Homo sentens hydroxyacu-Coenzyme A dehydrogenase/3-ketbacy-Coenzyme A thiolase/enoyi-Coenzyme A	4504326 NT	45043	4.0E-74	1.12	31271	18307	5185
Homo sapiens hydroxyscyl-Coenzyme A dehydrogenasal3-ketoacyl-Coenzyme A thiolase/encyl-Coenzyme A	2	4.0E-74 AB040938.1	4.0E-74	1.03	31224	18258	5133
- 1	7	217227 1	4.0E-74 Z17227	1.07		17870	4735
Homo sentens mRNA for transmebrane receptor protein		2812997	4.0E-74	1.86		17814	4679
Homo seriens KIAA0569 gene product (KIAA0569), mRNA	2 2	4.0E-74 AL 163247.2	4.0E-74	1.29	30315		4174
Homo sapiena chromosome 21 segment HS21C047	N	4.0E-74 AL163210.2	4.0E-74	1.1	29795		3616
Homo services chromosome 21 segment HS21C010	Z	4.0E-74 AJ006976.1	4.0E-74	6.22	29345	16335	3160
Homo centenc PI P nene			<b>V 2 1 3 3 3 3 3 3 3 3 3 3</b>				
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	m = =	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID
	- ` 						

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1							
Probe SEQ ID NO:	SEQID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top HI: Acession	Top Hit Database Source	Top Hit Descriptor
9582	2 22724	36294	5.27	2.0E-74	2.0E-74 AL163204.2	T	Hamo sapiens chramosame 21 segment HS21 0004
12526			2.87	20E-74	20E-74 AA196181.1	EST_HUMAN	zp98a06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
13169			1.16	2.0E-74	2.0E-74 BF002855.1	EST_HUMAN	
	64 13293	26308	1.5	1.0E-74	7657334 NT	'I	Homo saplens Misshapen/NiK-related kinase (MINK), mRNA
347		26586	3.71	1.0E-74	1.0E-74 AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-105 ST0234 Homo saptiens cDNA
512	2 13708	26734	1.8	1.0E-74	8922829 NT	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
519	9 13712	26739	2.59	1.0E-74 X02344)1	X02344)1	NT	Homo sapiens bela 2 gene
614	4 13803	26823	1.28	1.0E-74	4508020 NT	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
8 29 4	13984	27038	0.86	1.0E-74	1.0E-74 AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partiel cds
1024	4 14195		2.26	1.0E-74	1.0E-74 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2301			6.03	1.0E-74	1.0E-74 AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3209	0 16383	29394	2.82	1.0E-74	4768697 NT	NT	Homo sapiens mennosidase, elpha, class 2A, member 1 (MAN2A1), mRNA
3460	16627		1.29	1.0⊑-74	1.0E-74 AA258549.1	EST HUMAN	zr60c01.r1 Soares_NhHMP::_S1 Homo sapiens cDNA clone IMAGE:667776 5'
34 88	16627	29647	1.29	1.0E-74	1.0E-74 AA258549.1	EST_HUMAN	z/60c01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5
4031	Γ	Γ	0.84	1.0E-74	4504116 NT	3	Homo septens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4031	17187	30198	0.84	1.0E-74	4504116 NT	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4075	Π	30237	5.41	1.0E-74	1.0E-74 AL163268.2	4	Homo sapiens chromosome 21 segment HS21C068
4175	5 17326	30316	0.85	1.0E-74	1.0E-74 BE083030.1	EST_HUMAN	RC2-BT0642-270300-019-f06 BT0642 Homo sapiens cDNA
4383	17575	20508	0 0 7	200	1 00 74 00 467750 1		hz/3h08.x1 NCI_CGAP_Lu24 Horno saplens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12
88 44			1.29	1.0E-74	1.0E-74 M8991411	Z	Human neurofibromin (NF1) gene, complete cds
7804			1.05	1.0E-74	11417977 NT	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8246	6 21328	34844	1.27	1.0E-74	1.0E-74 BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8246	e 21328	34845	1.27	1.0E-74	1.0E-74 BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Hamo sapiens cDNA clone IMAGE:3456260 5'
9005	5 22084	35627	7.81	1.0E-74	1.0E-74 AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9034	4 22113	35656	0.67	1.0E-74	1.0E-74 BF351851.1	EST_HUMAN	MR0-HT0559-230500-021-a03 HT0559 Homo sapiens cDNA
10445	Π	Γ	0.65	1.0E-74	1.0E-74 AJ251550.1	N	Homo saplens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10445	5 23480	37087	0.65	1.0E-74	1.0E-74 AJ251560.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10699	9 23732	37337	1.77	1.0E-74	11420549 NT	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
12154	4 25124	38826	1.94	1.0E-74	11417856 NT	T	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12238	8 25182		4.97	1.0E-74	11417856 NT	NT	Homo saplens glutathlone S-transferase theta 2 (GSTT2), mRNA
12386	6 15433	28566	1.61	1.0E-74	1.0E-74 AB002069.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12925	5 25610	•	1.38	1.0E-74	1.0E-74 AF240786.1	Z	Homo septens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) to genes, complete cds

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Single Exon Probes Expressed in Placenta

5365	4283	3833	3431	3431	3258	3086	2494	2180	<del>1</del> 883	1028	1027	10924	8689	6898	6389	5646	5646	2910	1805	471	115	10439	9573	9395	9395	9317	9109	11780	2395		12552	2709	Probe SEQ ID NO:
18568	17428	16993	16599	10599	16432	16262	16621	16315	15027	14198	14198	24007	20048	20048	19568	18840	18840	16088	14954	13666	13346	23474	22715	22470	22470	22393	22188	24770	15526		25375	15827	Exan SEQ ID NO:
31434	30418	29995	29617	28010	29449	29279	28740	28444	28134	27256	27256	37642	33459	33458	32929	32121	32120	29101	28048		26973	37078	36283	36035	36034	36944	35731	38466	28654				ORF SEQ
1.15	2.92	0.6	0.93	0.93	1.09	0.96	4.39	1.44	2.23	3.59	3.6	10.62	1.4	1.4	5.18	0.68	0.68	5.64	1.08	1.68	2.1	2.64	1.1	0.47	0.47	0.77	1.09	1.39	1.25		3.07	6.1	Expression Signal
3.0E-75	3.0E-75	3.0∈-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	, 3.0E-75	3.0E-75	3.0E-76	3.0E-75	3.0E-75	4.0E-76	4.0E-75	4.0E-75	4.0Ε-75	4.0E-75	4.0E-76	4.0E-75	4.0E-76	4.0E-75	4.0E-75	5.0E-75	5.0E-75	5.0E-75	5.0E-75	5.0E-75	5.0E-75	6.0E-75	6.0E-76		8.0E-76	8.0E-75	Most Similar (Top) Hit BLAST E Value
11420956 NT	D87675.1	3.0E-75 M72383 1			3.0E-75 AB011153.1	3.0E-75 AL163201.2	4759153 NT	4507334 NT	3.0E-76 AB011153.1	3.0E-75 AF157623.1	3.0E-75 AF157623.1	7669505 NT	11417946 NT	11417946 NT	5579457 NT	11417948 NT	11417948 NT	4.0E-75 BE409464.1	4.0E-75 AW897230.1	4.0E-75 N36757.1	4.0E-75 BE081333.1	5.0E-75 Al638623.1	5.0E-75 BF690254.1	5.0E-75 BE561655.1	5.0E-75 BE561655.1	5.0E-75 AA132611.1	5.0E-75 BE272825.1	6.0E-75 BE791831.1	6.0E-75 AI817415.1		8.0E-76 AL163202.2	8.0E-75 AF176228.1	Top Hit Acession No.
TNT	NT	TN	TN	TN	TN	NT	NT	NT	NT	NT	NT	TN	TN	TN	TN	TN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NAMUH_TS3	EST_HUMAN		TN	NT	Top Hit Database Source
Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA	Homo sepiens DNA for amyloid precursor protein, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calclum-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Homo septens mRNA for KIAA0581 protein, partial cds	Homo sapiens chromosome 21 segment HS21 C001	Homo sepiens synaptosomal-associated protein, 29kD (SNAP29) mRNA	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Horno saplens mRNA for KIAA0581 protein, partial cds	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds		Homo saplens myosin, heavy polypeptide 1, skeletal muscle, edult (MYH1), mRNA	Homo saplens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo septens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo sapiens NIPSNAP, C. elegens, homolog 1 (NIPSNAP1), mRNA	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5	CM0-NN0057-150400-335-e11 NN0057 Homo sapiers cDNA	yx90h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268055 5'	QV1-BT0632-210200-079-e02 BT0632 Homo saplens cDNA	t31c12x1 NCI_CGAP_GC8 Homo sapions cDNA clans IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20.1 KD PROTEIN;	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'	601346909F1 NIH_MGC_8 Homo saplens cDNA done IMAGE:3887458 5'	801346909F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3687458 5'	2017e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'	601126068F1 NIH_MGC_9 Homo sapiens oDNA clone IMAGE:2889865 5'	601586109F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3840130 6	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);	wk38a08.x1 NCI_CGAP_Pr22 Homo saplens cDNA done IMAGE:2417654 3' similar to ob:M14123_cds4	Homo sapiene chromosome 21 segment HS21C002	Homo sapiens DNA cylosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds	Top Hit Descriptor

2486	45	45	12440	11351	11122	9628	962B	8609	7762	7762	3012	2377	8950	5790	9880	9185	7800	7800	7285	7285	6909	6909	6637	6637	5365	NO:	
8 15613	Г	5 13284	18502	24413	24194	- 1	22683	21689	П	20821	П	15508	22029	18982	22920	22263	20856	20856	20368	20368	20224	20224	19798	19796	18558	NO:	Exon
3	26293	26292	31538	3 38067	4	36254	36263	<u>v</u>	34312	34311	3 29213	28635	35570		36504	П		34346	.33822	33821	33655	33654	33186	33185	31435	iD NO:	ORF SEQ
0.94		2 0.89	8 1.97		6.68			3.12	0.64		2.95	10.98	1.36	1.34			2.66	2.66	4.12	4.12	1.57	1.67	0.59	0.59	1.16	Signal	Expression
Γ														T								3.0E-76	T	Γ		BLAST E Value	(Top) Hit
0.01-101-001-001	9.0E-76 A1652648.1	9.0E-76 AI652848.1	1.0E-/5 BE894194.1	1.0E-75 AF223391.1	.0E-/3 AA0043//	0E-75 BF313645.1	.0E-75 BF313645.1	1.0E-75 AA399270.1	0E-75 BE082528.1	.0E-75 BE082528.1	.0E-76 X62221.1	1.0E-76 AW168135.1	2.0E-75 AI311783.1	2.0E-75 AV /34650.1	181 27707#11.							11526319 NT	3.0E-75 AF123074.1	3.0E-/6 AF123074.1	IN OCEUZALL	N.	Top Hit Acession
	EST HUMAN	EST_HUMAN		NT LIMAN	1. 1010	EST HIMAN	TOT LINAN	EST_HUMAN	EO 1 HORSE	EG TOWN	201	EST_HUMAN	EST_HUMAN	nowe a	COT LIMAN	2 2	N 2	-	-	N	N	NT		1	27		Database
	TRAP1:  285b07.s1 Soares_fetal_liver_spleen_1NFLS_\$1 Homo septens cDNA done IMAGE:447541 3'	TRAP1:  TRAP1:  Wb30b10.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2307163 3' similar to TR:075235 075235.	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA done IMAGE:2307163 3' similar to TR:076235 075235	epliced 61437130F1 NIH MGC 72 Homo saplens cDNA clone IMAGE:3922303 6	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	ac77b08.s1 Strategene lung (#637210) Homo sepiens cDNA clone IMAGE:868599 3'	60190094F1 NIH MGC 19 Homo sapisns cDNA cione IMAGE:4129678 5	RIBOSOMAL PROTEIN S17 (HUMAN);  RN1900294F1 NIH MGC 19 Homo saptens cDNA clone IMAGE:4129678 5	257/h03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13932 40S	RC5-RT0840-020300-031-H03 BT0640 Homo sepiens cDNA	BC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA	PTR7 repetitive element;	POL/ENV GENE; xx60d02.x1 NCI_CGAP_Ut4 Homo sepiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.t1	qo91e02.x1 NCI_CGAP_Kid5 Homo saplens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q59386	AV734680 cdA Homo sapiens cDNA clone cdABED02 5'	Homo sepiens Drosophila Keloh like protein (DKELCHL), mRNA	Lorgo sapiens shell 1 (dropobbile homolog), zinc finger protein (SNA11), mRNA	Homo sanions Oncodene TIM (TIM) mRNA	Homo saniens Oncodene TIM (TIM) mRNA	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIKA), mk.vk. Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo saplens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mrava.		Homo sablens cytoplasmic dynein intermediate chain 1 mRNA, complete cds	Homo saplens cytoplasmic dynein intermediate chain 1 mRNA, complete cds	Homo saniens adeptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

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Table 4

Single Exon Probes Expressed in Placenta

HSCZQD042 normalized trians premi count hairs sa	EST_HUMAN	3.0E-76 Z4131411			T	Т	5350
TOTAL CONTRACTOR OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE O	EST_HUMAN	3.0E-76 BF375659.1		5.75	1	Л	3
DOE STOROG 180100-033-A03 ST0300 Homo sapien	EST TOWN	3.0E-76 BF375689.1		6.75	81 29691		3515
IBC5_ST0300-180100-033-A03 ST0300 Homo sapiens	45034/6/NI				81 27867		اۃ
	4503476 NT		3.0E-76	8.04		٦	6
Homo saniens eukaryotic translation elongation factor 1	ES L'IONNIN	BF61625	Γ	7 2.01			٦
IJJH-BW1-emz-b-04-0-UI.s1 NCI CGAP_Sub7 Homo	COLLINAVA	3.0E-76 BF516262.1			31 26856	646 13831	6
UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo	EST LINAN	4.0E-76 D81625.1			36855	30 23265	10230
HI IM178G01B Human fetal brain (TFujiwara) Homo se	EST LINAN	4.0E-76 D81628.1		5.48	36854		10230
HI IM178G01B Human fetal brain (TFujiwara) Homo se	EST DOMAIN	4.0E-76 BE /83412.1			36 31455		5384
1	TOT LOW	4.0E-76 BE814050.1			52 29473	78 16452	3278
L		6.0E-76 D638/4.1			38 28245	15138	1997
Human mRNA for HMG-1, complete cds	217	6.0E-76 D638/4.;1		9.61	18 28244	15138	1997
Himan mRNA for HMG-1, complete cds	212	5.0E-76 D63874.1	1		18 28243		1897
L	EO LONGA	6.0E-76 BE273201.1			97565		11753
	ч.	6.0E-76 BE396253.1		37.29	9		1282
		400/			1 30613	17631	4491
Homo septenterin reductase (7,8-dihydroblopterin:NADP+ oxidoreductase) (SPR) mRNA	450/184 NT			5.52	1 30612	1 17631	4491
Humo senients sepienterin reductase (7,8-dihydrobiopterin:NADP+ oxdoreductase) (SPR) mRNA	4 NIZOUCUCA				4 29558	2 16544	3372
Homo sanians lymphocyte antigen 75 (LY75) mRNA, and translated products	2 2	AFUCO48			8 29551	6 16538	3366
Homo saplens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partai cas	NIT .		Γ		6 27029	7 13976	797
Homo sapiens dihydrolipoamido dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo- gutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA	5016092 NT						
	1417007141		8.0E-/o	2.51		4 25550	12824
Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	10442821 N I		Γ		7 37619		10903
Homo saniens baculoviral IAP repeat-containing 6 (BIRC6), mRNA		M13/82			37231	23624	10589
Himen adenosina desprihase (ADA) gene, complete cds	101 N	17476961 N			35110		8482
Homo saniens AlM-1 protein (LOC51151), mRNA	11419212 NI				34289		7739
Library safety mitrochandrial carrier family protein (LOC55972), mRNA	15 NT			1.17	}		7658
Homo septens clivi dolinari Niraco (Circini) in RNA	42 NT		8.0E-76				830
FIGURE SECTION (CONT.), TO THE MARCH AND AND AND AND AND AND AND AND AND AND	7706724 NT	77067	8.0E-76	0.95	1		2976
Homo sapietis in lacus ( \companion) mRNA	74 NT	4504374 NT	8.0E-76	1.18	1	丁	8
TOTAL SEPTEMBER (Complement) (HF1) mRNA	74 NT	4504374 NT	8.0E-76	1.18	27194	╗	86
Human terrium neavy susum manus (HF1) mRNA	ZT	9.0E-76 M12937.1	9.0∈-76	5.44	36741	23143	10105
U for the Beaut subunit mRNA complete cds			Agrico				-
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E	Expression Signal	ORF SEQ	SEQ ID	SEQ ID

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Single Exon Probes Expressed in Placenta

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Probes Expressed in Placenta	1 000

					ſ	Г	į
H.sapiens mRNA for ubiquitin hydrolase	Z T	5.0E-77 X98296.1	1		T	Т	7490
Homo sepiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds	Z	5.0E-77 M13975.1				Т	803
DKFZp434G1728_r1 434 (synonym: htes3) Homo septents CUNA clone UKFzp434G1726 3	T_HUMAN	AL04385	٦			٦	5052
מוני (בטוב), וויייל		5031680 NT	5.0E-77	0.97	7	٦	4825
Homo explients Cyr-like repeats and dissolution around a Cyrill 20 mRNA			5.0E-77				4825
Homo sapiens upiquiun specific protesse to (vor to), illinora				0.65			3611
Homo sapiens cullin 1 (CCL1) IIINVN					29046		2822
Homo septens cousted like kinase i ( LLN ) minima, complete cas		AF16266		1.76		15866	2749
Homo septens distribution metalloprotease domain to (ACAMIN) illustra		4557250 NT					1391
7 Homo septens glucokinase (GCN) gerre, court 10 (ADAMAO) mBNA		5.0E-77 AF041015.1		2.89	27486		1264
adoid	EST HUMAN	6.0E-77 A1204068.1			27808		1574
ES J 308823 MAIGE resequences, MAIGE noting september 2018 done IMAIGE 1745083 3'	<u></u>	6.0E-77 AW957753.1	6.0E-77	1.05	27384		1165
Homo sapiens interieron (aprila, beta and oring/a) reversion 2 (ii 1972/2) iii 1972		4504600 NT	6.0E-77	4			273
Homo septens polymerase (KNA) if (LINA direction) polypopular ( (2007) (100 MBNA		-					2482
Homo septens polymerase (NNA) II (DNA directed) polypeptide E (1950) (BOI ROE) mRNA				278	28733	15609	2482
ZUB1801.61 Coares testis and inclina septents color could invocation (POI R2F) mRNA	T HUMAN	AA62575	7.0E-77	2.2			1983
MER 10 repetitive element;	HUMAN	8.0E-77 R00245.1	8.0E-77	32.5	31982	25637	12979
yessifo4.81 Soares fetal liver spieen 1NFLS Homo sapiens cunA cione liviAGE:123007 3 Similar of Chicalina					7	Т	
ze82e02,r1 Scares retina N2b4HK Homo sapiens culvia done invade 30007 31 cmiller is contains	EST HUMAN	8.0E-77 AA019770.1	8.0E-77	1.78	7	╗	11669
2662602./1 Socres retina N254HK Homo septens curva detre invasce0027/0	EST HUMAN	8.0E-77 AA019770.1	8.0E-77	1.78		П	11669
mRNA		4506230 NT	8.0E-77	1.37	31807	18766	5569
Hamo sapiens proteasome (prosome, macropain) 26S subunit, non-A i rase, / (wows nomocog) (ramo/)						Т	
801886926F1 NIH_MGC_17 Home septents curve course transcent to the course transcent to the course transcent to the course transcent transcent transcent transcent transcent transcent transcent transcent transcent transcent	EST_HUMAN (	8.0E-77 BF205181.1	8.0⊑-77	1.41		٦	4644
SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1;	EST_HUMAN	8.0E-77 R83144.1	8.0E-77	0.77	26443	13414	192
2010023007 1 Sparses hreast 3NhHBst Home sapiens cDNA clone IMAGE:187155 5' similar to	EG! HOWAN	9.0E-77 BE410354.1	9.0E-77	1.98		25652	13003
601012400F   NITUMICC   71 Home seniens cDNA clare IMAGE:3636753 5	1	9.0E-77 BE889525.1	9.0E-77	4.56	33530		7083
ES 137301 Empryo, a week i norrio saprens contro o circ		1.0E-76 AA333207.1	1.0E-76	0.7			6374
601589896FT NIH_MGC_/ Homo septens colve doile twinger. Septence of		1.0E-76 BE786537.1	1.0E-76	5.83			5564
Human mRNA for HMG-1, complete cas	L.	1.0E-76 D63874.1	1.0E-76	2.49		٦	4412
Human mRNA for HMG-1, complete case	NT	1.0E-76 D63874.1	1.0E-76	2.49	30539	٦	4412
Homo sapiens HIKA interacting protein 4 (answerse) (hinner 4), minner		7549807 NT	2.0E-76	2.44		24232	11161
Homo sapiens similar to ribosconal protein 320 (n. sapiens) (Lossonos), illinos de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya d		11437211 NT	2.0Ε-76	1.42			10489
Homo sapiens (PCR86 protein (PIST) RS6 (IL sapiens) (1 OCR3450) mRNA		11427410 NT	2.0E-76	1.82	34397	20895	7840
TDODGO (LOTDODGGD)DNIA			Value				
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	(Top) HII	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID
			Most Similar				

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Table 4
Single Exon Probes Expressed in Placenta

	7	٦			$\neg$		٦	٦	Т	Т	Т	Т	1	. T	_	П			_	٦	٦	٦	٦	Т	Z M Z
7325	88	6075	4891	4534	4534	4143	265 56	285	2170	2757	6 2	383	315	10488	10486	2029	2029	10708	10708	9788	9769	ğ	88	7767	Probe. SEQ ID NO:
20407	19474	19257	18021	17672	17672	17295	16067	18067	15305	15293	14618	14538	24187	23531	23531	15170	15170	23741	23741	22765	22765	21644	21644	20555	SEQ ID
33869	32829	32586	31008	30657	30656		28896			7		T		37140	37139	28278	28277	37347	37346	36336	36335	35184	35183	34027	ORF SEQ ID NO:
9 15.02	1.86	2.08	2.94	0.67	0.67	1.98	1.69		275	1.3			283	60	60	1.39	1.39	0.97	0.97	2.61	2.61	1.21	1.21	0.72	Expression Signal
									П			٦				3.0E-77		Γ				5.0E-77	5.0E-77	5.0∈-77	Most Similar (Top) Hit BLAST E Value
2.0E-77 AI833003.1	2.0E-77 BE787143.1	2.0E-77 BE298940.1	2.0E-77 AA653025.1	2.0E-77 AI613519.1	2.0E-77 AIB13519.1	2.0E-77 BE044316.1	2.0E-77 AB037836.1	2.0E-77 AB037836.1	7 7706315 NT	2.0E-77 L41825.1	2.0E-77 AW897712.1	2.0E-77 AV764617.1	3.0E-77 BF359917.1	3.0E-77 H65167.1	3.0E-77 H65167.1	5/30038 N		AB00228	5.0E-77 AB002207.1	11421928 NT			11428849 NT	39586X	Top Hit Acession No.
EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	3	NT.	5 NT	NT N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ON-	2 2	Z	N	BNT	BNT	NT	INI	NT	Top Hit Database Source
	60147690 A Barsteed colon HPI RB7 Homp sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311	OUT 1900/F 1911 JNOC SE Homo septions cDNA clone IMAGE:3879505 5	ns68g12.s1 NCI_CGAP_Pr2 Homo saplens cDNA cione IMAGE:1188838 similar to SW:RL29_HUMAN [] P47914 60S RIBOSOMAL PROTEIN L29. [1] ;contains element MSR1 repetitive element;	065245 F21E10.7 PROTEIN.;	O65245 F216 COAR BRIDGE FOUND SENSOR FDNA clone IMAGE: 280468 3' similar to TR: 065245	INASDOBAN SORIES NFC.   GODO, ST HOURS SORIES AND GAG POLYPROTEIN; SW.GAGZ_HUMÁN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN; SW.GAGZ_HUMÁN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN; SW.GAGZ_HUMÁN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN;	Homo septems menual for nixx 1413 protein, persons and a firme IMAGE 3040113 3' similar to	Homo sapiens mixiva (or NIAX 14 to protein, period cyc	Homo sapiens CGI-79 protein (LUCS1034), minutes	Homo septens CYP1/ gene, o end	RC3-BN0053-170200-011-001 BN0003 Floring Septemb CDIVA	AV784617 MDS Homo sapiens cunk cione MUSB ir id 3	PM3-M10V/8-USUBOU-UO-BUS M10-US IN THE SEPTEM STATES	NASQUILT WEZINERI CHECUTY EMPIRIUM I TUNIO CAPOTE N RY2G5 -; SP.S.17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -; SP.S.17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -;	SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -;	wasana ri Weizmenn Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to	Homo services SET domain and mariner transposase fusion gene (SETMAR) mRNA	Turnan rentanc SET domain and mariner transposase fusion gene (SETMAR) mRNA	Human mixix for NixAnces gene, partial cits	Homo Sapiens Surging Textus (Strong), Illinois	Homo sapiens sorung nearn o (SINAS), IIINNA	Homo sapiens 3-hydroxyiscouty/y-coercying or hydroxeso (1110-017), 111-1111	Tomo saluaris 3-1 yarayisaaniy yarayina aharaha aharaha aharaha aharaha	H. saplens mRNA for ubiquitin nyarolase  A hydrolase (HIBCH), mRNA	Top Hit Descriptor

4646

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SEQ ID ö 23236 13601 16286 13282 17909 17782 15641 16025 13501 18348 19739 20063 19233 19233 17948 16025 ORF SEQ ID NO: 36826 36826 26288 26289 35343 36366 36367 28533 28763 28213 27140 26534 30933 32557 30892 30592 307**64** 36085 36086 33120 33473 34402 34500 32558 37387 Expression Signal 5.68 5.68 0.47 0.47 15.97 0.82 0.71 2.62 1.68 205 . 28 0.83 1.48 0.61 Most Similar (Top) Hit BLAST E Value 2.0E-77 1.0E-77 1.0E-77 AW058119.1 1.0E-77 AB029024.1 1.0E-77 1.0E-77 1.0E-77 1.0E-77 1.0E-77 1.0E-77 1.0E-77 1.0E-77 1.0E-77 1.0E-77 X94354.1 1.0E-77 X94364.1 OE-77 .0E-77 AF086944.1 .0E-77 . 7 BF310349.1 AB033102.1 BF310349.1 U60321.1 AI362707.1 Top Hit Acession AB033102.1 AI273014.1 AB029396.1 Ş 11 NT 4885182 NT 6881412 NT 4502166 4503300 4502166 4502166 NT 1502166 1420159 Z EST NT NES Z 33 EST 3 Z Detabase Source Top Hit HUMAN HUMAN HUMAN HUMAN Human protain kinase C substrate 80K-H (PRKCSH) gene, exon 7
Human protain kinase C substrate 80K-H (PRKCSH) gene, exon 7
Human protain kinase C substrate 80K-H (PRKCSH) gene, exon 7
601895183F1 NIH\_MGC\_19 Home sapiens cDNA clone IMAGE:4124541 5 qy70c09x1 NC|\_CGAP\_Brn25 Homo sapiens cDNA done IMAGE:2017360 3' similar to WP:F29D11.1 CE05765 LOW DENSITY LIPID RECEPTOR-RLATED PROTEIN; ww83e05x1 Soares\_thymus\_NHFTh Homo sapiens cDNA clone IMAGE:2536160 3 Homo sapiens mRNA for KIAA1101 protein, complete cds Homo sapiens mRNA for KIAA1276 protein, partial cds Homo sapiene amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA Homo sapiens emyloid beta (A4) precursor protein (protease nexin-li, Alzhelmer disease) (APP), mRNA Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA drno saplens mRNA for KIAA1276 protein, partial cds Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA Homo sapiens elastin (supravalvular aortic stanosis, Williams-Bauren syndrome) Human von Willebrand factor gene, exon 20 Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28 Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28 qv06g04 x1 NCI\_CGAP\_Kid8 Homo sapiens cDNA cicre IWAGE:1981110 3 Homo saplens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-excris, mRNA Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 Homo sepiens CGI-60 protein (LOC51626), mRNA Homo sapiens 2,4-dienoy/ CoA reductase 1, mitochondrial (DECR1), mRNA Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Atzheimer disease) (APP), mRNA Homo sapiens cullin 1 (CUL1), mRNA Human mRNA for kidney epidermal growth factor (EGF) precursor Homo saplens hu-GloAT-P mRNA for glucurony/trensferese, complete cds H.sapiens DNA for Cone cGMP-PDE gene Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferese, complete cds H.sapiens DNA for Cone cGMP-PDE gene Top Hit Descriptor (ELN), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:

10389

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Table 4

Single Exon Probes Expressed in Placenta

7						011910	- LACIT 10500	Lyprosou III I Iacailla
Z	Probe SEQ ID	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
	10773	23806	37429	2.76	9.0E-78	9.0E-78 AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
	6576	19738	33118	2.29	8.0E-78	8.0E-78 AW947061.1	1	RC2-ET0023-080500-012-e05 ET0023 Homo saplens cDNA
	6676	19738	33119	2.29	8.0E-78	8.0E-78 AW947061.1	_	RC2-ET0023-080500-012-e05 ET0023 Homo saplens cDNA
	8	13323	26351	1.66	. 6.0E-78	6.0E-78 AU118789.1		AU118789 HEMBA1 Homo sapiens cDNA clone HEM3A1004354 5'
F	8	13323	26352	1.66	6.0E-78	6.0E-78 AU118789 1		AU118789 HEMBA1 Homo sapiens cDNA clone HEM3A1004354 5'
	3389	16559	29574	0.9	6.0E-78	6.0E-78 BF344101.1		602016926F1 NCI_CGAP_Brn64 Homo sepiens cDNA clane IMAGE:4152511 5
	6690	19848		2.54	6.0E-78	11432710 NT		Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
Γ	224	13446	26474	6.13	5.0E-78	11422486 NT	NT	=1
	2629	16752	28867	6.71	5.0E-78	5.0E-78 AW673424.1	EST HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B8A,8
	3472	16639	29659	5.09	5.0E-78 M55586.1		NT	Human collagenase type IV (CLG4) gene, exon 6
	5528	18725	31741	2.73	5.0E-78	3	TN	Homo sapiens Beet's macular dystrophy related protein mRNA, partial cds
	5693	18887	32177	18.13	6.0E-78	11416585	NT	
Ţ.,	7304	20386	33846	2.18	5.0E-78	20.1	EST_HUMAN	EST385180 MAGE resequences, MAGB Homo sapiens cDNA
<u></u>	9284 4	22360	35910	7.02	5.0E-78 U60889.1		NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
T_	9285	22361	35911	2.94	5.0E-78	5.0E-78 BE960836.1		601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
L	1168	14324	27379	1.29	4.0E-78	4.0E-78 AL0433;4.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
Ţ	<b>1</b>	14699	27778	1.81	4.0E-78		Z	Novel human gene mapping to chomosome 22
Ī,	2392	15523	28652	6.1	4.0E-78	4.0E-78 AF107405.1	NT	Homo septens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
Ţ	4442	17582	30560	6.17	4.0E-78	7656876 NT		Homo sapiens syncytin (LOC30816), mRNA
Ţ	4896	18026	31012	1.2	4.0E-78	4505806 NT		Homo sapiens phosphatidylinositol 4-kinase, catalytio, alphe polypeptide (PIK4CA) mRNA
Ţ	4896	18026	31013	1.2	4.0E-78	4505806 NT		Homo sapiens phosphetidylinositol 4-kineso, catalytic, elphe polypeptide (PIK4CA) mRNA
	5888	19076	32385	1.25	4.0E-78	11420732 NT		Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
	8302	19475	32830	0.71	4.0E-78	7662109 NT		Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
	6302	19475	32831	0.71	4.0E-78	7662109 NT		Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
	6703	19861	33251	0.74	4.0E-78	4506736 NT		Homo saplens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
	7660	20727	34203	0.69	4.0E-78	4506736 NT		Homo sapiens ribosomel protein S6 kinese, 70kD, polypeptide 1 (RPS6KB1) mRNA
Ţ.,	9054	22133	35677	1.15	4.0E-78			Homo sepiens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds
T	\ <u>\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\</u>	22133	36678	1.16	4.0E-78/	4.0E-78 AF012872.1	NT	Homo seplens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
	9568	22710	36278	0.61	4.0E-78	11417251 NT		Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
ā	10660	23694	37303	1.95	4.0E-78	11560151 NT		Homo sapiens hypothetical C2H2 zino finger protein FLJ22504 (FLJ22504), mRNA
100	10660	23694	37304	1.95	4.0E-78	11560151 NT	,	Homo saplens hypothetical C2H2 zino finger protein FLJ22504 (FLJ22504), mRNA
<u>_</u>	11705	24702	38394	1.84	4.0E-78 /	4.0E-78 AF169148.1	<u> </u>	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds

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Single Exon Probes Expressed in Placenta

Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hir Acession	Top Hit Database Source	Top Hit Descriptor
11854 24842	38538	6.72	4.0⋶-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
П	31991	3.93	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-5, complete cds
П	26417	1.69	3.0E-78	AF095601.1	NT	Homo sapiens eRF1 gene, complete cds
13390	26418	1.69	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
2488 15615	28736	1.01	3.0E-78	06705	NT	Homo saplens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
		0.81	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3918 17077	30074	0.78	3.0E-78	4507334	T	Homo sepiens synaptojanin 1 (SYNJ1), mRNA
17077	30074	0.82	3.0E-78	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
		5.44	3.0E-78	BE144758.1	EST_HUMAN	CM0-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
11227 24296	37837	2.5	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo saplens cDNA
3191 16366		2.49	2.0∈-78	UD4489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4122 17276		1.99	2.0∈-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5 end
20700	34177	1.09	2.0⊑-78	AW 402306.1	EST_HUMAN .	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo capiano oDNA clone IMAGE:3054139 5'
7631 20700	34178	1.09	2.0E-78	AW 402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7908 20960	34466	3.36	2.0⊱-78	BF689800.1	EST_HUMAN	602188529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288599 5
8230 21312	34832	2.49	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8646 21726	35262	1.72	2.0E-78	AI5575()9.1	EST_HUMAN	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8646 21726	35263	1.72	2.0€-78	AI557509.1	EST_HUMAN	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3
		, j				母50h05x1 NCI_CGAP_Brn25 Homo sepiens cDNA clone IMAGE:1859981 3' striller to WP:R90.1
Т	0040	8.00	2.00-70	WI ISLOOL !	EGI DOMAN	CLOSES FIXO I FINANCIA I
Г		1.47	2.0E-78	BE439409.1	EST_HUMAN	HTM1-026F1 HTM1 Homo sapiens cDNA
11386 -24447	38108	3.01	2.0E-78	N66951!.1	EST_HUMAN	za48f12.s1 Soares fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE:295823 3'
5420 18621	31697	3.16	1.0E-78	11417304	NT	Hamo sapiens GAP-like protein (LOC5/306), mRNA
7094 18521	31514	0.82	1.0E-78	AV648699.1	EST_HUMAN	AV648699 GLC Homo sapiens cDNA clone GLCBMC01 3'
Г		1.81	1.0E-78	U52373!1	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12324 25234	32107	1.83	1.0E-78	11430460	Z	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12422 25299	32086	2.44	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
17953	30938	4.04	9.0∈-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4986 18115	31093	1.6	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-o12 BN0074 Homo sepiens cDNA
5549 18746	31781	16.98	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
	32996	2.52	9.0E-79	6454145	Z T	Homo sepiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
6752 18808	33301	0.98	9.0⊑-79	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
Probe EQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Exan SEQ ID ID NO: 24842 24842 25568 13390 15615 17077 17077 17077 23528 24296 17368 17368 17378 20700 20700 21312 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 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21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726 21726	Exam ORF SEQ Express SEQ ID ID NO: Sign 1 25868 31991 13390 26417 13390 26418 17077 30074 17077 30074 17077 30074 17077 30074 17077 30074 17077 30074 17077 30074 17077 30074 17077 30074 17076 34178 24296 37837 16368 17276 35262 21726 35262 21726 35262 21726 35262 21726 35262 21726 35263 16521 31614 21434 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 26234 32107 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Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field Field F	Exam ORF SEQ Expression (170p) Hit SEQ ID NO: CIPNE SIgnal PLAST E NO: CIPNE SIGN (170p) Hit SIGNA: 25688 31991 3.93 4.0E-78 ADS344.1 25688 31991 1.09 3.0E-78 ADS344.1 25688 31991 1.09 3.0E-78 ADS344.1 25690 26418 1.09 3.0E-78 ADS344.1 25690 26418 1.09 3.0E-78 ADS344.1 25690 26418 1.09 3.0E-78 ADS344.1 25690 3.0E-78 ADS344.1 25690 3.0E-78 ADS344.1 25690 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS344.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 ADS345.1 3.0E-78 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2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 AF09560.1 1.99 2.0E-78 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Table 4
Single Exon Probes Expressed in Placenta

Homo septens guarrine nucleotide exchange factor for Rep1 (KIAA0277), mRNA	NT	6912455 NT	3.0E-78	0.87	34574	21062	8012
	NT	3.0E-79 AB014520.1	3.0E-79	2.58	33482	20071	7206
	NT	3.0E-79 AB014520.1	3.0E-79	2.58	33481	20071	7206
601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'	EST_HUMAN	3.0E-79 BE256893.1	3.0E-79	0.84	33445	20036	6884
Hamo sapiens netrin 1 (NTN1), mRNA	NT	11425770 NT	3.0E-79	3.87	32387	19077	5889
Hamo sepiens netrin 1 (NTN1), mRNA	NT	111426770 NT	3.0E-79	3.87	32386	19077	6889
60/1482143F1 NIH_IMGC_68 Homo saplens cDNA clone IMAGE:3884554 5'	EST_HUMAN	3.0E-79 BE789470.1	3.0⊑-79	0.93	32364		5866
601482143F1 NIH_MGC_68 Homo sepiens cDNA clone IMAGE:3884554 5'	EST_HUMAN	3.0E-79 BE789470.1	3.0E-79	0.93	32363		5886
Homo septens mRNA for KIAA0892 protein, partial cds	NT ·	3.0E-79 AB020699.1	3.0E-79	1.69	32337	19031	5841
Homo sapiens MSTP016 (MST016) mRNA, complete cds	NT	3.0E-79 AF110322.1	3.0E-79	7.05	31689	18676	5477
Human zinc finger protein ZNF131 mRNA, partial cds	NT	3.0E-79 U09410.1	3.0E-79	1.74	29351	16343	3168
Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cin) gene, complete cds	NT	3.0E-79 AF2327,08.1	3.0E-79	1.22	27233		<u>1</u> 81
Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	NT	3.0E-79 AF114488.1	3.0E-79	1.74	26569	13537	323
Homo sapiens chromosome 21 segment HS21C082	NT	5.0E-79 AL163282.2	5.0E-79	3.63	38473	24776	11786
zj94e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT;	EST_HUMAN	6.0E-79 AA699829.1	6.0E-79	5.44		25132	12169
Homo saplens chromosome 21 segment HS21C046	NT	6.0E-79 AL163246.2	6.0E-79	0.62		21923	8844
601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 31	EST_HUMAN	7.0E-79 BE619648.1	7.0E-79	6.38	29516	16498	3326
Homo sapiens chromosome 21 segment HS21C010	NT	8.0E-79 AL163210.2	8.0E-79	1.18	29998	16996	3836
Homo sapiens gemma-glutemytransferase 1 (GGT1), mRNA	NT	11417877 NT	9.0E-79	1.4	31967	25711	13088
Homo saplens suppressor of white apricot homolog 2 (SWAP2), mRNA	NT	11423827 NT	9.0E-79	2.94	38490	24792	11802
Homo saplens suppressor of white apricot homolog 2 (SWAP2), mRNA	NT	11423827 NT	9.0E-79	2.94			11802
Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds	NT	9.0E-79 AY008273.1	9.0⊑-79	1.61		24385	11322
Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds	NT	9.0E-79 AF062346.1	9.0E-79	1.05	37275	23666	10632
Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds	TN	9.0E-79 AF062346.1	9.0E-79	1.05	37274		10632
Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA	NT	11438643 NT	9.0E-78	0.82	37214	23609	10574
Homo saplens DNA for amyloid precursor protein, complete cds	N T	9.0E-79 D87675.1	9.0E-78	89.0		22722	9580
Homo sapiens casein kinase II alpha subunit mRNA, complete cds	NT	9.0E-79 J02853.1	9.0E-79	4.78	35891	22340	9263
Homo sapiens casein kinese II alpha subunit mRNA, complete cds	NT	J02853.1	9.0E-79 J02853	4.78	35890	.22340	9263
Homo sapiens threonyl-tRNA synthetase (TARS), mRNA	NT	11417260 NT	9.0E-79	0.52		21622	8541
Homo sepiens threonyl-tRNA synthetase (TARS), mRNA	NT	11417260 NT	9.0E-79	0.52	35158	21622	8541
	NT	11421735 NT	9.0€-79	0.63	34299	20808	7748
Homo septens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA	NT	11421735 NT	9.0€-79	0.ස	34298	20808	7748
Homo saplens hypothetical protein FLJ20345 (FLJ20345), mRNA	NT	11424427 NT	9.0E-79	66.0		25846	7505
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Table 4
Single Exon Probes Expressed in Placenta

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N	J271408.1	20E-79 A	1 25	T	1	2216
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a N	1083503	3.0E-79	0.59		3300	
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Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mKNA	NT		T			Г	8897
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Homo sapiens mRNA for Ipophilin B	DNT	5174540 NT			7 33176	19787	6827
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Human pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type it consider (County) Annual Pro-aipnat type	NT	1,0E-80 L10347!1	1		32603	Т	8 9
CO12/4300F1 NITE NITE CONTROL OF PRINTS 1-54 CONTROLS	EST_HUMAN	1.0E-80 BE386615.1		6.25	2	7	5440
Homo sapieris Fixix a society of the same sapiens cDNA clone IMAGE:3615433 5		1.0E-80 Y13932!1		3.32		Т	5343
Land Septime DRKY Ayon 7	2	.0E-80 AF077188.1		0.95	30703	$\neg$	4583
repetitive element;	EST HUMAN	1.0E-80 AI732656.1		2.42	<u>.</u>	15149	2009
GAP_Co9 Homo sapiens cuiva cione					T	1	
Homo sapiens chromosories 1: una perinting of the contains OFR.11 OFR	NT	1.0E-80 AF231920.1	1.0E-80		27055	T	Ş   Ş
Homo adplatis ciliculacione en respectivo de la laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de laboratorio de lab	Z	1.0E-80 AL163303.2	1.0E-80	1.62		Т	350
G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;	EST HUMAN	2.0E-80 AA393352.1	2.0∈-80	6.84	37816	24181	11109
770112 r1 Spares tests NHT Homo capters cDNA clone IMAGE:727727 5' similar to TR:G191315	2	2.0E-80 AJ00/3/8.1	2.0E-80	0.99	36603	23009	9970
Homo sariens GGT gene, exon 6	10000	2.0E-80 AW864270.1	2.0⊱-80		35994	22435	9360
EST376343 MAGE resequences, MAGH Homo septens cDNA	EST HIMAN	Z.UE-60 1/3Z13.11	2.0E-60	0.89	33947	20479	7401
SP:K1CR XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B;	EST HUMAN	178245 1			$\neg$	$\neg$	
Homo sapietis Golgi valispoi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collipse promi collips	3	11421930	2.0E-80	1.89	٦	Т	7053
nasuau i si i Nortono de Carroller profein (90 kDa) (GTC90), mRNA	EST HUMAN	2.0E-80 AA582952.1	2.0∈-80	0.96		-1	994
UNITED TO TO COAP Coa Home seplens oDNA clone IMAGE:10901773'	ES I HOMAN	2.0E-80 AL0431;6.2	2.0E-80	7.03	٦	- }	2116
DIEZ-43401323 r1 434 (syronym; hies3) Homo sapiens cDNA clone DKFZp434D1323 5	EO! TOWAN	2.0E-80 A 444821.1	2.0E-80	1.57		_	98
9800800.1 Soules Illian Court Homo Sapiens cDNA clone RET4B7	1_	R35321.1	2.0E-80 R35321.1	4.85	28087	14987	<u>\$</u>
26-06-1 Sarras Infant hrain 1NIB Homo saplens cDNA done IMAGE:38060 5	L		Value				
	Source	Z o	BLASTE	Signal	D NO:	SEQ ID	SEQID
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Exon	Probe
		09					

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				Γ			1700	4500	
12	Homo saplens hypothetical protein FLJ20481 (FLJ20481), mknyk	32 NT		1		T	Т	+ 80	
4	Homo sapiens glutamete receptor, ionotropic, kainase ( VSNIN ) III NVN	IS NT				1	Τ	100	
<u> </u>		NT	6715601 NT	8.0E-82	7 1.39	27927	14843	<u> </u>	
1	Homo sapiens glutathions peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2,	- 12	8.0E-82 ADUST 140.1		5 224	73 27755	0 14673	1520	
با	327 protein, partial cds	77	8.0E-82   UBBoo.				Г	910	
┸	Human CRFB4 gone, partial cds		8.0E-82 UU8986.1	Ī		27070	7 14015	837	
Lg:	Himen CRFB4 dene, partial cds	2 -	8.0E-82 U08988.1	Γ		26523	4 13492	274	
	Linean Copperation of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state	2	8.0E-82 AF161406.1			1 26251	7	109	
اپا	Light serious HSPC288 mRNA, partial cds	N.	8.0E-82 AF161406.1				٦	13	
		N.	11418138INI				7	12417	
<u>-</u> į	1	EST_HUMAN	BF2042	1.0E-81	1.89		_(	11812	
اتبا	L	EST HUMAN	.0E-81 AW960658.1	1.0E-81	2.46	0 31528	7	11550	
٠	FOTESTATO NACE recontences MAGE Homo sapiens	EST HUMAN	AW798167.1	1.0E-81	2.93	38069	7	11352	
	The Thursday 200700 011 and I I Monad Home sapiens	EST HOMAN	1.0E-81 AW798167.1	1.0E-81	2.93	38068	╗	11362	
ır.	L	ESI HUMAN	.0E-81 AW844986.1	1.05-81		9 38062	24409	11347	
		EST HUMAN	1.0E-81 AW844986.1	1.0E-81		9 38061	24409	11347	
لــا	1		8923698	1.0≅-81		1 37886		11182	
Ц.	1	המין הטאניוי	1.0E-81 AW250322.1	1.0E-81	0.49	37519	23896	10884	
	┸	EGI HOWAN	1.0E-81 AW89/550.1	1.0E-81		37367	23759	10726	
_		EST HOWAY	1.0E-81 BE /44030.1	1.0E-81		36951	23346	10310	
_	L	EST LINAN	1.0E-81 BE /44040.1	1.05-87		36950	23345	10310	
<b>!</b>	1	EST LIM	1.UE-81 AAGSU/04.	1.05-81		36948	23343	10308	
		GOT LIMAN							
	┸	EO I TOWN	1.0E-81 BE564367.1	1.0E-81	5.13	36804	23211	10174	
	601343180F1 NIH MGC 53 Homo saplens cDNA clone	EST HUMAN	1.0E-81 BE868278.1	1.0E-81		36811	23017	9978	
_	601645051F1 NIH MGC 56 Homo saplens cDNA clone	EST LINAN	1.0E-81 BE9582/8.1	1.0E-81		38610	23017	9978	
	┸	EST LINA	1.0E-81 AJ250408.1	1.0E-81				7972	
	Domo septiens Cil 13 dene for Cil 13 protein	Z	11432966 N I	1.0E-81	7.94	34509	_	7949	
	2)  Line actions polymerase (TINA directed), gamma (POLG), mRNA	3	1.0E-81 AJ133269.1	1.0E-81	1.09	33439	20029	6877	
		E.O. 1. 101812	1.0E-81 BF6/4041.1	1.05-37	1.81	32797	19448	6274	
_	L	TOT LI MAN	J52351.1	1.0E-81 U52351.1			18963	5771	
	Harmo sanions arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds								
	Hit Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID	
_									-

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7							T. P. COCCA III.
Probe SEQ ID NO:	ID SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
<u>~</u>	1481 14634	4	1.18	7.0E-82	7.0E-82 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862086 5'
,	2825 15939	28049	1.62	7.0E-82	7.0E-82 AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA cione HEMBA10007623'
<b>1</b>	1705 14857	7 27944	22.64	4.0E-82	4.0E-82 AF081484.1	NT	Homo sepiens alpha-tubulin isoform 1 mRNA, complets cds
g	5613 18807	7 31874	0.87	4.0E-82	4.0E-82 BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
8	П	31875	0.87	4.0E-82	4.0E-82 BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo saplens cDNA
S.	5876 19066	32374	1.1	4.0€-82	4.0E-82 M25833.1	NT	Human von Willebrand factor gene, exon 9
12016	116 25000	38702	4.71	4.0Ε-82	4.0E-82 AIS373(0.1	EST_HUMAN	wp75e09.x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE:2467624 3' similar to TR:075276 075276 PKD1 :
12683	183 25455	J	3.78	4.0E-82	2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
N	288 13506	26540	15.3	3.0E-82	4502166 NT	3	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
	721 13903	26944	2.5	3.0E-82	3.0E-82 BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-f02 BN0120 Homo sapiens cDNA
Ţ	810 13989	27043	8.44	3.0E-82	6174702 NT	Ŋ	Homo seplens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
	893 14069	27134	5.31	3.0E-82	4502188 NT	3	Homo sapiens amyloid bata (A4) precursor protein (protease nexin-ll, Alzheimer disease) (APP), mRNA
15	1086 14252	2	15.73	3.0E-82	3.0E-82 AA725848.1	EST_HUMAN	al23e05.s1 Scares_testis_NHT Homo sapiens cDNA clone 1343648 3'
13	Г		1.22	3.0E-82	3.0E-82 AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
<u>_</u>	T	27729	5.59	3.0E-82	3.0E-82 AL163285.2	NT	Homo saplens chromosome 21 segment HS21C085
18	1960 16093	28194	2.14	3.0E-82	3.0E-82 BE813232.1	EST HUMAN	RC1-BN0005-260700-018-g04 BN0005 Home sapiens cDNA
23	2062 15202	28318	1.11	3.0E-82	4501922 NT	Z,	Homo saplens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3345	45 16518	_	2.42	3.0E-82	5453811 NT	TN	
83	8346 21427	34952	2.68	3.0E-82	11425206 NT	TIN	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
87	Γ		0.89	3.0E-82	11432889 NT	TIN	Homo sapiens contactin 6 (CNTN6), mRNA
87	8753 21832	35372	0.89	3.0E-82	11432889 NT	NT	Homo saplens contactin 6 (CNTN6), mRNA
10029	Г		4.01	3.0E-82		TI	Homo sapiens mRNA for KiAA1077 protein, partial cds
10029	П		4.01	3.0E-82		NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
	Γ		2.49	2.0E-82		NT	Homo sepiens mRNA for KiAA0999 protein, partial cds
	Г		2.49	2.0E-82	L		Homo sapiens mRNA for KIAA0999 protein, partial cds
17	П	Γ	2.23	2.0E-82	13	EST_HUMAN	DKFZp434M117_r1 434 (tymonym: htes3) Homo septens cDNA clone DKFZp434M117 5'
38	Г		0.93	2.0E-82 D87675.1		NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4131	Γ	30279	0.68	2.0E-82 U76833.		NT	Human Integral membrane setine protease Seprase mRNA, complete cds
4348			0.9	2.0E-82	4116	NT	Homo sapians glutamate receptor, fonotropic, kainate 1 (GRIK1) mRNA
8	4680 17815	30803	1.52	2.0E-82	2.0E-82 AB029019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds

	-6.	S.OF-GO DEGOCOTO.		297	27978	4 4500	
601273346F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:3614362 o	EST HUMAN	9.05-83 5528333 1			6 37128	1 23516	10481
601117160F1 NIH_MGC_16 Homo sapiens cDNA cione IMAGE:3357734 5	EST HUMAN	9.0E-83 BF6/2/20.1			35530		8912
(UBE2D3) genes, complete ods 602150403F1 NIH_MGC_81 Homo septens cDNA clone IMAGE:4291561.5	NT HIMAN	9.0E-83 AF224569.1			31394	7 18424	5307
Homo septens mannosidese, beta A, lycosomal (MANBA) gene, and ubiquitin-conjugating enzyme Exp. 3	IV.	.0E-82 AL163246.2	T.	1.49	П	П	11258
Homo sapions chromosome 21 segment HS21C048	2 2	1.0E-82 AL163209.2			3 37698	╗	1880
Homo sapiens chromosome 21 segment HS21C009	EST_CONSIN	1.0E-82 BF515938.1		1.4		╗	10451
III-H-BW1-apa-f-03-Q-UI.s1 NCI_CGAP_Sub7 Homo septens cDNA clone IMAGE:3084030 3	E LI IMAN	1.0E-82 AB014562.1		4 0.51	3 36474	П	9853
Homo sapiens mRNA for KIAA0662 protein, partial cds	2 -	1.0E-82 AB037838.1		0.9		7	9143
Home seplens mRNA for KIAA1417 protein, partial cds	7 -	1.0E-82 AB0111,10.2	Γ	7 0.8	27537	٦	1315
Homo seniens mRNA for KIAA0538 protein, pertial cds	ESI HUMAN	1.0E-82 BE064386.1		1.38	27536	П	1314
BCA BT0310-110300-015-110 BT0310 Homo sapiens cDNA	'Iı	1.0E-82 BE885106.1		3.19		٦	1236
S01510859F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE:3912207 5	) Z	1760011		1.69	26813	П	95
Homo sapiens melanoma differentiation essociated protein-5 (MDA5), mKNA	1 2	AAOTT		3.72		П	12818
zi01g09.r1 Soares fetal liver_splean_tNFLS_S1 Homo septens cDNA clone IMAGE:428000 0	DOT HIMAN	2.0E-82 N94950.1		2.81	1	25177	12230
zb31d10.s1 Soares parathyroid tumor NbHPA Homo saptens cDNA clone INAGE 300203 3	EGT LI MAN	2.0E-82 U80/30:1	Γ		38323		11588
	NT	2.012-82 080 / 30.1	T		38322		11588
Homo sapiens CAGF9 mRNA, partial cds		11417101111	Γ		38280	24603	11547
Homo sapiens leucy/cystiny aminopeptidase (LNPEP), mRNA			2.0E-82			24603	11547
Homo saplens leucyl/cystinyl aminopeptidase (LNPEP), mRNA		100032.	Γ		36957	23350	10315
Human endogenous retrovirus-K, LTR U5 and gag gane		2.0E-82 Y08032.1	Π		36956	23350	10315
Human endogenous retrovirus-K, LTR U5 and gag gene		1007340 IV			П	21948	8869
Homo sepiene microrchidia (mouse) homolog (MORC), mRNA			205-82		35482	21948	8869
Homo sapiens microrchidia (mouse) homolog (MORC), mRNA			2.0E-82		35117	21581	8500
Homo sapiens siit (Drosophila) homolog 3 (SLIT3), mRNA		11 001 C789	2.01-82		34550	21038	7988
Homo sepiens hypothetical protein FLJ20128 (FLJ20128), mRNA	1 Clare	2.0E-82/A/4/6426.1	2.0E-82	1.19		28222	7858
tm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:21572723		AF234862.1	2.0E-82	4.63	32832	19477	6304
Homo septens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds		2.0E-82 AB0182/0.1	2.0E-82	2.89	31827	18782	5587
Hymo saplens mRNA for KIA40727 protein, partial cds		10 000 / UCF	2.05-82	1.56	31281	18313	5191
Homo sapiens tumor necrosis factor receptor superfemily, member 5 (TNFKSF5) mkn/A	2 2	450/560	2.0E-82	1.56	31280	18313	5191
replication factor C subunit 2 (RFC2) gene, complete cds  Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRVA	N N N N N N N N N N N N N N N N N N N	2.0E-82 AF045555.1	2.01-82	2.86	31100	10121	4992
Hamo sapiens wascr1 (WBSCR1) and wascr5 (WBSCR5) genes, complete cds, elternatively spliced and	2	2.0E-82 AB029019.1	2.0E-82/	1.62	30804	17815	4680
Homo senions mRNA for KIAA1096 protein, partial cds			Value				ö
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	<u>₽</u>	Expression   Signal	ORF SEQ	Exon SEQ ID	0 "

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Table 4

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1022				4554 17	П	3728 16	2108 18	969 14	12179 25		11821 24	8971 23	9971 23	9878 22	7671 20	П	5408 18	3653 168	Т	Т	T		416 13611	6176 19352	4936 18066	2928 16105		_	1715 15992	NO:	S	
14183	13843 26870	18312 31279	18312 31278	17692 30672		16889 29893		14142	25139		24810	23010 36605	23010 36604	22918 36503	20737 34215	19324 32669	18610 31582	16816 29828	Τ	58 292//			11 26650	52 32699	8	8			92 27956		ORF SEQ	
-		79 13.87						7.24	4.13		2.31	5 0.71				1,3	1.73	98.0		0.00			1.39		6.85	1.64		1.2	10.59		Expression Signal	
4.09		97 5.0E-83			T		Τ	Τ	Ī			1 0.0E-83	T			Γ		T	T	1			Γ			T				Value	Most Similar (Top) Hit BLAST E	
2000000	4.0E-83 AF224669.1	490/010/11		0.0E-83 AC 1034 10.4	9 1 1632-10 2 NT	ALIOSE	5.0E-83 AF000303.	5.0E-63 01769375 4	2 14 7002 4	6 0F-83 AF240786.1	6.0E-83 AA486105.1	11400047				AJ01077	4507866 NT		11430241 NT	R 0F_83 AF231919.1	6.0E-83 AW 5/3030.1	1	6.0E-83 M33320.1	1420007	7.0E-83 BF221813.1	7.0E-83 AA584655.1		7.0E-83 AW385529.1	8.0E-83 N66951.1		Top Hit Acession No.	
	NT EST HUMAN	-	SVIT	S NT	NT I	21	3	3	NT.	<u>=</u> -	EST_HUMAN		7 17	7 4 7 7	4 14 1	2 2	e NT		1 N	NT	EST HUMAN	DOT LIMAN	12	214	EST_HUMAN	HONAIN	TOT LINAN	EST HUMAIN	EST HUMAN		Top Hit Database Source	
	(UBE2D3) genes, complete cds  EST79542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2U 3		Homo sapiens catalase (CAT) mRNA	Homo sepiens chromosome 21 segment HS21C010	Homo sapiens deoxyribonuclease I (DNASE1), mRNA	Novel human gene mapping to chomosome X	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon o	genes, complete cds	THR. 2 THR repetitive element;	ab14e10.s1 Stratagene lung (#937210) Homo septens oDNA clone IMAGE:840810 3' similar to contains	Homo sapiens pre-mRNA splicing factor cimilar to S. cerevisiae Prp18 (PRP18), mRNA	Homo seciens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	Homo saplens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA	and translated products	Homo sapiens VAMP (vesicle-essociated membrane protein)-associated protein A (33KD) (VALA) III NAVA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mixiva	Homo capiens chromosome 21 unknown mRNA	QV4-ST0234-181199-037-105 ST0234 Homo sapiens cDNA	SW YBEB HAEIN P44471 HYPOTHETICAL PROTEIN HIDD34.	LEALON A Source NET T GRC S1 Homo septens cDNA clone IMAGE:2933526 3' similar to	Human platelet Givcoprotein (lb (GPlib) gene, exons 2-29	DJ207H1.1; Home sedens KIAA0100 gene product (KIAA0100), mRNA	7p37a07x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y3I6 Q9Y3I6		23-121 CT ANCI CGAP Phot Home septens cDNA cione IMAGE:1100497 3' similar to contains Alu	2848172.81 Spares Islantive: Spream Int. Co. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 1811 CO. 181	Carl line of the TNEI S Home septions cDNA clone IWAGE:295823 3'	Top Hit Descriptor	

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Single Exon Probes Expressed in Placenta

L	FO. 1.010 0.4	2.0E-83 ALT34434.1		1.04	37870	24239	11169
DKFZp547J135 r1 547 (synonym: hfbr1) Homo septens cDNA clone DKFZp547J135 6	TOT LIMAN	3 1104400411			37788	86 24160	11086
Homo sapiens KIAA0985 protein (KIAA0985), mRNA		AVV OUG	Γ		27 37034	92 23427	10392
UI-HF-BNO-amd-h-07-0-UI-1 NIH_MGC_50 Homo sepiens cDNA clone IMAGE:3081852 5	EST HIMAN	2.0E-83 AUT1/039.1			36967	22 23357	10322
AU117659 HEMBA1 Homo septens cDNA clone HEMBA1001910 5	EST LI MAN	2.0E-83 MZZ094.1				40 23275	10240
Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end	12-	2.0E-83 MZZ094.1	Γ			40 23275	10240
Human neural call adhesion molecule (N-CAM) secreted isoform mRNA, 3' end	217		Γ		38413	33 22833	9793
Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA	NT	5/5/3881 NT	2.05-83				9793
Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA	77	AFOI 192	T			)9 21590	8509
Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1	4	2.0E-83 AF01 1920.1	Γ			9 21590	8509
Homo saplens protein kinase CK2 catalytic subunit alpha gene, exon 1	3	2.UE-83 U66/07:1	I			6 21257	8176
Rattus norvegicus densin-180 mRNA, complete cds	1	20E-83 ABOUTOZO.					8026
Homo sapiens mRNA for brain ryanodine receptor, complete cds	27	2.0E-83 AB001025.1	Γ			П	8028
Home saplens mRNA for brain ryanodine receptor, complete cds	EGI DUMPIN	2.0E-83/BF105097.1	Γ		6 34548	7 21036	7887
601872090F1 NIH MGC 75 Homo sapiens cDNA clone IMAGE:4042318 5		2.0E-83 AF128533.1			4 34140	3 20684	7593
Homo sentens F-box protein Fbl3b (FBL3B) mRNA, partial cds	2	2.0E-83 AF128533.1			7 33446		6885
Homo seniens F-box protein Fbi3b (FBL3B) mRNA, partial cds	TO TOWN	2.0E-83 BE8854U1.1	١		8 32597		6086
R01507482F1 NIH MGC 71 Homo septens cDNA clone IMAGE:3909068 5	4)	11428081 N1			3 32468	7 19163	5987
Homo saplens membrane protein CH1 (CH1), mRNA	12	006679		0.91	7 31559	5 18587	5385
Human carcinoembryonic antigen gene family member 18 (CGM18) gene, exons A1 and B1	1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IN OGCOUT			30894	17910	4775
Homo saplens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA	N		2.0E-83		30893	5 17910	4776
Homo saplens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA	2	AF-2026)			30576	3 17598	4456
Homo saplens hematopoietic progenitor cell entigen CD34 precursor (CD34) mNNA, partial cas		ZUE-83 AL 103202.2				17033	3874
Homo sapienc chromosome 21 segment HS21C002	Z	NI TOOOT I		2.16		10515	3342
Homo saplens sal (Drosophila)-like 1 (SALL1), mRNA	11.÷	2.0E-83 DE020094.1			29103	П	2913
RCS-E 10046-280600-013-H12 E 10046 Homo septens cDNA	DOT LIMAN	2.0E-83 AD033080.1	Γ		28512	16384	2251
Homo sepiens mRNA for KIAA1272 protein, partial cds	NT I	A.O.C. ON ADDROOMS 4	2000		Γ	15121	1978
2948f12.s1 Soares fetal liver spieen 1NFLS Homo sapiens curva curve invocations	EST HUMAN	NAROS1	305.83		T	Τ.	100 A
Q92814 MYELOBLAST KIAA0216. ;	EST_HUMAN	2 0E-83 AA993492.1	2 0E-83	4 97		ヿ	
Q02614 MYELOBLAST KIAA0216.;	EST_HUMAN	2.0E-83 AA983452.1	2.0E-83	1.37	28089	14989	1843
064g05.s1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:19Z19SZ 3 simual w in George			0.00	20.0		19866	6708
qf73e05xf Soares_testis_NH   Home expense construction and control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control	EST HUMAN	3 0F-83 AI217223.1	3 0F-83	0.83		Т	1001
repetitive element:	EST_HUMAN	3.0E-83 AA632654.1	3.0E-83	1.6		$\neg \top$	383
TWA Close IMAGE: 1133292 similar to contains THR.12 THR			Value			NO.	Ö.
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	(Top) Hit BLAST E	Expression Signal	ORF SEQ	SEQ (D)	Probo SEQ ID
			Gimilor				
	Oliver Lynch Long	Brite					

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Single Exon Probes Expressed in Placenta

6232	3079	732	8264	7868	7642	6777	9		5835	5354	2471	1323	1323	3897	6835	5008	4359	3972	3251	2722	2076	1444	1444	12859	11168	Probe SEQ ID S
19407	16255	13914	21346	20922	20711	18969	10908	900	18829	18481	15598	14479	14479	17056	19988	18137	17502	17129	16425	15840	15216	14597	14597	25570	24238	Exan SEQ ID NO:
32756		26956	34861	34429	Γ	32274	0.00	39774	31905		28723	27646	27544	30056	33397	31111	30484	30132	29443	28951	28335	27674	27673		37871	ORF SEQ
0.62	1.91	1.32		1.05				0 99	1.91	218			298	3.62	1.59	2.74	2.22	7.78	0.72	1.21	1.15	2.26	2.26	3.26	1.64	Expression   Signal
				Γ	Γ	Γ		6.0E-84			Γ	Γ				1.0E-83	Γ		Γ		П	1.0E-83	1.0E-83	2.011-83	2.0E-83	Most Similar (Top) Hit BLAST E Value
5.0E-84 AA167678.1	5.0E-84 AF109718.1	5.0E-84 AA382811.1	6.0E-84 BE770189.1	6.0E-84 AF038391.1	6.0E-84 BE810371.1	11428718 NT		11428718 NT	6.0E-84 AA897339.1	6.0E-84 AL0428532	6.0E-84 AA776574.1	6.0E-84 BE838864.1	6.0E-84 BE838864.1	7.0E-84 BE901209.1	1.0E-83 AI027614.1	4502166 NT	1.0E-83 Z25822[1	1.0E-83 AF053768.1	7662349	BE88369	4503652 NT	4504326 NT	4504326 NT	2.0E-83 AB011399.1	2.0E-83 AL134452.1	Top Hit Acession
EST_HUMAN	2	EG! HOMAN	EG! HOMAN	1 2	ESI_HOMAN	1		<u>8 – N</u>	EST_HUMAN	EST HOWAY	EST HUMAN	EST HOMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	BNI	2	Z	NT	EST_HUMAN	1	NT	TNT	Z	EST_HUMAN	Top Hit Database Source
عربي 39هـ07.11 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632100 5' similar to TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;	I I III I I Galacia Americana	Lorno seriene chromosome 3 subletomeric region	ESTOSANA Testis I Hamo saplens cDNA 5' and	BNA STORAGE PROPERTY OF TRANSPORTED BY A STORAGE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T	Homo seriens pre-mRNA splicing factor (PRP16) mRNA, complete cds	MRNA  DAYOU TAOUR 190600 JONA-F02 LT0019 Home capiens CDNA	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endotherial certs (sixE),		VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);  VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);  VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	plazana en Spares NFI T GBC S1 Homo papions cDNA clone IMAGE:1460500 3' similar to gb:M14338	nkez-434H0322 r1 434 (synonym; htes3) Homo saplens cDNA clone DKFZp434H0322 5	RC2-FN0118-200000311-30011010101010100100000000000	RCZ-FNO118-2000000011-3001101101101101101101101101101101101101	6016/6023F I NIT IMSOLET I WITH SEPTING CONT.	PROTEIN (HUMAN):	Homo sapiens amyloid bela (A4) precursor protein (protease nexin-il, Abheimer discaso) (APP), mRNA	n. Septem Sporter to missession and the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september 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september of the september of the september of the	Ratius not regions drait apostrio conserno de la la somerase, exen 3	Tromo sapiens cen i coognitudi inclosed control (CBP90 mRNA, partial cds	OUTDU/370F I NIT WISC / I TOLING CAPTER OF THE PROPERTY (KIAAOB68), mRNA	Homo sapiens fath-ecid-Coenzyme A ligase, very long-critain 1 (100 to 1) in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 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Table 4

Single Exon Probes Expressed in Placenta

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9546	8579	8579	8247	6774	5843	5643	3027	3000	2172	2172	11118	3843	2063	2016	1178	326	11158	9112	9112	7825	6398	5680	5680	8377	5065	5084	1443	1407	11952	11952	11838	Probe SEQ ID NO:
22611	21660	21660	21329	19920	18837	18837	16203	16185	15307	15307	24180	17002	15203	16155	14341	13540	24228	22191	22191	20880	19567	18874	18874	18579	18183	18192	14596	14501	24838	24938	24827	Exan SEQ ID NO:
36179	35201	35200		33326	31915	31914	29226	29209	28436	28435		30005	28319	28260	27395	26572	37859	35736	35735	34381	32928	32163	32162	31448	31168	31167	27672	27635	38641	38640	38516	ORF SEQ ID NO:
1.24	0.58	0.58	1.55	0.92	0.93	0.93	1.22	9.21	6.46	6,46	6,78	5.53	2.36	2.39	1.53	2.16	4.76	1.12	1.12	13.68	2.14	1.8	1.8	1.62	1.52	0.66	4.47	1.34	1.99	1.99	2.85	Expression Signal
2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0€-84	2.0€-84	2.0E-84	2.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	5.0E-84		5.0E-84	Most Similar (Top) Hit BLAST E Value
2.0E-84 AU120230.1	2.0E-84 AL 163204.2	2.0E-84 AL 163204.2	2.0E-84 AI298674.1	2.0E-84 H63370!1	2.0E-84 BF511575.1	2.0E-84 BF511575.1	X89211.1	2.0E-84 AF036943.1	2.0E-84 BE695397.1	2.0E-84 BE695397.1	3.0E-84 AI983801.1	3.0E-84 AF014459.1	3.0E-84 AL096830.1	5453855	4758081	3.0E-84 AF026200.1	4.0E-84 AB032656.1	4557526 NT	4557526 NT	11421326 NT	4.0E-84 AF059650.1 NT	1138516	11386168 NT	4.0E-84 AF022835.1	4.0E-84 AF069601.2	4505928	4.0E-84 AI685321.1	4.0E-84 AB037735.1	5.0E-84 AB032957.1	5.0E-84 AB032957.1	11428740 NT	Top Hit Acessian
EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	S NT	NT	N	NT	8 NT	26 NT	6 NT	NT	X8 NT	NT NT	NT .	NT		EST_HUMAN	NT	NT	NT	TNO	Top Hit Database Source
AU120280 HEMBB1 Hamo saplens cDNA clone HEMBB1000339 5"	Homo sepiens chromosome 21 segment HS21C004	Homo saplens chromosome 21 segment HS21C004	qm87c09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 31	yr56e11.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2093243'	UI-H-BI4-eol-e-02-0-UI.e1 NCI_CGAP_Sub8 Homo septens cDNA clone IMAGE:3084883 3	UI-H-BI4-ad-a-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clane IMAGE:3084863 31	H.sapiens DNA for endogenous retroviral like element	Homo sepiens myelin transcription factor 1-like (MYT1-1) mRNA, complete cds	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA	wu20d05.x1 Soares_Dlockgreefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similer to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);	Homo sepiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete odo	Novel human mRNA containing Zinc finger C2H2 type domains	Homo sapiens pericentriclar meterial 1 (PCM1) mRNA	Homo sapiens chondroitin sulfete proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens Bach1 protein homolog mRNA, partial cds	Homo sepiens mRNA for KIAA1130 protein, partial cds	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sepiens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens multidrug resistance protein (MRP), excn 13		Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA	wa76c04.x1 Scares_NFL_T_GBC_S1 Homo sapians cDNA clone IMAGE:2302086.3' similar to SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR;	Homo saplens mRNA for KIAA1314 protein, pertial cds	Homo septens mRNA for KIAA1131 protein, partial cds	Homo sapiens mRNA for KIAA1131 protein, partial cds	Homo septens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

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- 1	11418185 NT	105.84	T			25 25236	12325
TOUTO SEPARTO 2 mitro-handrial (ACO2), mRNA	11417812 NT	1.06-84	٦		T	Г	9994
Homo services purineratio receptor P2X-like 1, orphan receptor (12/14-1); ""	400104014	1.05-84	1.6	28	1	Ţ	3
Homo sepiens ubiquitin specific protease 13 (Isophymusor 1975) mRNA	AEO TA NIT	1.01		27	88 31527	18488	9994
Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquitin specific processor (1977) Homo sepiens ubiquiti processor (1977) Homo sepiens ubiquitin specific processor (1977	784			6		72 23011	9972
Homo supieris Cata-Turium Provincia 13 (Isonophidase T.3) (USP13) mRNA	24511.1 NT	1 0E-84 AF224511.1	T		Γ	36 22800	9736
nomo sapraria ruscian catan caban CABP3 (CABP3) gene, exon 6 and partial cds	5031984 NT	1.02-84			T	Т	7777
in price riches fransbort factor 2 (placental protein 15) (PF16) mixix	11430846IN	1.06-84	234		1	Т	
Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NOC 1)	1143004014	1.品学	1.07		٦	7	7777
Homo capiens NGFI-A binding protein 1 (ENG) of the AVANDED PRINA	14 120000 NT	1.05-04	10.45			٦	7637
Homo sapiens polymerase (UNA director), elpina (Company) in 1 (NAB1) mRNA	8	2 2			33789	6 20339	7256
Novel human gene mapping a construction of the (POI A) mRNA	19794.1 NT	A DE BA DI 049794.1	Ī			Г	7020
NOVE NUMBER GENERAL TO CHARMAGE 13	9734.1 NT	1.0E-84 AL049734.1			T	Т	7020
the latest married to chomosome 13	9784.1 NI	1.0E-84 AL049784.1			T	Т	97.0
nt) Now himse dese mapping to chomosome 13		1.0E-84 S73482.1	2.84		32849	10401	9
uterine water channo=28 kda erynnocyte illioglia illiumater r		1.05	0.00		6 32549	19226	6043
Homo septens special-type ("Oz Prousi") and homo protein homolog (human, uterus, mRNA, 1340	11434422 NT	200	T			17676	5031
Homo sapiens goy to come work (SPOP), mRN/	N	4 0E-94 AJ229041.1	T		Γ	Γ	4821
L	3314.2  EST HUMAN	1.0E-84 AL043314.2			T	T	404
1	E-01	.0E-84 AL043314.2	ļ	3.03	1	Т	
1		1.0E-84 AJZZBU4 1.1		5.89		Т	4538
┙		1.00-04			5 30007	$\neg$	3845
		1.01.01			28562	16430	2298
	27197 NT	200				15252	2114
L	2137.1 EST HUMAN	1.0F-84 BE392137.1	Ī		1	Ī	1321
L	EST	1.0E-84 AA984379.1			27542	1777	3 3
85511 s1 Stratagene schizo brain S11 Homo sapiens	2703	1.0E-84		1.19		3	3
(YWHAZ) mRNA Homo sapiens complement component 5 (CS), mRNA Homo sapiens complement component 5 (CS), mRNA  TNA John MACE: 1629885 3'	4507952 NT	1.0E-84		10.87	26781	13766	663
Homo sapiens tyrosine 3-monoxygenaseu yhuqueur			T	6.1	26568	13536	322
_		1 DE 84 AF114483.1	T		T	25316	12449
<b>!</b>	000.1 EST_HUMAN	2.0E-84 BF448000.1		1 29			
nae30a02.x1 Lupski_sympathetic_trunk Homo saptens cDNA clone IMAGE:4090251 3' similar to	DO0.1 EST_HUMAN	2.0E-84 BF448000.1	Γ	1.81	32092	25316	12449
11000000000 1775RG23 1 ·	_	-				1012	8500
P26644 BETA-2-GLYCOPROTEIN I;  P26644 BETA-2-GLYCOPROTEIN I;  P26644 BETA-2-GLYCOPROTEIN I;	1.1 EST_HUMAN	2.0E-84 H22841.1		0.64	36564	22972	3093
ym49e11.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:01303 3 silliliar 2007 2007		-					
TAPOH RAT	Source		Value	Signal	D NO:	NO C	SEQ ID
OP THE CONSIDER	ession	_	(Top) Hit	Expression	ORF SEQ	9	
T Lis December	Top Hit	<u> </u>	Most Similar				
do Expression	Single Exor Flores Expressed						

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Single Exon Probes Expressed in Placenta

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5019	1821	1327	10798	8021	6276	6278	13127	11381	6567	5587	4552	2410	12060	11702	11702	11943	1159	13046	5032	5001	4366	3870	1709	1609	1609	1098	1098	Probe SEQ ID NO:
18148	14970	14484	23831	21074	18450	19450	17690	24442	18784	18764	17690	15540	25041	24699	24699	24929	14323	14860	18160	18130	17509	17029	14860	14762	14762	14263	14263	Exon SEQ ID NO:
	28062	27551		34688	32799	32798		38101	31805	31804		28668	38750	38392	38391		27378	27949	31137		30490		27949	27842	27841	27320	27319	ORF SEQ ID NO:
1.03	4.8	0.91	1.8	3.43		1.39	1.72	2.31	1.59	1.69	0.71	4.09	2	2.56	2.56	5.61	4.64	1.78	1.16	68.0	0.92	8.0	3.59	1.12	1.12	2.89	2.89	Expression Signal
									П			Γ		6.0E-85	6.0E-85	7.0E-85	7.0E-85		9.0E-85				9.0E-85					Most Similar (Top) Hit BLAST E Value
11024695 NT	3.0E-85 T97485.1	3.0E-85 AF096157.1	4.0E-85 BE079263.1	4.0E-85 BE882304.1	4.0E-85 BF677910.1	4.0E-85 BF677910.1	5.0E-85 AF211189.1	6.0E-85 AF224669.1	5.0E-85 BF035674.1	5.0E-85 BF035674.1	5.0E-85 AF211 89.1	5.0E-85 AL163284.2	6.0E-85 AA403053.1		11438573 NT	AF113210.1	L05094.1	7657020 NT	AL163268.2	5901979	AL163280.2	9.0E-85 AL163209.2	7657020	9.0E-85 M33282.1	9.0E-85 M33282.1	9.0E-85 U51432.1	9.0E-85 U51432.1	Top Hit Acession No.
5 NT	EST_HUMAN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	N <sub>1</sub>	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	3 NT	3 NT	NT	NT	ONT	NT		NT	NT	ONT	NT	NT	NT	NT	Top Hit Database Source
Hamo sepiens F-bax only protein 24 (FBXO24), mRNA	ye53g09.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'	Homo sapiens protein phosphatase 2A BR gamma suburit gene, exon 6	RC1-BT0823-120200-011-c07 BT0623 Homo sapiens cDNA	601505022F2 NIH_MGC_71 Homo papient cDNA clane IMAGE:3806940 5'	602084730F1 NIH_MGC_83 Homo sapiens cDNA clane IMAGE:4249087 5'	802084730F1 NIH_MGC_83 Homo sapiens cDNA clane IMAGE:4249087 5"	Homo sepiens T-type celctum channel alphat subunit Alphati-a Isoform (CACNAti) mRNA, complete cds	Homo sepiens mannosidase, bela A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	801458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'	601458646F1 NIH_MGC_63 Homo sapiens cDNA cione IMAGE:3862402 5'	Homo sepiens T-type calcium channel alpha1 subunit Alpha1I-a Isoform (CACNA1I) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21 C084	zt62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN. ;	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box potypeptide 10 (RNA helicase) (DDX10), mRNA	Homo sapiens MSTP030 mRNA, complete cds	Homo sapiens ribosomal protein L27 mRNA, complete cds	Homo saplens DKFZp434P211 protein (DKFZP434P211), mRNA	Hamo sapiens chromosome 21 segment HS21C068	Hamo sepiens heat shock transcription fector 2 binding protein (HSF2BP), mRNA	Hamo sapiens chromosome 21 segment HS21 C080	Homo sapiens chromosome 21 segment HS21 C009	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Human plasminogen gene, exon 7	Human plasminogen gene, exon 7	Homo sapiens nuclear protein Skip mRNA, complets ods	Homo sapiens nuclear protein Skip mRNA, complete cds	Top Hit Descriptor

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Prebe SEQ ID NO:	SEQ ID	ORF SEQ	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5019	18148	31128	1.03	3.0≅-85	11024695 NT	NT	Hamo septens F-bax only protein 24 (FBXO24), mRNA
5080		,	0.91	3.0€-85	7383442 NT	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5517	18715	31729	6.36	3.0E-85	11436001 NT	NT .	Homo sepiens lecrimal proline rich protein (LPRP), mRNA
6210	19385	32734	0.72	3.0E-85	11422024 NT	NT	Homo sepiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
0262	19436	32782	4.92	3.0E-85	7652309 NT	NT	
6282	19436	32783	4.92	3.0E-85	7662309 NT	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7091	20185		7.96	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chein (DNAH9 gene)
7555	20827	24102	0 84	3 05 85	11416870	T	Homo saplens GTPese regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621) mBNA
8058	21139	34659	1.44	3.0E-85 U44953.1	J44953.1	N.T	Homo sapiens DENN mRNA, complete cds
8706	21786	35319	0.48	3.0E-85	11525829 NT	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
9178			4.39	3.0€-85	11430889 NT	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9089			0.84	3.0E-85)	11421422 NT	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
9508	22772	36344	0.84	3.0E-85	11421422 NT	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA
10700	П	37338	0.72	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scremblase mRNA, complete cds
11798	24788	38484	1.48	3.0E-85	5031660 NT	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
12898	25848		3.02	3.0E-85	11418177 NT	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
985	14157	27218	0.62	2.0E-85	7657266 NT	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1065	Г	27289	2.35	2.0E-85	AF248640.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1436	Γ	27662	1.19	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1451		27682	13.02	2.0E-85	5174775 NT	NT	Homo saplens apolipoprotein C-II (APOC2) mRNA
1451	14604	27683	13.02	2.0E-85	5174775 NT	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2304	16436	28668	2.92	2.0E-85 U10525.		NT	Human DNA polymerase beta gene, exons 12 and 13
2884	14523		4.22	2.0E-85	7657468 NT	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3087	Г	29280	3.57	2.0E-85	2.0E-85 M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4454	17594	30574	4.66	2.0E-85	4505880 NT	NT	Homo sapiens plasminogen (PLG) mRNA
4687	17822	30810	0.74	2.0E-85	4826977 NT	Z T	Homo sapiens reelin (RELN) mRNA
5030	18159	31136	1.21	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9473	22530	36094	1.78	2.0⊑-85	2.0E-85 AI7608:20.1	EST HUMAN	wi67h08.x1 NCI_CGAP_Kid12 Homo capieno cDNA obne IMAGE:2398431 3' similar to contains element MSR1 repotitive element ;
9849	22889	38469	. 0.82	2.0Ε-85	2.0E-85 Al914459.1	EST_HUMAN	wd49d03_x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2331481 3'
10469	Г	37118	0.94	2.0E-85	2.0E-85 AI886384.1	EST_HUMAN	wm94d12.x1 NCI_CGAP_U/2 Homo septens cDNA done IMAGE:24436073"
2360	15491		3.66	1.0E-85	1.0E-85 BE 794308.1	EST_HUMAN	601591416F1 NIH_MGC_7 Harno septens cDNA clone IMAGE:3945818 5!

	00 (30300) 1 1111 1 110 0	EST HOMAN	3.0E-86 BE886479.1			1	Τ		
AVIZZOSE I NIH MGC 71 Homo sapiens cDNA clone IMAGE:3911303 5	ENTENDEDE NIH MGC 7	EST HUMAN	3.0E-86 AV722329.1			T	Т	8457	
AVZ22230 HTB Homo saplens cDNA clone HTBBSD04 5	AV72230 HTB Homo saple	EO HONON	3.0E-86 AW340948.1				Л	5713	
x-62h12 x1 NCI CGAP Lu24 Homo sapiens cDNA done IMAGE:28/1/193	VZOZNIO XI NCI CGAP LUZ	TO THE MAN	3.0E-86   BE86// Va. 1			30531	04 17547	4404	
601443262F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3847455 o	601443262F1 NIH_MGC_69	EST HIMAN	4.UE-86 BE34/1/3.1		1 2.34	19 26471		11517	
801072594F1 NIH MGC_12 Homo saplens cDNA clone IMAGE:3430630	601072594F1 NIH_MGC_12	EST HIMAN	4.UE-00 DE 23UTV.			32680	59 19335	6159	
17 Homo sepiens CUNA Conte INFOCT SAFERSON FO	601176865F1 NIH_MGC_17 Homo sepient cuna con	EST HUMAN	DECORRAS 1	1			217 13439	2	
601072594F1 NIH_MGC_12 Homo sapiens CUNA Cipire INVACE: 3731053 5	601072594F1 NIH_MGC_12	EST HUMAN	RE54717	T		Ī	Г	1322	
e dehydrogenase (lippamide) (OGCn) iiii No	Homo sapiens oxoglutarate d	ZNI		80E-86		Π	Γ.,	12117	
Homo sepiens coagulation factor XIII, A1 polypeptide (F13A1), mr.NA	Homo sapiens coagulation fa	3 NT	11418903 NT	T			П	11204	
anscription factor CA150 (H. sapiens) (LOCo3170), Illinois	Homo sapiens similar to transcription factor CA150 (H.	2NT		T				11204	
anscription factor CA150 (H. sapiens) (LOCos 170), INNIA	Homo saptens similar to transcription factor CA150 (H.	3 NT	110700	Τ			0 22999	0988	
	Homo sapiens DiGeorge syndrome critical region gene	7 NT	14505307 NT	Γ		Г		989	
g protein 7 (RANBP7), mRNA	Homo sapiens RAN binding protein 7 (RANBP7), mRN.	7 17 -	7.0E-86 L38557.7	١			╗	8943	
Homo sapiens galactocereorosidase (GALC) gene, exon 15	Homo sapiens galactocereore		17421/3/141		6.43	31499	٦	7118	
in T-cell leukemia virus type I) binding protein 1 ( I AX18F1), mixivo	Homo capiens Tax1 (humen T-cell leukemia virus type l	2 2	NIOSOODES			32854	_	6325	
Homo sapiens tumor endothellal marker 7 precursor (TEM7), mRNA	Homo sapiens tumor endothe	NIT	0000000 N1	7.01-86	0.97	32853	5 19497	6326	
Homo sapiens tumor endothetial marker 7 precursor (TEM7), mRNA	Homo sapiens tumor endother	EG LIONS	7.0E-86 AA86UGUT. I	7.0E-86		27193	$\neg$	98	
ai88(08.s1 Soares_parathyroid_tumor_NbHPA Homo septens cDNA clone IMAGE: 1400000	ai88f08.s1 Soares parathyroid	ECT LIMAN	7.0E-86 AA86U8U1.1	7.0E-86		27192	٦	88	
ai88f08.51 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone INAGE. 1400000	ai88f08.s1 Soares parathyroid	EGT HIMAN	1002247	7.0E-86		26480	13454	233	
Homo sapiens KIAA0680 gene product (KIAA0680), mRNA	Homo sapiens KIAA0680 geni	1	11 CVC632	8.0E-86		32774	19428	6254	
Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), ITINIVA	Homo sapiens similar to CDC	ı,	9.0E-80 BE2/421/.1	9.01-86	25.01		14613	1460	
801120778F1 NiH_MGC_20 Homo sepiens cDNA clone IMAGE: 2967690 5	601120778F1 NIH_MGC_20 I	EOT LIMAN	1141/00Z N	1.0E-85	2.92	32046	7	12601	
inding protein 1 (KIAA0330), mRNA	Homo saplens calcineurin binding protein 1 (KIAA0330),	1	1112007141	1.05-85	4.68	32045		12330	
	Homo sapiens calcineurin binding protein 1 (KIAA0330),	Į,-	1.0E-85 AIT88420.1	1.01-85/	3.29	38757	26049	12068	
125 Homo sapiens cDNA clone IMAGE: 1860/455 3	di56a07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA doi	EST HI MAN	1.0E-85 BF311302.1	1.05-85	1.88	37954		11245	
601897003F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:4128440 5	601897003F1 NIH_MGC_19 h	EST HIMAN	.0E-85 BF311562.1	1.0E-85	1.86		П	11245	
9 Homo sepiens cDNA clone IMAGE:4128440 5	601897003F1 NIH MGC 19 Homo sapiens cDNA clone	TOT LINAN	I.0E-85 AA778785.1	1.0E-85/	. 2.79	37866		11164	
r spicen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453243 3	2445f03.s1 Soares fetal liver_spicen_1NFLS_S1 Homo	EST DUMAN	1.0E-85 AA778785.1	1.0E-85 A	2.79	37865	7	11164	
spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3	รุปผริการ sal Source fetal liver splean_INFLS_S1 Homo	1_	1.0E-85 AW813525.1	1.0E-85 A	0.76	37055	╗	10416	
RC1-ST0198-081099-011-605-ST0196 Homo saplens cDNA	RC1-ST0198-081099-011-d05	L	1.0E-85 BE25/91/.1	1.0E-85 B	2.13	36615	7	1888	
6 Homo sapiens cDNA cione IMAGE:3350553 5	R01109738F1 NJH MGC 16 Homo sapiens cDNA clone		1.0E-85 BE062951.1	1.0E-85 B	0.61	34545	21032	7983	
NEC-ST0284-221199-002-03 BT0264 Homo sepiens cDNA	MB0-810264-221189-002-103	Ł		1.0E-85 B	9.36	28720	15594	2467	
7 Hamo sapiens cDNA clone IMAGE:3866021 5	601462817F1 NIH MGC 67 Homo sapiens cDNA clone	1_		1.0E-85 B	9.36	28719	16594	2467	
	601462817F1 NIH MGC 67 Homo saplens cDNA clone	1_		Value			Ş		
		Source	No.		Signal	ID NO:	SEQ ID	SEQ ID	
Top Hit Descriptor		Top Hit	Top Hit Acession	Most Similer		200	Exen	Probe	

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Table 4

Single Exon Probes Expressed in Placenta

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Table 4
Single Exon Probes Expressed in Placenta

1627	12980	12789	11143	10721	10667	10664	10664	8518	9104	8772	1	8772	8189	. 7221	0000	Į,	5993	4910	4161	3840	3840	3502	2342	2265	1217	427	277	12300	11803	11720	10425	NO.	Probe SEQ ID	
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9 27864	8	7 32006	5 37842	4 37360	1 37311	в 37308		36153	35728		1	35392	34803	33501	T	1		31030			30001	1			27437		26525		38491	37529	37086		ORF SEQ	
2.15	2.58	6.3		1.25								2.62	0.58					3.21	2.59	2.29			1.56	8.53	3.33	2.69	1.56	3.38	1.37	4.87	3.54		Expression Signal	
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Homo separa management	repetitive element;	placenta N52HP Homo saplens color o	Homo sepiens mRNA for KIAA1414 protein, particular to contains Alu	Homo capiens chromosome 21 segment read rode			Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (L. Courtes, minus)		Homo saplens mRNA for KIAA1081 protein, partial cds	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), minux		Human mRNA from chromosome 16 gene with homology to MHC-HLASB-1 intron A	ox59h01.s1 Soares NhHMPu S1 Homo sapiens cDNA done IMAGE:1660507 3	DKEZ6434N0323 rf 434 (synonym: htes3) Homo sapiens oDNA cidile DKEZ643	DKFZp434N0323_r1 434 (synonym: htes3) Homo saptene cDNA ctone UKFZp434N0323_5	II 5-HT0702-160600-103-d09 HT0702 Homo sapiens cDNA	L3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA	MR0-NT0039-020500-004-d11 NT0039 Homo sepiens cUNA	7h85f02x1 NCI_CGAP_Co16 Homo sapiens cDNA done IMAGE 3322779 3	NA done IN	O cuniculus mRNA for elongation factor 1 elpha	Homo sapiens a disintegrin and metalloproteinase domein 22 (ADAMZZ), mixiva	SW:K1CJ_MOUSE P02536 KERATIN, TYPE TOTIONAGE TO MRNA Home sablens a disintegrin and metalloproteinase domain 22 (ADAN22), mRNA	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens colve construction	Home saplens chromesome 21 segment HS21CU84	Homo sapiens chromosome 21 segment HS21C084	Homo saplenis synaptojanin 1 (SYNJ1), mRNA	Homo saplens chromosome 21 segment HS21C100	Homo sepiens ohromosome 21 segment HS21C009	Homo capiens chromosome 21 segment HS21C009	Human gamma-glutamyl transpeptidase mRNA, complete cas	Homo sapiens fibulin 5 (FBLN5) mRNA	Top Hit Descriptor	

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Single Exon Probes Expressed in Placenta

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601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 6	EST HUMAN	2 DE 87 RE531136 1	T		30208	Т	8589
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SO117503251 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3631511 5	EOI TOWAR	2.0E-8/ AV604143.1		0.75		20235	6920
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v/21e07.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:243386 6	EST HI MAN	2.0E-8/ BE30/193.1			Ī	Π	6456
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1	EST HUMAN	4 0E-87 RE247234 1					
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(MLT4) mRNA  (MLT4) mRNA  (MLT4) mRNA  (MLT4) mRNA  (MLT4) mRNA	4 NT	5174574 NT	4.0E-87	3.61	29732	16718	3553
Homo saniens mysloid/lymphoid or mixed-lineage laukemia (trithorax (Drosophila) homolog); translocated to, 4	2	1 N 6929077	4.0E-87	66.0	28739	16820	2493
Totilo Sapietra CGLen protein (LOCS1626) mRNA	9 N		4.0E-87		28738	15620	2493
repentive element,	EST_HUMAN	4.0E-87 R78133.1	4.0E-87	1.29	28403	15279	2143
y/80f10.r1 Socres placenta Nb2HP Homo sapiens CDNA Gidle IMAGE. 1707 6 Communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the c		,				T	
y80/10/1 Soares placettle Nozini nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulliu sepirelia comitati nulli sepirelia comitati nulli sepire	EST_HUMAN	R78133.1	4.0E-87	1.29	28402	16279	24.63
NA CIPE 145579 & similar to contains Alu			Value			ç	2
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E	Expression Signel	ORF SEQ	Expan SEQ ID	Probe SEQ ID
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Table 4
Single Exon Probes Expressed in Placenta

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3064	2704	1875	9223	4384	4384	3717	2189	1380	1380	1130	13228	13228	.12701	11247	10970	10584	9833	9833	9110	9110	8307	7707	7558	7333	6356	6356	3828	3801	1463	1463	1209	Probe SEQ ID NO:
16240	15822	15019	22301	17527	17527	16878	16324	14635	14535	14295	25798	26798	26190	24316	24050	23619	22873	22873	22189	22189	21389	20772	20630	20414	19526	19526	16988	16962	14616	14616	15989	Exon SEQ ID NO:
29260	28939		35845	30509	30508	29883	28449	27610	27609	27350	31891	31890			37683	37225	36457	36456	36733	35732	34912	34257	34105	33876	32884	32883	29991	29966	27699	27698		ORF SEQ ID NO:
0.62	3.65	1.22	4.04	2.97	2.97	1	0.99	2.94	2.94	8.48	1.22	1.22	2.31	1.66	2.11	0.88	2.92	2.92	0.05	0.95	9.93	0.92	1.05	1.09	1.63	1.63	2.3	5.18	1.61	1.61	2.2	Expression Signal
				9.0Ë-88		9.0E-88		Г					1.0E-87	1.0E-87	1.0E-87	1.0E-87												1.0E-87	1.0E-87	1.0E-87	1.0E-87	Most Similar (Top) Hit BLAST E Value
5.0E-88 AF114;88,1	5.0E-88 N89399.1	7661887	6.0E-88 AF003528.1	X91929.1	X91929.1	9.0E-88 AL163209.2	7661701	9.0E-88 AB037320.1	6.0E-88 AB037320.1	9.0E-88 AF167,465.1	AF169558.1	1.0E-87 AF169558.1	7657632	D10083.1	5729867	M34426.1	1.0E-87 BE818183.1	1.0E-87 BE818183.1	1.0E-87 AB022918.1	1.0E-87 AB022918.1	1.0E-87 AF214562.1	4506786	11431590	4506786	1.0E-87 AF073371.1	1.0E-87 AF073371.1	4758827	Y00052.1	1.0E-87 AW361977.1	.0E-87 AW 36/1977.1	7705683	Top Htt Acession No.
NT	EST_HUMAN	7 NT	NT	3	NT	NT	1 NT	NT	NT	NT	NT	NT	2 NT	TN	7 NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	6 NT	ONT		T	ZT	7 NT	NT	EST_HUMAN	EST_HUMAN	3 NT	Top Hit Database Source
Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	K9719F Human fetal heart, Lambda ZAP Express Homo sepiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1	Homo saplens KIAA0063 gene product (KIAA0063), mRNA	Homo sepiens X-linked enhidroitio ectodermel dysplasia protein gene (EDA), exon 2 and flanking repeat regions	H. saplens ECE-1 gene (exon 9)	H.sapiens ECE-1 gene (exon 9)	Hamo sapiens chromosome 21 segment HS21 C009	Hamo saptens DKFZP586P1522 protein (DKFZP586P1522), mRNA	Homo sepiens mRNA for KIAA1399 protein, partial cds	Homo sapiens mRNA for KIAA1399 protein, partial cds	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9	Hamo sapiens beta-urektopropionase (BUP1) gene, expn 9	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	Hamo sapiens RGH1 gene, retrovirus-like element	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Human L-plastin mRNA, 5' end	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA	RC6-BN0276-050700-012-E02 BN0276 Homo sepiens cDNA	Hamo sapions mRNA for alpha2,3-sialytransferase ST3Gal VI, complete cds	Homo saplens mRNA for alpha2,3-sialytransferase ST3Gal VI, complete cds	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA	Homo sapiens protein kinese C, beta 1 (PRKCB1), mRNA	Hamo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA	Hamo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8	Hamo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exan 8	Hamo sapiens neurexin III (NRXN3) mRNA	Human mRNA for T-cell cyclophilin	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA	Homo saplens putative glycolipid transfer protein (LOC51054), mRNA	Top,Hit Descriptor

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mkiva, complete cas	NT	3.0E-88 AF034374.1	Γ	7 1.58	71 34897	8390 21471	83
Homo saplens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein City	28 NT	11421726 NT	3.0E-88	7 9.3	87 34707	05 21187	8105
Long ceniens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA					T	7712	Ţ
Homo Subjets reuniculational Province	NT	11436400 NT	٦		T	Т	
	Z	3.0E-88 AF279265.1			٦	T	1
Librar content ruinting anion transporter 1 mRNA, complete cds	- NOT	11418210INI		0.84	٦	1	8543
Homo sapiens activator of S phase kinase (ASK), mRNA	N N			0.84		7	6543
Homo sabiens activator of S phase kinase (ASK), mRNA	ON T			0.72		7	6290
Homo seplens Interleukin 13 (IL13), mRNA	ST NI				12 32318	╗	5822
Homo sapiens v-rai simian laukemia viral oncogene homolog A (ras related) (RALA), mixiva	00 NT				32188	П	<b>5703</b>
Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA	3 N N N				16 31590	П	5414
Home series valosin-containing protein (VCP), mRNA			Γ	4.81		17737	4600
Home saciens hypothetical protein FLJ20220 (FLJ20220), mRNA	22			0.81	8 30478	$\neg$	4355
Hamo senieno a disintegrin and metaloproteinase domain 23 (ADAM23) mRNA	N		Γ	0.81	30477	٦	4355
Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA	בטן חטואאויו	3.0E-88 N66951:1		6.08	9 29214	7	3013
TRACETTO ST Socres fetal liver spieen 1NFLS Homo sapians cDNA clone IMAGE 295823 3	4	4508020 N I			٦	1	1855
Home soliens zinc (inger protein 259 (ZNF259) mRNA	2 2					П	750
Homo saplens hypothetical protein FLJ21634 (FLJ21634), mRNA	27	/86194/ N1		1.72		╗	11779
Homo seriens KIAA0152 gene product (KIAA0152), mRNA		N /#8100/		1.72	38464	9 24769	11779
Homo saplens KIAA0152 gene product (KIAA0152), mRNA	\$ 10 -	10 450 2020 IN			37849	0 24221	11150
Homo sepiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) ITITALY	217	11410303 NT	4.0E-88		0 33936		7392
Homo saplens transforming growth fector, beta-induced, 68kD (TGFBI), mRNA	EST HOMAN	4.0E-88 BF670714.1	4.0E-88	0.65		$\Box$	5244
BO21407951 NIH MGC 81 Homo sapiens cDNA clone IMAGE:4290975 5	EST HONAN	4.0E-88 BF091229.1	4.0E-88	0.96	7	7	138
BM1. TN0028-050800-004-f10 TN0028 Homo sapiens cDNA	EO TOWN	4.0E-88 BF091Z/9.1	4.0E-88	96.0	27589	П	136
PM1-TN0028-050900-004-10 TN0028 Homo septens cDNA	EST LI MAN	5.0E-88 BF680206.1	5.0E-88	0.53	36143	╗	9512
SOZI SAGERET NIH MGC 83 Homo saplens cDNA clone IMAGE:4295775 5	N	5.0E-88 AL1632E4.2	5.0E-88/	2.67		П	8114
Homo saplens chromosome 21 segment HS21C084	EOI TOWN	110932.1	5.0E-88 H10932.1	2.67		П	6910
winding 1 Soares Intent brain 1NIB Homo sapiens cDNA clone IMAGE:47129 5		5.0E-88 AF114488.1	5.0E-88/	0.71		П	4869
Homo saplens intersectin short isoform (ITSN) mRNA, complete cds	12	6.0E-88 AF1144E8.1	6.0E-88/	0.75	29806	П	3625
I come seniens intersectin short isoform (ITSN) mRNA, complete ode	EST HUMAN	5.0E-88 A1693217.1	5.0E-88	2.78		16643	3476
wd88h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu	2	5.0E-88 AF114488.1	5.01-88	0.71	29273	П	3075
Homo saplens intersectin short Isoform (ITSN) mRNA, complete cds	212	5.0E-88 AF114488.1	5.0E-88 A	0.71	29272	16251	3076
Homo sapiens intersectin short Isoform (ITSN) mRNA, complete cds	7						;
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E	Expression   Signal	ORF SEQ	SEQ ID	Probe SEQ ID

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Table 4
Single Exon Probes Expressed in Placenta

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Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hii Acession No.	Top Hit Database Source	Top Hit Descriptor
9834	21077	34589	2.14	3.0€-88	11526262 NT	NT .	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
10132	23170	36767	0.76	3.0E-88	3.0E-88 AB015/28.1	TN	Homo saptens mRNA for RALDH2-T, complete cds
10132		36768	0.76	3.0E-88		NT	Homo sepiens mRNA for RALDH2-T, complete cds
10162		36794	0.6	3.0E-88	11439065 NT	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12424			2.49	3.0E-88	11417974 NT	NT	
12439		31676	1.63	3.0E-88	11430460 NT	ZT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13223	25796	31889	1.31	3.0E-88	11526140 NT	NT	Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA
1061	14227	27283	6.85	2.0E-88	7305198 NT	NT	Homo saplens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1653	14806	27891	4.24	2.0E-88	2.0E-88 AF246218.1	NT	Homo sepiens SNARE protein kinase SNAK mRNA, complete cds
1789	Г	28031	6.83	2.0E-88	2.0E-88 AF246219.1	NT	Homo sepiens SNARE protein kinase SNAK mRNA, complete cds
3554	16718	29733	2.9	2.0E-88		NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4545	17683	30665	1.93	2.0∈-88	31666	NT	Homo sapiens dynein, axonemai, light polypeptide 4 (DNAL4), mRNA
6032	19216	32536	4.98	1.0Ε-88	1.0E-88 AW 139565.1	EST_HUMAN	UI-H-B11-aea-d-04-0-UI.e1 NCI_CGAP_Sub3 Homo expione cDNA clano IMAGE:2718750 3'
6032	19215	32537	4.98	1.0E-88	1.0E-88 AW 139565.1	EST_HUMAN	UI-H-Bi1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6783	18938	33334	21.66	1.0E-88	1.0E-88 AB007877.1	NT	Homo septens KIAA0417 mRNA, complete cds
6783	19938	33335	21.66	1.05-88	1.0E-88 AB007877.1	NT	Homo septens KIAA0417 mRNA, complete cds
7271	20354	33807	1.52	1.0E-88	1.0E-88 AI969034.1	EST_HUMAN	wq70a12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2476606 31
7334	20415	33877	3.7	1.0E-88	1.0E-88 AA488981.1	EST HUMAN	las54s11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:80272.2 CE00851 ;
8331	21413	34939	0.51	1.0E-88	1.0E-88 AF135183.1	NT	Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
9443	22559	36122	0.76	1.0E-88	1.0E-88 AA190368.1	EST_HUMAN	2087602.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA cione IMAGE:627170 5 similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN
9778	22818	36396	2.83	1.0E-88	1.0E-88 AL0433:14.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5
11730	23916	37541	3.35	1.0Ĕ-88	1.0E-88 AA991479.1	EST_HUMAN	os91g03.s1 NCI_CGAP_GC3 Homo sepiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
12865	25442		4.28	1.0E-88	1.0E-88 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13232	П	31850	1.54	1.0E-88	-	EST_HUMAN	UI-H-BI3-alk-b-03-0-UI.91 NCI_CGAP_Sub5 Homo septens cDNA clone IMAGE:2737084 3
11184	24263	37898	8.14	9.0E-89	1238	N,	Homo saplens transgelin 2 (TAGLN2), mRNA
2795	15910	29019	1.75	8.9⊟-89	8.0E-80 BE311557.1	EST_HUMAN	
7072	20125	33541	1.14	68-30.8	11421514 NT	Z	Homo caplono similar to soma domain, immunoglobulin domain (Ig), short basio domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
446	13642	26680	1.41	7.0E-89	7657213 NT	NT	Horno septens hormonally upregulated neu turnor-associated kinase (HUNK), mRNA
446	Ι.	26681	1.41	7.0E-89	7657213 NT	Z	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5005	18134	31108	2.71	7.0E-89	4557390 NT	3	Homo sapiens complement component 8, beta polypeptide (C88) mRNA

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1	EST POWER	OF 80 AV705749 1	T		16 31863	25916		
- 1		3.0E-89 AV/00451.1				39 24118	11039	
UMAN AV/08-31 CO Trans sariens cDNA clone ADBBGA01 3	1	3.0E-88 NO. 301	2.29 3.0		37751	 :	_	
1	EST HUMAN	157067		_				
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cDNA clone I CBAT VOCA NTANA2 Homo saplens cDNA	not E	_			Ī	6 18308	5186	
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_		_	T		31380	18413	2002	
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anians low density lipoprotein-realize in laritemia Baylor-HGSC project - 1 Con 1997	6806918[NT		T		30874	T		
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Homo sepiens PXR2b protein (PXR2b), mknA	Homo sapiens PXR2b protein (PXR2b), mRNA	Top Hit Descriptor	

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Table 4
Single Exon Probes Expressed in Placenta

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14380	13384	21603	21603	19285	19285	17485	17485	16312	16312	23706	23375	23375	23256	22244	22244	21699	14036	24021	24021	21836	16035	16035	14254	14254	21503	21603	Exan SEQ ID NO:
27439		35141	35140	32619	32618	30468	30467	28325	28324	37314	36986	36985	36844	35788	35787			37655	37654	35377	27592	27591	27309	27309	35036	35035	ORF SEQ
6.22	27.59	4.01	4.01	2.84	2.84	11.21	11.21	1.16	1.16	0.62	4.2	4.2	0.46	2.13	-2.13	2.14	6.81	1.38	1.38	0.6	3.26	3.26	2.91	4.38	1.07	1.07	Expression Signal
Г		6.0E-90	6.0⊱-90			6.0E-90											7.0E- <del>9</del> 0										Most Similar (Top) Hit BLAST E Value
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Human gamma-aminobutyric acid transaminase mRNA, partial cds		Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo sepiens HsGCN1 mRNA, partial cds	Homo sepiens HsGCN1 mRNA, pertial cds	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo saplens hypothetical protein FLJ10388 (FLJ10388), mRNA	H.sapiens ECE-1 gene (exon 6)	H.sapiens ECE-1 gene (exon 6)	802071208F1 NCL CGAP_Brn64 Homo sapiens cDNA done IMAGE;4214257 5'	yr85e04.51 Soeres fetal liver spleen 1NFLS Homo septens cDNA clone iMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;	yr88e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;	xv24e02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814026 3'	601655837R1 NIH_MGC_66 Homo sapiens cDNA clore IMAGE:3855824 3'	601655837R1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:3855824 3'	ai63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	qg98c08x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	qg96c08,x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	RC1-HT0598-120400-022-b08 HT0598 Hamo sepiens cDNA	7e36f08x1 NCI_CGAP_Lu24 Hamo sepiens cDNA clone IMAGE:3284583 3'	7e36f08x1 NCI_CGAP_Lu24 Hamo sepiens cDNA clone IMAGE:3284583 31	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Top Hil Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression   · Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1864	15010	28116	1.07	5.0E-90	5.0E-90 AI222035.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
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4662	Т	Π	4.61	5.0E-90	6354	NT	Homo sapiens pregnancy-zone protein (PZP) mKNA
4683	Т	Γ	0.78	5.0E-90	.2	Z	Homo sapiens chromosome 21 segment HS21C001
5708	Т	32198	2.85	5.0E-90		N	H.sapiens mKNA encoding phospholipase c
5910	18919	37207	0.72	5.00-90	5.0E-90 APOU8915.1	2 2	Homo sapiens EVIS mRNA, complete cas
5882	T	Ì	2	F 0F 00		NT	H sasians mRNA encoding phospholinasa c
6869		33430	. 0.95	5.0E-90	9910365	NT	Homo sapiens Cerbonic enhydrase-related protein 10 (LOC56934), mRNA
6869		33431	66.0	5.0E-90	9910365 NT	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7364	20443	33906	2.04	5.0E-80	5.0E-80 AF113708.1	NT	Homo sapiens anglopoletin 4 (ANG4) mRNA, partial cds
7364	20443	33906	2.04	5.0E-90	5.0E-90 AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
7736	20787	34286	7.98	5.0E-90	4557258 NT	NT	
8488	21569	35107	4.89	5.0E-90	11345483 NT	NT	Homo saplens hypothetical protein FLJ13222 (FLJ13222), mRNA
9882	22922	36506	1.17	5.0E-90	11419429 NT	N T	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10488			0.71	5.0E-90	5.0E-90 AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10663	23697	37306	9.68	5.0E-90	11433721 NT	NT	Homo sapiens ATPass, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
· 10723		37362	0.53	5.0E-90	7662051 NT	NT	Homo sepiens KIAA0317 gene product (KIAA0317), mRNA
10723	23756	37363	0.53	5.0E-80	7662051 NT	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12948	25659		1.77	5.0E-90	5.0E-90 AB011399.1	NT	Homo sepiens gene for AF-8, complete cds
13000	25849		4.54	5.0E-90	5.0E-90 AI523368.1	EST_HUMAN	er78h05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
313	13529	26562	2.04	4.0E-90	4.0E-90 AF231920.1	NT	Homo saplens chromosome 21 unknown mRNA
313	13529	26563	2.04	4.0E-80	4.0E-80 AF231820.1	TN	Homo sapiens chromosome 21 unknown mRNA
1110	14275	27332	4,36	4.0E-90	4505316 NT	TN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1724	14874	27966	13.42	4.0E-90 X99033		NT	H. saplens gene encoding discoidin receptor tyrosine kinase, exon 16
2923	1		0.74	4.0E-90	6806918 NT	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
52.RZ	19191	01167	0./4	4.01-80	INIBLEGORG	7	nomo sepiens low gensily ilpoprotein-realied protein z (LKFz), mKNA

SEQ ID Probe 8036 4939 3088 4919 10165 5903 5896 5896 4811 3948 1200 9993 888 386 SEQ ID 16101 21119 18069 18049 17914 19084 17944 14362 23032 19092 23032 13505 13895 15983 15983 ORF SEQ 30900 29114 29115 34638 31047 26473 27421 38619 34639 30103 30830 27422 32406 32395 31135 26539 26628 26628 26932 37571 36796 36795 36623 36624 Expression Signal 0.91 28.7 6.48 3.80 285 .6 3.08 1.46 0.99 1.05 228 <u>.</u> .46 (Top) Hit BLAST E Most Similar Value 3.0E-90 4.0E-90 2.0E-90 BE537913.1 3.0E-90 BF516168.1 3.0E-90 BE563833.1 4.0E-90 1.0E-90 AF231920.1 1.0E-90 AF231920.1 1.0E-90 AF231920.1 1.0E-90 AJ237689.1 2.0E-90 2.0E-90 Al138213.1 2.0E-90 AB006627.1 2.0E-90 2.0E-90 2.0E-90 2.0E-90 2.0E-90 2.0E-90 20E-80 2.0E-90 .0E-90 AJ237589.1 Top Hit Acession BF516168.1 AW672686.1 AU118985.1 AU118985.1 Š 6806918 NT 11024711 1162590 11427320 11427320 NT 5729855 5031748 NT 5031748 4502166 Z EST\_HUMAN EST\_HUMAN Z EST\_HUMAN EST HUMAN Z Z EST HUMAN 3 3 3 Z Top Hit Database Source HUMAN Homo sepiens low density lipoprotein-related protein 2 (LRP2), mRNA Homo sepiens low density lipoprotein-related protein 2 (LRP2), mRNA Homo sepiens DNA for emyloid precursor protein, complete cds UI-H-BW1-any-b-04-0-UI.s1 NCI\_CGAP\_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3 601335244F1 NIH\_MGC\_39 Homo sapiens cDNA clone IMAGE:3689147 5 Homo septens high-mobility group (nonhistone chromosoma) protein 17 (HMG17), mRNA qc54c02.x1 Scares\_placanta\_8tc9wecks\_2NbHP8tc9W Homo septens cDNA clone IMAGE:1713410 3' 601067378F1 NIH\_MGC\_10 Homo saplens cDNA cione IMAGE:3453834 5 UI-H-BW1-any-b-04-0-UI.s1 NCI\_CGAP\_Sub7 Homo saplens cDNA clone IMAGE:3083839 3 Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA Human prohormone converting enzyme (NEC2) gene, exon 6 Horno sapiens low density lipoprotsin-related protein 2 (LRP2), mRNA Homo sapiens mRNA for KIAA1244 protein, partial ode similar to SW:OLF3\_MOUSE P23275 OLFACTORY RECEPTOR OR3. Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA ba49d05.y3 NIH\_MGC\_10 Homo septens cDNA clone IMAGE:2899881 5' similar to TR:075208 075208 HYPOTHETICAL 35.5 KD PROTEIN.; Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5' Homo sepiens RaP2 interacting protein 8 (RPIP8), mRNA Homo sapiens GRB2-related adaptor protein (GRAP) mRNA Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA Homo sapiens RaP2 interacting protein 8 (RPIP8), mRNA Homo sapiens mRNA for KIAA0289 gene, partial cds Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial Homo sapiens chromosome 21 unknown mRNA Homo sapiens chromosome 21 unknown mRNA Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial Homo sapiens amyloid beto (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA Top Hit Descriptor

Single Exon Probes Expressed in Placenta Page 412 of 550 Table 4

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SEQ ID Probe Š 3954 3954 8 5792 334 9021 4543 4313 9516 3563 8501 8 8400 6750 SEQ ID Š 14299 13929 16093 15094 14491 22100 22550 22581 22581 18983 20085 19145 17681 14853 21582 20904 4491 21481 16728 18060 ORF SEQ 30663 32286 32460 30112 27561 27560 29106 28195 34408 35640 33500 36149 36148 30756 29744 30755 37163 35118 35581 Expression Signal 17.93 3.46 6.46 0.73 0.59 2.08 1.68 231 0.65 1.14 0.67 .33 123 Most Similar (Top) Hit BLAST E 1.0E-90 BE378884.1 1.0E-90 11420 1.0E-90 6005 1.0E-90 AB020710.1 1.0E-90 AB020710.1 1.0E-90 AF167340.1 1.0E-90 AB014533.1 1.0E-90 AF264750.1 1.0E-90 AF264750.1 1.0E-90 1.0E-90 1.0E-80 5.0E-91 5.0E-91 5.0E-91 AU143539.1 8.0E-91 D12234. 5.0E-91 AA702794.1 1.0E-90 1.0E-90 1.0E-90 5.0E-91 5.0E-81 AU143539.1 1.0E-90 5.0E-91 7.0E-91 .OE-91 AF096154.1 ) AF096154.1 Top Hit Abession U91834.1 AI9041,51.1 AF163864.1 BF314582.1 AV649878.1 A1879995.1 ř 11422109 NT 4.1 EST 11419234 NT 11422086 6005720 11422109 NT 1420514 NT 1507828 1426910 1142675B 7110634 NT 7110634 퐄 3 ¥ N Į Z Z EST HUMAN EST\_HUMAN EST HUMAN EST\_HUMAN Top Hit Database Source HUMAN NAMOH Homo oxpiens protein phosphatase 2A BR gamma subunit gane, exon 3
Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
60118956372 NIH\_MGC\_53 Homo sapiens cDNA clone IMAGE:3511118 5 Homo sapiens ALR-like protein mRNA, partial cds Homo sapiens Kruppel-like factor 7 (ubiqui Homo sapiens ALR-like protein mRNA, partial cds and complete cds, alternatively spliced Homo sapiens mRNA for KIAA0903 protein, partial cds Homo sapiens chromosome 8 open reading frame 2 (OSORF2), mRNA HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA cione s381 3 Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA **MRNA** Homo sepiens KIAA0623 gene product (KIAA0623), mRNA Homo sapiens mRNA for KIAA0633 protein, partial cds Homo sapiens mRNA for KIAA0903 protein, partial cds Homo saptens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) geno, exon 8, atternative exons 9 Homo sapiens SNCA Isoform (SNCA) gene, complete cds, elternetively spliced Homo capiens CGI-15 protein (LOC51009), mRNA Homo sapiens solute carrier family 1 (high effinity aspartate/glutamate transporter), member 6 (SLC1A6), au49f09\_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' stmillar to SW;ASPG\_FLAME Q47868 N4-(BETA-N-ACETYLGLUCOSAMINYL)+L-ASPARAGINASE PRECURSOR 1601801624F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4130933 5' AU143539 Y79AA1 Homo sepiens cDNA clone Y79AA1002087 5 z80b04.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:448015 3 CM-BT043-090299-075 BT043 Homo sepiens cDNA Homo sepiena CGI-15 protein (LOC51006), mRNA Homo sepiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2) luman retina-derived POU-domain factor-1 mRNA, complete cds Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA AU143539 Y79AA1 Homo saplens cDNA clone Y79AA1002087 5 AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3 saplens chromosome 22 open reading frame 5 (C22ORF5), mRNA tous) (KLF7), mRNA Top Hit Descriptor **TRNA** 

Single Exon Probes Expressed in Placenta

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Table 4

12685 12376 12376

ORF SEQ 29466 37875 35582 29465 32020 32074 32019 32119 31193 30832 29730 29729 27886 28077 28605 27885 32298 Expression Signal 3.27 3.27 3.22 1.58 <u>.</u>61 4.4 9 8 4.85 1.16 .58 2.08 Most Simila (Top) Hit BLAST E Value 5.0E-91 4.0E-91 AF156776.1 5.0E-91 AI193566.1 3.0E-91 4.0E-91 M77994,1 4.0E-91 M77894.1 4.0E-91 4.0E-91 1.0E-91 AF156776.1 1.0E-91 AL163284.2 3.0E-91 3.0E-91 3.0E-91 3.0E-01 AF265555.1 3.0E-91 3.0E-91 AF084530.1 3.0E-91 3.0E-91 AL163233.2 3.0E-91 AB033104.1 3.0E-91 AV649878.1 M77994.1 M77994.1 Top Hit Acession AL163285.2 AB033104.1 Z 11430193 11497611 11434964 Single Exon Probes Expressed in Placenta 4502740 Z EST\_HUMAN Z EST\_HUMAN 333 EST\_HUMAN 목목목 33 EST\_HUMAN EST\_HUMAN EST HUMAN Top Hit Database Table 4 AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3' Retrovirus-related gag polyprotein Retrovirus-related gag polyprotein
EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein EST01579 Hippocampus, Strategene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Homo sepiens chromosome 21 segment HS21C084 Homo sapiens lysophosphatidic acid acyltransferase-delia (LPAAT-delia) mRNA, complete cds Homo sapiens lysophosphatidic acid acyltransferase-delia (LPAAT-delia) mRNA, complete cds MIR.b2 MIR MIR repelitivo element; ge70f11.x1 Soeres\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:1744385 3' similar to contains Homo sapiens solute carrier family 4, enion exchanger, member 3 (SLC4A3), mRNA Homo sapiens solute carrier family 4, enion exchanger, member 3 (SLC4A3), mRNA EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein EST01579 Hippocampus, Strategene (cat. #936205) Homo sepiens cDNA clone HHCMC60 similar to Homo sapiens mRNA for KIAA1278 protein, partial ods Homo sapiens cyclin-D binding Myb-like protein mRNA Homo sapiens mRNA for KIAA1278 protein, partial cds Homo sepiens ubiquitin-conjugating BIR-domain வேதாக APOLLON mRNA, complete cds Homo sapiens chromosome 21 segment HS21C085 Homo sepiens chromosome 21 segment HS21C085 Human Ku (p70/p80) subunit mRNA, complete cds Homo capiens chromosome 21 segment HS21C083 Homo sapiens gamme-aminobutyric ecid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA Homo sapiens epididymal secretory protein (19.5kD) (HE1 Top Hit Descriptor complete cds 1), mRNA

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SEQ ID

SEQ ID

12971

25631

8960

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3272

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25267 25457

6713

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34368 34369 34735 33263

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19871 20871 20871

2.98 4.48 4.48

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11497611

Z

Homo sapiens gamma-eminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript verlant 2, mRNA Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11

Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11

Human mRNA for very low density lipoprotein receptor, complete cds Homo saplens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA Z

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Table 4
Single Exon Probes Expressed in Placenta

g	82	86	6677	9013		9000		1866	1866	22		9474	8569	8569	89 41	80 <u>4</u> 1	6583	6722	5579	5309	1270	1270	12540	12130	6983	6983	5529	1274	4	13037	13037	11480	11480	9488		SEQ ID	Probe
8620 21700	8283 21365	6680 19839	Г	T	19900	Т	Т	Т		296 13613		П	П		21124	21124	19745	2 18915		9 18426		Г		0 25110	3 20211	П		П	7	╗	7	24539	24539	22545			E XS
00 35236	Γ	39 33228		I	00 31877	T	1		12 28118	13 26547	26357	П		35191	4 34645	34644	5 33127		4 31820					38814		33640	31742	П		31431	31430	38208	38207	36108		D NO:	22.25
																													2.84	8.54	8.54		1.49			Signal	
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9.0E-92 LD41:00.1	92	14416061	8 0F-92 AF179428.1	8.0E-92 AJ000979.1	8.0E-92 AF264717.1		8.0E-02 AB046820.1	92 11434722 NT		BEJOOS	8.0E-92 W 2030/ 1	92 11422060 NI	AB0409	9.0E-92 AB040945.1	9.0E-92 AJ250550.1	9.0E-92 AJ250566.1	9.0E-82 AF310705.1		8.0E-92 JUSOO7:1	9.0E-92 MB020-00-1	8.0E-82/20001003.1	9.0E-92 N.001680 1	1.0E-91   110212-1	T.UE-91 AV/03033.	1.0E-91 BF348152.1	1.0E-91 BF348182.1	1 143440Z NI	AW 449	1.0E-91 AL163284.2	3.0E-91 AF169555.1	3.0E-91 AF169555.1	3.0E-91 AB029003.1	3.0E-91 AB029003.1	3.06-91 (480 11 190.1	AD0444684	N <sub>o</sub>	Top Hit Acession
	Z Z		NT.	N T	NT		2	22 N I	N.		EST HIMAN	DOT LIMAN				7 7	2	NIT -	TIN	3	212	Z	Z I	EST HIMAN	EST HIMAN	EST HIMAN	41	EO LOIMAN		12	12	2	1	1	Z	Source	Top Hit
	Human lens membrane protein (mp19) gene, exon 11	Homo sapiens AiM-1 protein (LOC51151), mRNA		Homo sapiens MCF-4 gene	ods	Homo sapiens in YVC domain-culturining over speciments and speciments	Inditio separation of the separation of the separation phosphatase FYVE-DSP2 mRNA, complete		Home seriens diacylolicerd kinase, gemma (90kD) (DGKG), mRNA	Homo saplens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA	601273513F1 NIH MGC 20 Homo saplens cDNA clone IMAGE:3614887 5	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Homo saplens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA	Home series mRNA for KIAA1512 protein, partial cds	Homo sablens mRNA for KIAA1512 protein, partial cds	Homo seplens partial TM4SF2 gene for tetraspanin protein, exon 5	Homo saplens partial TM4SF2 gane for tetraspanin protein, exon 5	Homo sepiens NALP1 mRNA, complete cds	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA		Homo sapiens mRNA for KIAA0833 protein, partial ods	Homo saplens NKG2D gene, exon 10	Homo sapiens NKG2D gene, exon 10	ym30e03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE: 49567 5		602022088F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4157804 5	E0202088F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4157804 5	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA	III.H.RIG.sks-d-01-0-UI.s1 NCI CGAP Sub5 Homo saplens cDNA clone IMAGE:2735280 3	Librar sarriers chromosome 21 segment HS21C084	Homo saniens bala-ureidopropionase (BUP1) gene, exon 6	Homo sapiens bata-ureidopropionase (BUP1) gone, exon 6	Homo sablens mRNA for KIAA1080 protein, partial cds	Homo sepiens mRNA for KIAA1080 protein, partial cds	Homo sepiens mRNA for KIAA0594 protein, partial cds	1	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

		3.0E-92/A1360#.1		7 3.26	37717	2 24081	11002
Human mRNA for elpha-actinin	21	X45004.1				2 24081	11002
Human mRNA for alpha-ecunin		VAEBOA 4	T		Γ	7 19182	5997
EST91020 Synovial sarcoma Homo sapiens cUNA 6 end similar to similar to incoming processing	EST HUMAN	2 0E-02 AA378336 1	T		Ī	Т	2824
601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5	EST HUMAN	3.0E-92 11434014 IN				1	2178
dominant, atavin 3) (MJD), mRNA	21					٦	
dominent, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 3) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva  Long content, atexin 4) (MJU), minva	NT NT	11434814 NT	3.0E-92	0.98	3 28441	8 15313	2178
Homo sepiens Machado-Joseph disease (spinocerebellar ataxia 3, olivoponicoerebellar ataxia 3, autosorika		7.05-82 /-	76-30.7	5.51	8 31448	18578	6376
Zw66d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5	EST HUMAN	AAAAAA	20E-92				5284
Homo sapiens prospero-related homeobox 1 (PROX1) mRNA	N	AROSA IS NOT	70-02		Γ	Γ.	4710
	3	7 05-00 571824 1	7 0E-03				
nf]  N. CANTALE Ido peural cell adhesion molecula fhuman, small cell lung cancer cell line OS2-R, mRNA, 2960	N	7.0E-92 S71824.1	7.0E-92	1.19	30828	17845	4710
N-CAM=145 kda neural cell adhesion moleculo [human, small cell tung cancer cell line OS2-R, mkNA, 2800		100,000	7.012-92	0.7	29610	18466	3426
Homo sapiens T-cell lymphoma invasion and metastasts 1 (TIAM1) mRNA	NT	4507500 NT	7.01-92			18466	3426
	2017		7.05-92			15903	2787
Homo sapiens NRAS-related gene (D1S155E), mRNA	2	AF16770	7.0E-92			П	2630
Homo saniens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	50315/0 N	7.0E-92	3.85			2260
Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	ON I		7.0E-92			$\neg$	2280
Homo seniers ARP2 (entin-related protein 2, yeast) homolog (ACTR2), mRNA	\$ N -		7.0E-92	1.94	27533		1309
Homo saplens B-cell CLUlymphoma 7b (BCL7B) mRNA	2	7.0E-92 AHOO/822.1	7.0E-92	1.68			604
Home seniens cytoplasmic Seprese truncated isoform mRNA, complete cds	12	7.0E-92 AB018301.1	7.0E-92	1.71	26489	16008	246
Homo saplens mRNA for KIAA0758 protein, partial cds	1	7.0E-82 AB018301.1	7.0E-82	1.71	28498	16008	246
	1 -	7.0E-92 M606/6:1	7.0E-92	1.91			88
Human von Willebrand factor pseudogene corresponding to exons 23 (trough 34	NA.	17434/V4 N	8.0E-92	1.69	32028	26491	12740
mKNA Homo sapiens fracile X mental retardation, autosomal homolog 1 (FXR1), mRNA	277	4503340 NT	8,0€-92	1.93	38415	24722	11642
Hamo sapiens dinydrolipoamae Seuccinylualista ass (LE company)							1.00
Homo septens nuclear mitogen- and stress-ectivated protein kinase-1 (MSK1) mRNA, complete cds	ZT	8.0E-02 AF074353.1	8.0E- <del>0</del> 2/	2.86	37765	24121	11043
TOMO SECIETA III AND TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR	N.	(13629.)	8.0E-82 Y13829.	0.91	36857	23267	10232
ions advantage and for MRNI profein		8.0E-92 AB014511.1	8.0E-92/	2.53	35889	22339	33.CB
Users and For KIAA0611 protein, partial cds		17420508 N	8.0E-92	0.71	35337	21801	8721
Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA		04183.1	8.0E-92 L04183.1	5.05	35236	21700	8620
Urman lans membrana protein (mp19) gene, exon 11			Y QU'O				
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	_ <del></del>	Expression   N	ORP SEQ	SEO E	Probe SEQ ID
				1			

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Single Exon Probes Expressed in Placenta

Homo sapiens mRNA for KIAA1093 protein, partial cds	ZT	2.0E-92 AB0290 16.1	2.0E-92	8.46	32035	25502	12758
CM4-LT0026-161299-062-g06 LT0026 Homo saplens cDNA	EST_HUMAN	2.0E-92 AW836290.1	2.0E-92	5.71	38135	24470	11409
CW4-LT0028-161299-062-g06 LT0026 Homo sapiens cDNA	EST_HUMAN	2.0E-92 AW836290.1	2.0E-92	5.71	38134	24470	11409
Homo saplens zinc finger protein 198 (ZNF198), mRNA		11434759 NT	2.0E-92	3.22	37965	24326	11257
Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA	NT	11434900 NT	2.0E-92	4.68	37709	24076	10997
hd02h02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:002711 PRO-POL-DUTPASE POLYPROTEIN;	EST_HUMAN	4.1	2.0E-92	1.26	35880	22135	9056
Human NPY Y1-like receptor pseudogene mRNA, complete cds	NT		2.0E-92	0.64		20697	7657
Human NPY Y1-like receptor pseudogene mRNA, complete cds	NT	2.0E-92 U67780 1	2.0E-92	0.61		20697	7627
Homo sapiens mRNA for KIAA1088 protein, partial cds	NT	2.0E-92 AB028991.1	2.0E-92	26	33297	19904	6748
Homo septens Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA	NT	4504756 NT	2.0E-92	7.19		19589	6431
Homo capiens P-glycoprotein (mdr1) mRNA, complete cds	NT	2.0E-82 AF016535.1	2.0E-82	0.64	32377	19069	5879
DKFZp434C0414_r1 434 (synonym: htes3) Homo capions oDNA clone DKFZp434C0414 5'	EST_HUMAN	2.0E-92 AL040437.1	2.0E-92	4.1		1	6108
Human endogenous retroviral DNA (4-1), complete retroviral segment	TIN	2.0E-92 M10976.1	2.0E-92	1.17	30530	17546	4403
Homo sepiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA	NT	5803180 NT	2.0E-92	7.02	29944	16938	3777
Homo saplens chromosome 21 unknown mRNA	TN		2.0E-92	1.02	29865	16862	3701
Homo sepiens chromosome 21 unknown mRNA	NT	2.0E-92 AF231919.1	2.0E-92	1.02	29864	16862	3701
Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA	NT	6912457 NT	2.0E-92	22.36	28954	15843	2725
Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA	NT	4506860 NT	2.0∈-92	5.35	28366	16245	2106
Homo septens transforming growth factor, beta 3 (TGFB3), mRNA	Ŋ	4507464 NT	2.0E-92	1.01	28266	15161	2020
Homo sepiens transforming growth factor, beta 3 (TGFB3), mRNA	<u> </u>	4607464 NT	2.0E-92	1.01	28265	15161	2020
wk27d07.x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;	NAWOH_TSE	2.0E-92 AI818119.1	2.0E-92	2.53	28237	15132	1990
wk27d07.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;	EST_HUMAN	2.0E-92 AI818119.1	2.0E-92	2.53	28236	15132	. 1990
mrg≖mas-related [human, Genomic, 2416 nt]	NT	2.0E-92 S78653.1	2.0E-92	1.62		14801	1752
601118337F1 NIH_MGC_17 Homo saplens cDNA cione IMAGE:3028304 5'	EST HUMAN	2.0E-92 BE289180.1	2.0E-92	5.49	26998	13949	768
601118337F1 NIH_MGC_17 Homo saplens cDNA clans IMAGE:3028304 5'	NAWOH_TS3	2.0E-92 BE299190.1	2.0E-92	5.49		13949	768
Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA	TN	11422946 NT	2.0E-92	4.28	26434	13405	183
Homo saplens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA	TN	11422946 NT	2.0E-92	4.28		13405	<b>18</b>
Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA	NT	4501898 NT	2.0E-92	1.54	26266	13264	26
RC1-GN0021-240800-012-e11 GN0021 Homo sapiens cDNA	EST_HUMAN	3.0E-92 BF367138.1	3.0E-92	1.67		26198	12878
Top Hit Descriptor	Top Hit Database Source	Top Hil Acession No.	Most Simfler (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:

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Table 4
Single Exon Probes Expressed in Placenta

	2	6.0E-83 AF045555.1	1.75 6.0E	<u>-</u>	16410	10	
renlication factor C subunit 2 (RFC2) gene, complete cds	<u>-</u> -				10181	91 0283	T <sub>g</sub>
where (WBSCR1) and where (WBSCR5) genes, complete cas, alternatively spilote and	2	5.0E-93 M22878.1			T	Т	ا
10	1 -	5.0E-93 X04201.1		3.73	١	T	Ţ
Human skeletal muscle 1.3 kb mRNA for tropomyocin		5.0E-93 AJ28/ 10.1		23 1.03	16049 28123	Т	T
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Homo saplens chromosome 21 segment rock (Not) is gene) is from 2	Z	0.0E-83 A107 T 101.1			92 27667	1439 14592	
wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens culvo civilo into	EST HUMAN	5.0E-83/A1074104.1	T		92 27666	٦	1439
wc09c08.x1 NCI_CGAP_Pr28 Homo salpana colora (MAGE:2314870 3)	EST HUMAN	3.0E-90 AIS74134 1	T		66 27640		1412
Homo sepiens mRNA for KIAAGE I Process, person IMAGE:2314670 3	NT	03 AB014511 1	T			56 20109	7056
	Z	6 0E-03 4E095771.1	T			19 19972	6819
Homo sapiens mRNA for KIAA1207 protein, per uni con RNA, complete cds	NT	ABOAR	T			16320	3144
Hall Page	76 NT	7.0E-93 Ar 23   010:	Τ		75 26506	13475	256
Homo sapiens chromosome 21 unknown makes 1 (TIAM1) mRNA		AE231010 1	Ī		80 33271	19880	6723
	EST HUMAN	BEOGRA	Ţ			7 24933	11947
Homo capiens ribosomal protein Live (12 Live).	즤	11418526	T		29867	Г	3703
601281867F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3803832 5	EST HUMAN	9.0E-93 AF223391.1	Π			2 15830	2712
spiced	-					Т	
protein L29 Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	EST_HUMAN	9.0E-93 AA316723.1		20.41	Б	0 15240	2100
EST188414 HCC cell line (matastasis to liver in illustration)		0.00	T	3.03	5 28347	5 15225	2085
AU121681 MAMMA1 Homo sapiens CDIVA Civil In mouse of Homo sapiens CDIVA 5' end similar to ribosome	EST_HUMAN	O DE 03 AL 121631.1	T			3 22440	9365
MER17 repetitive element;	EST HUMAN	A DE 02 A 1380353 1					
O18825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element;					T	224.22	COER
MER17 repetitive element;  MER17 repetitive element;  MER17 repetitive element;	EST_HUMAN	1.0E-92 Al380356.1		3.24	35999		3
Q16825 PROTEIN-TYROSINE PHOSPHATASE Dit ; contains Alu repetitive element contains element.			,		T	73017	8441
THIM 1200 MINISTER OF A 11 Home sapiens cDNA clone IMAGE:2107467 3' similar to SW:F INF_DUMNIN	EST HUMAN	1.0E-92 BE439625.1	1.0E-92		35051	T	2135
IN ASSECTION Home sapiens CDNA	ı	4506668 N	1.0E-92		Ī	1	8
Urmo saniens ribosomal protein, large, P1 (RPLP1) mRNA	HUNNA	0E-92 R78078.1	1.0E-92		T		100
Assence of Science placenta Nb2HP Homo sapiens CDNA Contributions	1000	1.0E-92 R/80/8.1	1.0E-92	295		Т	
v80e08.r1 Soares placenta Nb2HP Homo sapiens CUNA cibite IMACE: 145574.5	ECT LIMAN	1047180	2.0E-92	73.58	28954	٦	13066
Homo saplens calcineurin binding protein 1 (KIAA0330), mKNA	27	AF10665	2.0E-02	1.36	32005	25524	12782
Homo sablens edenylosuccinete lyase gene, complete cds			Value			2	NO:
	Source	70.	BLASTE	Signal	D NO:	SEQ ID	SEQ ID
Top Hit Descriptor	Top Hit Database	Top Hit Accession	Most Similar (Top) Hit	Expression	ORF SEQ	E E	Probe
	Single Exolit Floor	Singn					

		6.00			14407	3410	186
Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds		AB015610 1		F. 60		Т	11048
wb02d05.xt NCI_CGAP_GCB Homo sapiens CUNA CAR is important to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the	EST HUMAN	A 18248			1	Т	9
Homo sepiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA	B2 NT	11426182 NT	3.0E-93	1.31	33242	10851	990
1 Wine - apr	-	3.0E-93 AF 220690.1		2.6	3	0 17493	4350
Home series tensin mRNA, complete cds	TO LONG	3.0E-93 Brosugau.		7 12.26	3 29907	2 16903	3742
602246554F1 NIH MGC 62 Hamo sepiens cDNA clone IMAGE:4332036 5	EST HOWEN	3.0E-83 Br690630.1	Γ		3 29906		3742
R02246554F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'	EOT DUNAN	4.0E-83 AV692051.1			9 38123	3 24469	11398
yb94c12.r1 Stratagene liver (#937224) Homo seplens cDNA clone (MAGE: /8836 o striller to enimer to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN , AV632041 GKC Homo seplens cDNA clone GKCDRF07 5'	EST_HUMAN	4.0E-93 T46864 1			2 32255	18952	5760
I to the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and the complete and t	2	//0880N1	4.0E- <del>0</del> 3	0.76	29831	16819	5136
Homo sepiens tumor entiden SLP-8p (HCC8), mRNA	AN		4.0E-03		30306	17310	4159
Homo sanlens interleukin 18 receptor 1 (IL18R1) mRNA	GN-		4.0E-93		29831		3656
	N		4.0E-93	1.16			2672
Homo septions TNF-Individual CG12-1 (CG12-1), mRNA	2	4.0E-93 AF157476.1	4.0E-93	1.19		╗	2318
Library State (No. 1997) Annual State (REV3) MRNA, complete cds	2	4.0E-83 AF047677.1	4.0E-93	4.37	28284	_ [	2033
Homo septems (typoureuse promining to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o	8 NT	8923658 NT	4.0E-93	2.12	1		1210
nonio sepieris pessenine (Listerine) 20031 (FL) 20731), mRNA	ANT	7657454 NT	4.0E-83	1.16		П	785
Humo sapiens pessedille (zahrefish) hondog 1. containing BRCT domain (PES1), mRNA	N.	7657454 N I	4.0E-93	1.16		٦	783
nomo sapiens inicirioni ganinina cooper. (incomparing BRCT domain (PES1), mRNA	9 N T	4557879 N I	4.0E-93			П	48
Lucius exploris interior names receptor 1 ([FNGR1] mRNA	9 N	4557879 N	4.0E-93	2.38	28690	٦	458
P37397 CALPONIN, ACIDIC ISOFORM:	EST HUMAN	4.0E-93 AA459953.1	4.0E-93	6.63		13325	98
TERMO 1 Scams tests NHT Home septens cDNA come IMAGE:795688 3' similar to SW:CLPA_RAT		1747/8//NI	5.0E-93	2.31	31921	26791	12651
Homo saciens gamma-glutamytransferase 1 (GGT1), mRNA	NA PART	IN GROSEPLI.	5.0E-83		Γ		11084
Homo seriens aucleobindin 2 (NUCB2), mRNA	7	5.0E-93 AF069313.2	6.0E-93		36906	23310	10275
Homo senions WSB1 protein (WSB1) mRNA, complete ods	N	1N 991280G	5.0E-93	1.35	П	23050	10012
Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds		5.0E-93 AF274863.1	5.0E-93	2.02	36443	29822	9822
HOILD saturate more, may (proceptions)		4557526 NT	5.0E-93	0.73	35423	21883	8804
Tulib squaris usas; mass (cream) homolog 2 (chapsyn-110) (DLG2) mRNA		4567626 N I	5.0E-93	0.73	35422	21883	8804
Homo sabiens protein prosprintess— i regulatory socialities (1000) product alternatively spliced product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000) product (1000)		5.0E-63 AF067138.1	5.0E- <del>0</del> 3 /	3.52	34450	20944	7892
Top Hit Descriptor	Top Hit Database Source	Top Hit Accession No.	(Top) Hit BLASTE	Expression   Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:

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Table 4
Single Exon Probes Expressed in Placenta

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Table 4

Single Exon Probes Expressed in Placenta

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	20 6	382	2578	2534	2414	1376	1265	1265	1194	895	613	55	<u>6</u>	<u> </u>	12930	12624	12525	11333	11333	6822	5768	5764	5680	55 44	<u> </u>	525 <u>4</u>	2555	2199	8	2	띯	185		
Г	Т	14480	15702	15659	15544	14531	14422	14422	14356	14071	13802	13724	13341	13341	25813	25420	25358	24396	24388	18975	18960	18946	18854	18741	18730	18374	15680	6334	14789	13547	13547	13418	L	NO:
I	Т	0 27546			4 28672	27604	2 27488	27487		27136	28822	26760	26369						38044			32248		31775	31746	31340	28805	28461	27884	26578	26578	26448		ORF SEQ
			129	3.06	2 1.08	9.7						7.76			5.34	3.25	1.78		1.39	1.2		1.08		0.7		1.19	1.02		3.8	6.74	13.77	5.59		Expression Signal
ĺ						Γ		1.0E-93	Γ			6 1.0E-93	Ι.	Γ.			Γ											П		Γ		Γ		Most Similar (Top) Hit BLAST E
	1.0E-93 BE297369.1	1.0E-93 BE 297369.1	1.0E-83 AL137200.1	1.0E-93 AF055066.1	1.0E-93 AF231981.1	1.0E-93 AF16//06.1	3 10170768			D87675.1	1.0E-93 AI1487,55.1	3 /05/010/11	AF 23899	1.0E-93 AF238597.1	2.0E-93 BF035327.1	2.0E-83 L41825.1	2.0E-93 AA126735.1	2.0E-93 AV721846.1	2.0E-93 AV721846.1	2.0E-93 AW 502002.1	2.0E-93 U74313.1	11430039	BF3514	4758153	AW9643	2.0E-83 BE253201.1	2.0E-93 BE252982.1	2.0E-93 U40763.1	2.0E-93 AF225896.1	2.0E-93 AL163285.2	2.0E-03 AL163285.2	2.0E-93 AB015610.1		Top Hit Acession
	EST_HUMAN	EST_HUMAN	NT	Z	NT		N N	NT V	ZNI	2	EST_HUMAN	2	77	2	ES! HUWMIN	2	EST_HUMAN	EST HOMAN	EST_HOMAN	ESI HUMAN	EST_HUMAN		EST_HUMAN	Z	EST HUMAN	EST_HUMAN	EST HUMAN	N	N	2	Z	2		Top Hit Database Source
	601177686F1 NIH_MGC_17 Homo sapiens cuna doi a livro curvo	601177080F1 NITI MOSC IT ISSUE SPACE TO INA GET 3532985 5	Nover numan gene mapping to cramposine cDNA done IMAGE:3532965 5'	TIGHTO SEPTEMBER WITH CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE	Homo sapiens long chain polyuncaturated fatty acid elongation enzyme (HELO1) mRNA, complete cas	I WING Superior 2		Homo saplens hypothetical protein FLJ20291 (FLJ20291), mRNA		Homo sablens diutamate decarboxylase 1 (brein, 67kD) (GAD1), transcript varient GAD67, mRNA	ZINC FINGER PROTEIN.;  Homo saniers DNA for amyloid precursor protein, complete ods	oy64b08x1 NCI_CGAP_CLL1 Homo sapians cDNA clone IMAGE:1872503 3' similar to TR:Q62384 Q62384	Homo saniens hypothetical protein (DJ328E19.C1.1), mRNA	Homo seniens CTR1 pseudogene		801458531E1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5	1250 IV.s Course in 8 and	1200-10 st Spares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:503346 3'	AV733348 HTB Hamp senions cDNA clone HTBAUB04 5	AV777888 HTB Homo seniens cDNA clone HTBAUB04 5	HSU/4313 Human childringswise 14 Hamio septems cDNA clone IMAGE:3078329 5'	none saparis riyou readan (2-27)	QV3-H IUS I3-2803W- (20-liv4   1 0013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-1013   31-101	TOTIL SEPTET SESTION 128 AND HT0513 Home septens CDNA	LO 10 O Windows alloword dominant 5 (DFNA5), mRNA	COTTOTALES MACE rescallences MAGH Homo sabiens cDNA	CONTRACTOR VIII MCC. 16 Homo septems cDNA clone IMAGE:3357243 5		Transaction in the Complete ode	Dans spriene tensin mRNA complete cds	Light opposite chromosome 21 segment HS210085	Library chromosome 21 segment HS21C085	Characehus aethiops mRNA for ribosomel protein S4X, complete cds	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

Agorigous i ocures real mear, rudnin lew nomo sapiens curva cione image: 44554 3 083405.s1 Soares_total_feitus_Nb2HF8_9w Homo sapiens cDNA cione iMAGE:1823369 3*	EST_HUMAN	5.0E-84 AI015800.1	5.0E-94	1.45	33726	20285	7150
Homo sapiens mkina for kinadiotiz protein, partial cos	2	5.0E-94 AB014512.1	5.0E-94	3.51	31699	Т	248
Homo sepiens mRNA for KIAA0612 protein, partial cds	NT	5.0E-94 AB014512.1	5.0E-94	3.51	31698	Г	5483
Homo sapiens transcription enhancer factor-5 mRNA, complete cds	NT	6.0E-84 AF142482.1	6.0E-94	1.94	30233	Τ	4070
Homo sapiens chromosome 21 segment HS21C009	NT	8.0E-84 AL163209.2	8.0E- <del>9</del> 4	1.13		23852	10819
Homo sapiens glutathione S-transferase theta 2 (GSTT genes, complete cds	Z <sub>T</sub>	1.0E-93 AF240786.1	1.0E-93	1.42		26173	13123
Homo sapiens calcineurin binding protein 1 (KIAA0330).	2 NT	11417862 NT	1.0E-93	1.36	31941	25723	13108
Homo saplens glutathlone S-transferase theta 2 (GSTT	NT	11417856 NT	1.0E-83	3.71		25608	12923
Homo sapiens GGT1 gene, exon 1	NT	1.0E-93 AJ230125.1	1.0E-93	1.62		26547	12820
Homo sapiens ryanodine receptor 3 (RYR3), mRNA	SNT	11433646	1.0E-93	0.59	36994		10349
Novel human gene mapping to chomosome 13, similar to rat RhoGAP	TN	1.0E-93 AL049801.1	1.0E-93	1.24	36655		9926
Human PreA4 gene for Alzhelmer's disease A4 amyloid	NT	.0E-93 X13474.1	1.0⋶-93	3.9	36404	22827	9787
Human PreA4 gene for Alzheimer's disease A4 amyloid	NT	1.0E-93 X13474.1	1.0E- <del>9</del> 3	3.9	36403	22827	9787
Homo sapiens Trio isoform mRNA, complete cds	F	1.0E-93 AF091395.1	1.0⊑-93	1.14	34612		9656
Homo sapiens mRNA for KIAA1485 protein, partial cds	NT	1.0E-93 AB040918.1	1.0E-83	2.03	34608	21094	9851
Homo sapiens protein kinass inhibitor gamma (PKIG) mi	NT	1.0E-93 AF182032.1	1.0E-93	1.14	35468		8850
H.sapiens mRNA for MEMD protein	TN	1.0E-93 Y10183.1	1.0E-93	1.15	35353	21819	8740
Homo sapiens mRNA for KIAA1411 protein, partial cds	NT	1.0E-93 AB037832.1	1.0E-93	2.29	35066	21536	8455
Human mRNA for NF1 N-isoform-exan11, complete cds	NT	D42072.1	1.0E-93 D420;	3.24	33946	20478	7400
Homo sapiens protein kinase C, beta 1 (PRKCB1), mRI	UT	11431500 NT	1.0⊑-93	1.94	33679	20246	6931
Homo saplens KIAA0672 gene product (KIAA0672), mRNA	NT	7662241 NT	1.0E-93	4.8	32855		6326
Homo sapiens neurofibromin 1 (neurofibromatosis, von mRNA	Z NT	4557792 NT	1.0E-93	10.78	32543	19220	6037
Homo sapiens candidate taste receptor T2R14 gene, co	NT	1.0E-93 AF227138.1	1.0E-93	1.2	32383	19074	5885
Homo sapiens glucocorticold receptor (GRL) gene, intron D, exon 5, and intron E	NT	1.0E-93 U78509.1	1.0E-93	2.39	32168		5684
Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E	NT	1.0E-93 U78509.1	1.0E-93	2.39	32167		5684
Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6	IN	1.0E-93 AF123498.1	1.0E-93	0.92	31427	18461	5348
Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6	INT	1.0E-93 AF123498.1	1.0E-93	0.92	31426	18461	5348
Homo sapiens chromosome 21 segment HS210084	NT	I.0E-93 AL163284.2	1.0E-93	3.28	30668		4549
Homo sapians long chain polyunsaturated fatty acid elor	NT	1.0E-93 AF231981.1	1.0E-93	1.23		16461	3287
Homo saplens DNA for amyloid precursor protein, comp	NT	1.0E-93 D87675.1	1.0E-93	5.86	29197	16176	3000
	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:

7/7/S/10 OM

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	EOI TOWAY	1.0E-94 BEZX6/14.1	Γ	0 3.07	8 26410	3 13378	153
F01175782E1 NIH MGC 17 Homo saplens cDNA clone IMAGE:3531038 5	TOT HOMAN	2.0E-94 AJ910393.1		0.67	36588		9954
WISON 11 X INC. CGAP Co16 Homo saplens cDNA done IMAGE:2391813 3'	EST HOMAN	2.0E-94 AI910393.1		7 0.67	36587	П	9954
LIBITIAN 1 NOT CRAP Co16 Home sapiens cDNA done IMAGE:2391813 3'	2	3.0E-94 U26711.1			38662		11976
	_	4/5/821		9 1.94	38079		11362
Homo seriens gyonal transport of synaptic vesicles (ATSV) mRNA		AF08794		7.29	38410	$\neg$	9791
Homo serviens altromenin-11 mRNA complete cds	2	3.0E-94 AB014579.1				7	8787
	2	3.0E-94 AF152309.1		0.96		$\Box$	8383
Homo sories protoceriberio elpha 13 (PCDH-elpha13) mRNA, complete cds	3 N -	4826863 N		0.63	7 34541	7	7978
Home serviens neumanal cell adhesion molecule (NRCAM) mRNA	2 2		3.0 €-94		3 33125		6581
Homo saniens chromosome 21 open reading frame 18 (C21ORF18), mRNA	ZI Z	AB0115			3 32801	19453	6279
Homo sapiens mRNA for MEGF2, partial cds	N N	11496268			8 32292	18988	5798
Homo seplens zinc finger protein 277 (ZNF277), mRNA	EG! HOWAIN	AA7818	Γ		П		4437
ANOUGO: 1 Soares testis NHT Homo sepiens cDNA clone 1375163 3	1_	3.0E-94 AA464805.1			П	17449	4306
Tuestant of Spares total febus Nb2HF8 9w Homo septems cDNA clone IMAGE:774782 5	77	450/000				14962	1813
Homo seniens E1A binding protein p300 (EP300) mRNA	N	AF167/0			8 28022	14928	1779
Homo saniens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	7	3.0E-94 AF167/706.1	Γ		8 28021	14928	1779
Homo saniens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds		4502506	Γ		26961	П	739
Long seriens complement component 5 (C5) mRNA	2	AB02278		1.76	26833		626
Long septems ASH2 gane complete cds, similar to Drosophila ash2 gene		4.0E-94 L27386.1		0.9	5	20105	7052
Homo seplens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA		11440670 NT	4.0⊑-94	1.48	33145	19757	6597
Homo saplens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA		11440670 NT	4.0E-94	1.48	33144	19757	6597
PROTEIN TYROSINE PHOSPHATASE;	EST_HUMAN	4.0E-94 AI591312.1	4.0E-94	3.06	30983	17973	4840
n52 Homo sapiens cDNA clo	EST HUMAN	4.0E-84 AW 197351.1	4.0E-94	1.12	29926	16923	3762
WIBSTIZM Scenes NET T GBC S1 Homo sabiens cDNA clone IMAGE:2701679 3	1_	4.0E-94 AW 197851.1	4.0E-94	1.12	29926		3762
Homo sapialis protein prospiration (1, 1991). Homo sapiens cDNA clone IMAGE:2701679 3	NT	4506008	4.0E-94	66'0	28952	П	2723
Homo sapiens noosomal protein LZ/ IIIN/NA, complete vo	Z	4.0E-94 L05094.1	4.0E-94	16.49		Т	1890
ydyspu4.51 Coales letai live spacer live to living spreads	EST_HUMAN	T89398.1	5.0E-94 T89398	3.6		Т	12503
Homo sepiens edenyiere kinese a (Ana), illinas		11423962 NT	5.0E- <del>0</del> 4	1.43		Т	11215
Hans equilis equilyade virase & (2007) ONIV		11423962 NT	5.0E- <del>9</del> 4	1.43	37822	$\neg$	11215
	THUMAN	5.0E-94 BF529115.1	5.0E- <del>0</del> 4	0.85	35457	21919	8840
Top Hit Descriptor		Top Hit Acession No.		Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
			Most Similar				

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
3158		29342	2.05	1.0E-94	1.0E-94 BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE 3352559 5'
3158	16333	29343	2.05	1.0E-94	1.0E-94 BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3352559 5'
4478	17618	30600	1.11	1.0E-94	9506692 NT	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6198	18373	32724	0.69	1.0E-94	1.0E-94 AE000269.1	TN	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6396	Γ	32925	1.91	1.0E-94	1.0E-84 AL040518.1	EST_HUMAN	DKFZp434G0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6405	19574	32936	0.82	1.0E-94	1.0E-94 H08270.1	EST_HUMAN	y/87/02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:45053 5
6648	Г	33194	0.66	1.0E-94	1.0E-84 AV725682.1	EST_HUMAN	AV725992 HTC Hamo sapiens cDNA clone HTCBEF05 5'
8304	Π	34908	- 0.8	1.0E-94	1.0E-94 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8304	21386	34909	0.8	1.0E-94	1.0E-84 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9456	Г	36138	2.17	1.0E-94	11428710 NT		Homo sepiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9990	23029	36820	1.35	1.0E-94	1.0E-94 BE780478.1	EST HUMAN	601468748F1 NIH_MGC_67 Homo sepiens cDNA clone IMAGE:3872099 5'
11321	24384	38028	3.11	1.08-94	1.0E-94 U65590.1	TN	Homo sapiens IL-1 receptor entegonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11697	24650	38334	1.88	1.0E-94	1.0E-84 AI2722.44.1	EST_HUMAN	ap22e02x1 Schiller digoderdroglioma Homo sepiens cDNA clone IMAGE:19561223' similar to TR:Q62845 Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR.;
12051	25032	38738	1.34	1.0E-94	11418871 NT	NT	Homo sepiens KIAA0164 gene product (KIAA0184), mRNA
12639	13378	28410	2.02	1.0E-94	1.0E-94 BE295714.1	NAWOH_TSE	601175762F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:3531038 5
12968	13378	26410	1.73	1.0E-94	1.0E-94 BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Hamo sepiens cDNA clone IMAGE:3531038 5'
1506	5 14859	27741	6.05	9.0E-95	9.0E-95 AF027302.1	Z	Homo sepiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3224	16398	29409	1.09	9.0E-96	7682027	NT	Homo sepiens KIAA0255 gene product (KIAA0255), mRNA
3224	16398	29410	1.09	9.0E-95	7662027	NT	Homo capione KIAA0255 gane product (KIAA0255), mRNA
5521	18718	31733	1.46	9.0E-95 X82569.1	X8250e.1	NT	M.musculus glyT1 gene (exons 1c and 2)
5521	18718	31734	1.46	9.0E-95	9.0E-95 X82569.1	NT	M.musculus glyT1 gene (exons 1c and 2)
8446	3 21527	35054	1.58	9.0E-95	9.0E-95 AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
148	13374	28407	2.9	8.0⊑-85	8.0E-95 AF154830.1	NT	Homo sepiens carbamyl phosphate synthetase I mRNA, complete cds
4658	17794	30779	1.68	8.0E-95	8.0E-95 A1700998.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
4658	3 17794	30780	1.68	8.0E-95	8.0E-95 AI700998.1	EST_HUMAN	we08e04.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
7087	20181	33605	0.73	8.0E-95	11419376 NT	NT	Homo septens KIAA0193 gene product (KIAA0193), mRNA
7390	20468	33934	1.4	8.0E-95	11426529 NT	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7390	20468	33935	1.4	8.0E-95	11426529 NT	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8391	$\Gamma$	34998	208	8.0E-95	8.0E-95 AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9565	22707	36273	1.98	8.0E-95	11420944 NT	Z	Homo sapians KIAA0255 gene product (KIAA0255), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA	NT	5453665 NT	2.0E-05	1.5	28744	15624	2497
Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA	NT	5453665	2.0E-05	1.5	28743	15624	2407
601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5	EST_HUMAN	BE393873.1	2.0E-95	3.97	28246	15139	1998
Homo sepions tissue inhibitor of metalloproteinese 3 (Scrsby fundus dystrophy, pseudcinflammatory) (TIMP3) mRNA	NT	4507512 NT	2.0E-95	73.27	28242	15136	1995
Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	NT	7662027 NT	2,0E- <b>9</b> 5	3.52	27912	14828	1676
Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	NT	7662027 NT	2.0E-95	3.52	27911	1	1678
601846212F1 NIH_MGC_55 Homo septens cDNA cbne IMAGE:4070451 5'	T_HUMAN	3.0E-95 BF213446:1	3.0E-95	0.86	36581	22987	9948
Homo sepiens KIAA0763 gene product (KIAA0763), mRNA		7662289 NT	3.0E-⊖5	1.62	36191	22820	9555
Homo sepiens KIAA0763 gene product (KIAA0763), mRNA	NT	7662289 NT	3.0E-95	1.62	36190	22620	9555
EST370191 MAGE resequences, MAGE Homo sapiens cDNA	EST_HUMAN	AW956121.1	3.0E- <del>0</del> 5	2.01	34072	20588	7525
EST370191 MAGE resequences, MAGE Homo sapiens cDNA	EST_HUMAN	1	3.0E-95	2.01	34071	20598	7525
Z97d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'	EST_HUMAN	3.0E-95 AA412321.1	3.0€-95	0.73	33860	20397	7315
zl97d01.r1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'	EST_HUMAN	3.0E-95 AA412321.1	3.0E-95	0.73	33859	Ι_	7315
Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA	NT	4503354 NT	3.0E-95	0.94	32285		5791
602071146F1 NCI_CGAP_Bm64 Homo sapiens cDNA done IMAGE:4214147 5	EST_HUMAN	BF526041.1	3.0E-95	1.52	31794	18766	6658
AV648361 GLC Hamo sapiens cDNA clane GLCBIF01 3'	EST_HUMAN	3.0E-95 AV648361.1	3.0E-95	0.82	26468		215
HTM1-288F HTM1 Homo sapiens cDNA	EST_HUMAN	4.0E-95 BE439625.1	4.0E-95	0.62	36058		9418
Homo sapiens chromosome 21 segment HS21C046	NT	7.0E-95 AL163246.2	7.0E-95	1.09		17673	4535
Hamo septens Ly-6-like protein (CD59) mRNA, complete cds	NT	7.0E-95 M95708.1	7.0E-95	15.92	30608	17626	4486
Human hepatocyte growth factor gene, exon 8	NT	7.0E-95 M75973.1	7.0E-95	1.37	28768	16646	2519
Human hepatocyte growth factor gene, exon 8	NT	7.0E-95 M75973.1	7.0E-95	1.37	28767	Г	2519
Homo sapiens DNA for emyloid precursor protein, complete cds	NT	7.0E-95 D87675.1	7.0E-95	6.07	26538	13504	286
Homo sapiens DNA for amylold precursor protein, complete cds	NT		7.0E-95	6.07	26537	13504	286
zu84b01.s1 Soares_testis_NHT Homo septens cDNA clone IMAGE:744649 3' stmitar to contains L1.t1 L1 repetitive element;	EST_HUMAN	8.0E-95 AA629056.1	8.0E- <del>0</del> 5	17.21		25588	12887
Hamo sapiens zinedin (ZIV), mRNA	NT	7019672 NT	8.0E-85	1.32	38670	24867	11982
Homo sapiens zinedin (ZN), mRNA	NT		8.0E-95	1.32	38669	24987	11982
Homo sapiens HCF-binding transcription factor Zhengfel (ZF), mRNA	NT	10864024 NT	8.0E-95	1.72	38461		11773
Homo sepiens developmental erteries and neural crest EGF-like protein mRNA, complete cds	NT	8.0E-95 AF112152.1	8.0E-95	1.59	37670	24035	10953
Homo sepiens early growth response 2 (Krox-20 (Drosophile) homolog) (EGR2), mRNA	NT	9845523 NT	8.0E-95	0.81	37079	23475	10440
Homo saplens mRNA for KIAA1395 protein, partial cds	NT	8.0E-95 AB037816.1	8.0E-95	2.92		23121	10083
Homo sapiens proline dehydrogenase (proline oddase) (PRODH) mRNA	NT	5174844 NT	8.0E-95	2.45	36693	23091	10053
Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	NT	11420944 NT	8.0E-95	1.98	36274	22707	9565
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:
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Table 4
Single Exon Probes Expressed in Placenta

38692 1.69 2.0E-95 76 1.67 2.0E-95 AF161420.1
1.69 2.0E-95
1.35 2.0E-95
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3.25 2.0E-95 AF2677
0.0 2.0E-95
3.86 2.0E-95 M59724
32352 0.63 2.0E-05 11525132 NT
1.24 2.0E-95 1
4.12 2.0E-95
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0.99
31242 3.6 2.0E-95 7681979 NT
1.38
30006 0.62 2.0E-95 A1290264.1
29870 0.81 2.0E-95 AB037807.1
3.6 2.0E-95
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21
28828 1.34 2.0E-95 47
28784 3.62 2.0E-95 AF24078
ORF SEQ Expression (Top) Hit Top Hit Acession ID NO: Signal BLAST E No.

	Probe SEQ ID NO: 1272: 13067 6732 7683
7683 9963 22 8388 2388 456 10 456 11 4018 11 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11839 11	8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
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Table 4
Single Exon Probes Expressed in Placenta

Probe Exon SEQ ID SEQ ID	ORF SEQ	Expression		Top Hit Acession	Top Hit	Top Hit Descriptor
	D NO:	Signal	BLAST E Value	70	Source	Top I III Desori possi
7163 20298	33740	0.91	5.0E-96	5.0E-96 AB0231/77.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
П	34231	0.76	5.0E-96		NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
	34900	1.87	5.0E-96		NT	Human type IV collagenase (CLG4B) gene, exon 5
	34901	1.87	6.0E-96 M68347.1	VI68347:1	NT .	Human type IV collagenass (CLG4B) gene, exon 5
	38769	1.33	5.0E-96	661973	TN	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
П		15.95	3.0E-96 H68656	1	EST_HUMAN	yr87h12.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
428 13623		6.76	2.0E-96	4503098 NT	TN	Home sapiens chendreitin sulfate proteeglycan 4 (melanoma-essociated) (CSPG4), mRNA
	26994	1.1	2.0E-96	2.0E-96 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1834 14981	28079	1.03	2.0E-96	6205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4880 18011	30895	1.56	2.0≣-96	2.0E-96 BE148074.1	EST_HUMAN	RC3+HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
7620 20690	34165	0.59	2.0E-98	2.0E-96 BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-512 GN0120 Homo sapiens cDNA
7620 20690	34166	0.59	2.0E-96	2.0E-96 BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo saplens cDNA
9181 22259		4.9	2.0E-96	2.0E-96 AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5'
12288 25214		2.54	2.0E-06	2.0E-86 AW 248440.1	EST_HUMAN	2819351.5prime NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2819351 51
638 13823	26845	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell edhesion molecule (NRCAM) mRNA
638 13823	28846	0.86	1.0E-98	4826863 NT	NT .	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
688 13872	26905	3.08	1.0E-96 Y18890.1		TN	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1822 14971	28063	9.97	1.0E-96 /	1.0E-96 AW 955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1822 14971	28064	9.97	1.0E-96	1.0E-96 AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
5331 18444		1.59	1.0E-86	5453913 NT	TN	Hamo sapiens phospholipid transfer protein (PLTP) mRNA
7105 18532	31487	. 1.19	1.0E-96	0912735 NT	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7194 20059	33470	0.71	1.0E-96	6912455 NT	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8407 21488	35017	0.9	1.0E- <del>0</del> 6	7661803 NT	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8407 21488	35018	0.9	1.0E-96	7661803 NT	FN	Homo sapiens HSPC144 protein (HSPC144), mRNA
						Homo saplens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214),
8913 21892	35531	21.44	1.0E-96	11419429 NT	NT	mRNA
9051 22130	35674	2.22	1.0E-96	1.0E-96 AF274853.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
	37007	0.68	1.0E-96		NT .	Homo sapiens mRNA for KIAA1290 protein, partial cds
10362 23397	37008	0.68	1.0E-96 /	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
12274 13823	26845	3.29	1.0E-88	4826863 NT	NT	Homo sapiens neuronal cell adhesion molocule (NRCAM) mRNA
12274 13823	26846	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3405 16575	29590	0.72	6.0E-97	6.0E-97 BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7730 20792		3.4	6.0E-97	6.0E-97 BE141849.1	EST_HUMAN	IL5-HT0117-011089-004-D07 HT0117 Homo sapiens cDNA

7/7/S/10 OM

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value 6.0E-97	t Similer Top Hit Acession No. Astr E No. 6.0E-97 BE898012.1	Top Hit Database Source	Top Hit Descriptor
9134 9134			0.75 0.75	6.0E-97	6.0E-97 BE898012.1 6.0E-97 BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10821	23854	37475	0.65	6.0⊑-97	6.0E-97 AA320332.1	NAMUH_TS3	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' and
10821	23854	37476	0.65	6.0E-97	6.0E-97 AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
11692	Г	38381	2.42	6.0E-97	6.0E-97 X15804.1	TN	Human mRNA for alpha-actinin
8204	21286	34809	1.73	6.0E-97	6.0E-07 AL043314.2	NAWOH_TSE	DKFZp434N0323_r1 434 (synonym: https3) Homo sapiens cDNA clone DKFZp434N0323 5
8336	21417	34943	11.21	6.0E-97	6.0E-97 AA418326.1	EST_HUMAN	z/97e12.61 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:767758 3' similar to TR:G1304125 G1304125 PMS4 MRNA ;
9877	22917	36502	3.12	5.0∈-97	5.0E-97 BF154912.1	NAMUH_TS3	RC0-BT0812-250900-032-e09 BT0812 Homo sapiens cDNA
11840	24829	38519	1.68	5.0E-97	5.0E-97 BE148597.1	EST_HUMAN	MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
11840	Г	38520	1.68	5.0E-97	5.0E-97 BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
962	Г	27196	2.13	4.0E-97	4.0E-97 BE004436.1	EST_HUMAN	CM0-BN0106-170300-293-e06 BN0108 Homo sapiens cDNA
1959	П	28202	1.41	4:0E-07	5463672 NT	TN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5683	18877	32166	0.92	4.0E-97	4557326 NT	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6962	20190	. 33615	6.47	4.0E-97	4.0E-97 Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6962	20190	33616	6.47	4.0E- <del>0</del> 7	4.0E-07 Y11339.2	NT	Homo sepiens mRNA for GelNAc alpha-2, 6-slaly/transferase I, long form
7161	20294	33737	1.09	4.0E- <del>0</del> 7	7710125 NT	NT	Homo sepiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7214	20079	33492	0.92	4.0E-97	11422155 NT	3	Homo saplens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8329	21411	34937	1.08	4.0E- <del>9</del> 7	4557708 NT	NT	Homo sepiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8553	21634	35171	1.43	4.0E-97	11421783 NT	NT	Homo sepiens v-src avian sercoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8779	21858	35401	0.51	4.0E-97	11431060 NT	N	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
8820	21899	35438	0.82	4.0E-97	11423233 NT	NT.	Homo sepiens cytochrome P450, subfemily IVB, polypeptide 1 (CYP4B1), mRNA
9449	22565	36128	1.06	4.0E-97	4.0E-97 AB011166.1	NT	Homo sepiens mRNA for KIAA0594 protein, partial cods
9449	22565	36129	1.06	4.0E-97	4.0E-97 AB011188.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10652	23686	37296	0.55	4.0E-97	11431060	NT	Homo saplens N-myc (and STAT) Interactor (NMI), mRNA
11435	24496	38162	1.99	4.0E-97	11863122 NT	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11435	24486	38163	1.99	4.0E-97	63122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11710	23906	37628	4.61	4.0E-97	4.0E-97 AB042567.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete ods
12472	25325		5.26	4.0E-97	11418318 NT	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
253	13473	26504	1.58	3.0E-97	3.0E-97 AB032398.1	T	Homo sepiens mRNA for KIAA 1172 protein, pertial cds
897	14073	27138	7.16	3.0E-97	4502166 NT	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

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PM4-B10/24-010400-008-812 B10/24 Homo sapiens CUNA	EST_HUMAN	9.0E-98 BE090973.1	9.0E-98	4.97	27163	14099	12487
Homo sepiens mRNA for KIAA 1005 protein, partial cds	NT	9.0E-98 AB023222.1	9.0E-98	2.62		Г	11253
Homo sapiens mRNA for KIAA 1005 protein, partial cds	NT	9.0E-98 AB023222.1	9.0E-98	2.62	37962	24322	11253
Homo saplens protease-activated receptor 3 (PAR3), mRNA	44 NT	11431544 NT	9.0E-98	0.5	37215	23610	10575
Homo capiono inocitol polyphocphato 1-phosphatase (INPP1) gene, complete cds	Z	9.0E-98 AF141325.2	9.0€-98	0.67		23502	10467
Homo saplens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	70 NT	4507070 NT	9.0E-98	1.28	36277	22709	9567
Homo saplens SWI/SNF releted, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	70 NT	4507070 NT	9.0E-98	1.28	36276	22709	9567
Homo sapiens 17-beta-hydroxysteroid dehydrogenese IV (HSD17B4) gene, exon 8	Z	9.0E-98 AF057726.1	9.0E-98	0.81		22805	9540
	TN	9.0E-98 AB037/86.1	9.0E-98	1.6	36112	22549	9492
Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA	90 NT	11321580 NT	9.0E-98	1.12	36064		9425
Human mRNA for amyloid A4(751) protein	TN	9.0E-98 X06989.1	9.0E-98	1.78		22392	9316
Homo saplens death-associated protein (DAP), mRNA	19 NT	4758119 NT	9.0E-98	5.62	34712	21191	8109
Homo sapiens death-associated protein (DAP), mRNA	19 NT	4758119 NT	9.0E-98	5.62	34711	21191	8109
Homo saptens mRNA for KIAA1636 protein, partial cds	NT	9.0E-98 AB046356.1	9.0E-98	4.13		21072	8020
Homo sapiens mRNA for KIAA1636 protein, partial cds	TN	9.0E-98 AB046856.1	9.0E-98	4.13	34583		8020
Homo saptens CLDN12 gene for claudin-12	TN	9.0E-98 AJ250713.1	9.0E- <del>9</del> 8	0.79		18600	6432
Homo saptens cat eye syndrome critical region gene 1 (CECR1), mRNA	92 NT	8393092 NT	9.0⊑-98	1.32	27528	14461	1305
PM4-BT0724-010400-008-a12 BT0724 Homo saplens cDNA	EST_HUMAN	9.0E-98 BE090973.1	9.0E-98	2.34	27163		924
Homo sapiens ribosomal protein S15 (RPS15), mRNA	72 NT	11426272 NT	1.0E-97	8.3		23942	11756
Homo saplens ribosomal protein S15 (RPS15), mRNA	72 NT	11426272 NT	1.0E-97	8.3	37688	23042	11766
nk29g02.s1 NCI_CGAP_Co11 Hamo sapiens cDNA clane IMAGE:10149623'	EST_HUMAN	1.0E-97 AA553761.1	1.0E-97	1.38	38324	24642	11589
Homo saplens KIAA0649 gene product (KIAA0649), mRNA	57 NT	11427757 NT	1.0E-97	2.84			10946
Homo saplens KIAA0649 gene product (KIAA0649), mRNA	57]NT	11427757 NT	1.0E-97	2.84		24027	10945
yf38c08.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:1291343'	EST_HUMAN	1.0E-97 R10887.1	1.0E-97	1.02	36600		9966
Homo saplens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA	31 NT	5453881 NT	1.0E-97	0.69	33509	20092	7039
601339520F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3881821 5	EST_HUMAN	1.0E-97 BE566486.1	1.0E-97	2.72	36088		6557
Homo saplens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	70 NT	4503470 NT	1.05-87	22.23			4902
Homo saplens pericentrin (PCNT) mRNA	78 NT	5174478 NT	3.0E-97	0.96			3333
Human beta-primo-adaptin (BAM22) gene, exon 7	NT	3.0E-97 U36255.1	3.0E-97	2.4	28755	15998	2508
Homo sapiens N-myc (and STAT) Interactor (NMI), m:RNA	13 NT	4758813 NT	3.0E-97	1.94	27712	16039	1473
Homo seplens amylold beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	36 NT	4502166 NT	3.0E-97	7.16	27139	14073	897
Top Hit Descriptor	Top Hit Datebase Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:
						1	

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Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA	NT	11428813 NT	2.0E-98	4.44	35427	21886	8807
Homo saplens SH3-domain GRB2-like 2 (SH3GL2), mRNA	TN	11428813 NT	2.0E-98	4.44	35426	21886	8807
Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA	NT	11431271 NT	2.0E-98	1.25	34349	20857	7801
Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA	NT	11431271 NT	2.0E-98	1.25	34348	20857	7801
Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA	NT	4605798 NT	2.0E-98	1.7	33347	19948	6793
Homo sapiens PDZ domain-containing guanine nucleotide exchange factor I (LOC51735), mRNA	NT	7706512 NT	2.0E-98	4.76	31708	18691	5492
Homo sapiens attractin precursor (ATRN) gene, exon 16	NT	AF218902.1	2.0E-98	1.39	31053	18078	4948
Homo saplens attractin precursor (ATRN) gene, exon 16	NT	AF218902.1	2.0E-98	1.39	31052	18078	4948
Homo sapiens fathy-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA	NT	2.0E-98 4758331	2.0E-98	4.23	30577	17599	4459
Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	NT	AF032897.1	2.0E-98	0.82	30538	17553	4411
Homo sapiens chromosome 21 segment HS21C002	NT	2.0E-98 AL163202.2	2.0E-98	2.21	28578	15443	2311
601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5	EST_HUMAN	2.0E-98 BE294281.1	2.0E-98	4.08	28399	15277	2141
601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'	EST_HUMAN	BE261694.1	2.0E-98	0.67	26980	13935	754
Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	NT	11418177 NT	3.0E-98	3.01		25739	13138
	EST_HUMAN	3.0E-98 AI159975.1	3.0E-98	2.22	38504	24808	11819
Human fumarase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds	NT	3.0E-98 U69309.1	3.0E-98	2.66	37899	24264	11195
601673686F1 NIH_MGC_21 Homo sepiens cDNA done IMAGE:3956517 5*	EST_HUMAN	3.0E-98 BE900454.1	3.0E-98	0.89	37330	23724	10891
AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone i8	EST_HUMAN	3.0E-98 AJ403124.1	3.0E-98	. 1.82	36727	23126	10087
AJ403124 3.4 (downregulated in larynx carcinoma) Homo saptens cDNA clone 18	EST_HUMAN	3.0E-98 AJ403124.1	3.0E-98	1.82	36726	23125	10087
Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA	NT	8922096	3.0E-98	0.54	36115	22553	9497
yo17g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178240 5'	T_HUMAN	3.0E-98 H46698.1	3.0⊑-98	4.07	35571	22030	8951
Homo sapiens activator of S phase kinase (ASK), mRNA		11419210 NT	3.0E-98	1,99	33603	20179	7085
Homo sapiens activator of S phase kinase (ASK), mRNA		11419210	3.0E-98	1.89	33602	20179	7085
7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01	EST_HUMAN	3.0E-98 AA077498.1	3.0E-98	5.04		15921	2807
Homo septens mRNA for KIAA0707 protein, partial cds	NT	3.0E-98 AB014807.1	3.0E-98	2.1	28910	16793	2673
AJ403124 3.4 (downregulated in laryrx carcinoma) Homo sapiens cDNA clone i8	EST_HUMAN	AJ403124.1	3.0E-98	1.35	28508	15380	2247
601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 6	EST_HUMAN	6.0E-98 BE885973.1	6.0E-98	0.96	32732	19382	6207
Human mitochondrial creatine Kinase (CKMT) gene, complete cds	NT	8.0 <b>E-98</b> J04469.1	8.0E-98	6.45	30055	17055	3896
Homo sapiens PMS2L16 mRNA, partial cds	NT	8.0E-98 AB017007.1	8.0⊑-98	2.79	28010	14914	1765
Homo sapiens PMS2L16 mRNA, partial cds	NT	AB017007.1	8.0E-98	2.79	28009	14914	1765
Homo sapiens IL2-Inducible T-cell Kinase (ITK), mRNA	NT	5031810 NT	8.0∈-98	1.1	27826	14743	1591
Homo sapiens iL2-inducible T-cell kinase (ITK), mRNA	NT	5031810 NT	8.0E-98	1.1	27825	14743	1591
Homo sapiens hPAD-colony10 mRNA for peptidylarginine delminase type I, complete cds	NΤ	AB033768.1	8.0E-98	0.83	27631	14557	1403
Top Hit Descriptor	Database Source	No.	(Top) Hit BLAST E Value	Signal	ID NO:	SEQ ID	SEQ ID
	Top Hit		Most Similar	,		E SS	Probe
						]	1

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nomo seprens CUS4 enugen (CUS4) mixina	2	4502000	6.0E-99	1.42	30880	COUBL	800
EST388473 MAGE resecuences, MAGN Homo sapiens cDNA	EST_HUMAN	6.0E-99 AW976364.1	6.0€-99	2.8	30160	Т	3995
Homo sepiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA		11430555 NT	6.01-89	6.2	28457		2196
Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA	T	11430555	6.0⊑-99	6.2	28456	15331	2198
Human G2 protein mRNA, partial cds	NT	6.0E-89 U10991.1	6.0E-89	0.72	26713	13678	484
Homo sapiens NK-receptor (KIR-G2) gene, linker region exan	NT	7.0E-89 AF001886.1	7.0E-89	1.91	38599	24896	11909
Homo sapiens oscillin (hLn) gene, exon 5	NT	7.0E-89 AF036808.1	7.0E-89	9.25	32458	19142	5956
Human endogenous retrovirus, complete genome	NT	9635487	8.0E-99	1.19	35542	22003	8924
zn90d02:r1 Stratagene lung cardnoma 937218 Homo sapiens cDNA clone IMAGE:565443 5: similar to TR:G662994 G662894 GPI-ANCHORED PROTEIN P137. ;	EST_HUMAN 1	9.0E-99 AA134504.1	9.0E-89	1.72	38389	24897	11700
IM69h07.X1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:2183421 3' similer to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST;	EST_HUMAN F	9.0E-89 Al479829.1	9.0E-89	1.85	38106	24445	11384
tm69h07.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST;	EST_HUMAN F	9.0E-89 A1479829.1	9.05-89	1.85	38105	24445	11384
EST380711 MAGE resequences, MAGJ Homo sepiens cDNA	EST_HUMAN E	9.0E-99 AW968636.1	9.0E-99	4.01	32688	19341	6165
QV-BT073-191298-012 BT073 Homo sapiens cDNA	EST_HUMAN (	9.0E-99 A1905004.1	9.0E-89	1.05	32439		5939
QV-BT073-191298-012 BT073 Homo saplens cDNA	EST_HUMAN (	9.0E-89 AI905004.1	9.0E-89	1.05	32438	19125	5939
Homo seplens beta-tubulin mRNA, complete cds	I. TN	1.0E-98 AF141349.1	1.05-98	0.59	35816	22277	9199
Homo septens beta-tubulin mRNA, complete cds	NT	1.0E-98 AF141349.1	1.0E-98	0.59	35815	22277	9199
601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'		1.0E-98 BE390527.1	1.0E-98	0.97	32173	18881	5687
601284986F1 NIH_MGC_44 Hamo sepiens cDNA clone IMAGE:3606692 5'	EST_HUMAN 6	1.0E-98 BE390627.1	1.0E-98	0.97	32172	18881	5687
zp98c09.r1 Stratagene muscle 937/209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806562 NEBULIN. ;	EST_HUMAN (	1.0E-88 AA195354.1	1.0E-98	3.3	31610	18632	5432
yv23f05.r1 Soares fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosemal protein L29 - human ;	EST_HUMAN F	1.0E-98 N49813.1	1.0E-98	26.16	28086	14986	1840
PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA	EST_HUMAN F	1.0E-98 AW998611.1	1.0E-98	3.27	26698	13662	467
w36504.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2261743 3" similar to SW:RL2B_HUMAN P28316 60S RIBOSOMAL PROTEIN L23A.;	EST_HUMAN F	1.0E-98 AIB82007.1	1.0E-98	27.52	26653	13613	418
Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	NT	11435947	2.0E-98	2.23	32062	25340	12492
Homo sepiens mRNA for KIAA1590 protein, partial cds	NT TN	2.0E-88 AB046513.1	2.0Ε-98	1.61		25116	12136
Homo capiens AIM-1 protein (LOC61161), mRNA	NT	7705868	2.0E-98	1.66			10624
H.saplens arginase gene exon 3 (EC 3.5.3.1)	II TN	2.0E-98 X12661.1	2.0€-98	1.58		22802	9737
Homo sapiens NKAT4b mRNA, complete cds	NT I	L76668.1	2.0E-98 L7656.1	0.8	35504	21988	8889
Homo sapiens NKAT4b mRNA, complete cds	NT	2.0E-98 L76668.1	2.0돈-98	0.8	35503	21968	8889
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:

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Single Exon Probes Expressed in Placenta

		4503730 NT	1.0E-99	121	28224	15123	1980
Homo saplens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	TIN	j	1.0E-99	1.16	27820	14739	1587
Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds	TN	1.0E-99 AF192523.1	1.0E-99	1.18	27819	14739	1587
Human Ku (p70/p80) subunit mRNA, complete cds		1.0E-99 M30938.1	1.0E-99	3.61	27684	14605	1452
Homo saplens GA-binding protein transcription factor, elpha subunit (60kD) (GABPA), mRNA	NT	26150	1.0E-99	1.75	26632	13596	390
Homo sapiens intersectin tong Isoform (ITSN) mRNA, complete cds	TN	1.0E-99 AF114487.1	1.0Ε-99	1.49	26671	13639	326
Homo saplens potassium channel, subfamily K, member 10 (KCNK10), mRNA	NT	33960	20E-99	1.64	38767	25061	12081
Homo sapiens myosin X (MYO10) mRNA, complete cds		2.0E-89 AF247457.2	2.0Ε-69	3.16	38085	24428	11367
			2.0E-99	0.75	35986	22428	9353
zb48d06.r1 Soares_fetal_lung_NbHL19W Homo septens cDNA clone IMAGE:306635 5' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);	EST_HUMAN	2.0E-89 W23507.1	2.0E-89	10.79	35523	21983	8904
Homo saplens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	NT	2.0E-99 AF257737.1	2.0E-99	0.76	34410	20906	7851
Homo capiono chort chain L-3-hydroxyacyi-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene	NT	2.0E-69 AF095703.1	2.0E-09	1.82	30787	17800	4665
	NT	2.0E-99 M30938.1	2.0E-99	1.4	29522	16504	3331
დ08e06.X1 NCI_CGAP_HN9 Homo sapiens cDNA clame IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);	EST_HUMAN	2.0E-99 AW <i>2747</i> 92.1	2.0E-99	7.26		14426	1268
Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds	NT		3.0E-99	4.95		21597	8510
601513167F1 NIH_MGC_71 Hamo sepiens cDNA clone IMAGE:3914391 5'	EST_HUMAN	5.0E-99 BE890177.1	5.0E-99	249		25346	12502
Homo sapiens T cell receptor bela locus, TCRBV7S3A2 to TCRBV12S2 region	NT	5.0E-99 AF009380,1	5.0E-99	1.81	30809	Г	4686
H.sapiens IMPA gene, exon 8	NT	Y11365.1	5.0E-99	1	28268	15163	2022
Homo saplens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA	NT	9910279	6.0E-99	202	37554	23928	11742
Homo sepiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA	TN		6.0E-89	2.02	37553	23928	11742
Homo saplens BH3 interacting domain death agonist (BID), mRNA	NT		6.0E-99	3.15	37674	П	10958
	TN	11431994 NT	6.0E-89	0.59	35745	Г	9123
Homo septens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA	NT	11431894 NT	6.0E-99	0.59	35744	22202	9123
Homo capiens lodestar protein mRNA, complete cds	NT		6.0E-99	7.6	35689		9064
	TN	6.0E-99 AF080.255.1	6.0E-99	7.6	35688	22143	9064
Homo sapiens NDST4 mRNA for N-deacet/lase/N-sulfofransferase 4, complete cds	NT	6.0E-99 AB036429.1	6.0E-99	2.67	35586	22043	8964
Homo capiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	NT	6601589	6.0E-99	0.59	34921	21396	8314
	TN	1.1016BX	6.0E-99	1.85	34899	21378	8296
	NT	6.0E-99 L43610.1	6.0E-99	0.74	33377	18969	6816
Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30	TIN	L43610.1	6.0E-99	0.74	33376	19969	6816
Homo saplens GAP-like protein (LOC51306), mRNA	NT	TN 8613077	6.0≣-99	0.94	33280	19888	6732
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
						1	]

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Single Exon Probes Expressed in Placenta

1						9		C TYPI COOK III I INCUITA
SEC	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	1980	15123	28225	1.21	1.0E-99	4503730 NT	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
	3154	16329	29339	0.93	1.0⊑-99	1.0E-99 J03171.1	NT	Human Interferon-alpha receptor (HulFN-alpha-Rec) mRNA, complete cds
	4499	17639	30621	2.64	1.0⊑-99	1.0E-99 AF098018.1	NT	Homo sapiens fatty acid emide hydrolase (FAAH) gene, exon 14
	4489	17639	30622	2.64	1.0⊑-99		NT	Homo sapiens fatty acid emide hydrolase (FAAH) gene, exon 14
	6943	20256	33694	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
	6943	20256	33695	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
<u> </u>	7289	25842	33827	0.81	1.0E-99 X98022.	X98022.1	NT	H.sapiens E6-AP gene exon 2
_	9400	22474		0.75	1.0E-99	11419721 NT	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
	9720	22785	36356	1.7	1.0E-99	1.0E-99 AW340174.1	EST HUMAN	hd02h02x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2908371 3' similar to TR:002711 002711 PRO-POL-DUTPASE POLYPROTEIN;
=	11403	24464	38128	2.56	1.0≝-99	7427514 NT	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
=	11403	24464	38129	2.66	1.0≅-99	7427614 NT	NT	Homo capiens huntingtin interacting protein 1 (HIP1), mRNA
<u> </u>	11462	24521	38191	1.68	1.0E-99	5901979 NT	NT	Homo sepiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
=	11659	24738	38429	2.83	1.0E-99	1.0E-99 AB023:222.1	NT	Homo saplens mRNA for KIAA1005 protein, partial cds
<u></u>	11996	24981	38687	2.45	1.0E-99	11417191 NT	NT	Homo sapiens leucy/cystinyl aminopeptidase (LNPEP), mRNA
	12257	25183		4 50 _	1 05-50	1 0E-99 AF240.786 1	4	Homo septens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
	_	13241	26241	1.7	1.0⊑-100	1.0E-100 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
	2	13241	26241	2.91	1.0E-100	1.0E-100 AL163247.2	NT	Homo sepiens chromosome 21 segment HS21C047
Γ	8	13307	26329	1.62	1.0E-100	11418230 NT	N <sub>1</sub>	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
	70	13307	26330	1.62	1.0E-100	11418230 NT		Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
Γ	8	13324	26353	0.82	1.0E-100	1.0E-100 AW276237.1	EST_HUMAN	xv78b11.x1 NCI_CGAP_Bm53.Homo sapiens cDNA clone IMAGE:2824605 3'
<u> </u>	173	13397	26425	0.89	1.0Ё-100	1.0E-100 AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
<u> </u>	327	13541	26573	1.84	1.0E-100	1.0E-100 AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
Γ	353	13564	26592	1.87	1.0E-100	1.0E-100 T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo saplens cDNA clone HFBCR32
	450	13646		2.24	1.0E-100	1.0E-100 AF003528.1	Z	Homo sapiens X-linked enhidrotite ectodermal dysplasia protein gene (EDA), exen 2 and flanking repeat regions
	502	13697		5.88	1.0E-100 X89831.1	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
	823	13716	26742	1.21	1.0E-100	1.0E-100 BE180309.1	EST_HUMAN	RC3-HT0625-040500-022-509 HT0625 Homo sapiens dDNA
Γ.	104 14	14210	27266	4.57	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
Γ.	1044	14210	27267	4.57	1.0E-100	7661685 NT	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
	1577	14730		1.3	1.0E-100	1.0E-100 AW 207555.1	EST_HUMAN	
	1681	14733	27814	1.66	1.0E-100	1.0E-100 AI200857.1	EST_HUMAN	qf62f09.x1 Soares_tests_NHT Homo sepiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81061 CYSTATIN ;

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PMO-BN0065-100300-001-c06 BN0066 Homo sapiens cDNA	EST_HUMAN	1.0E-100 AW888611.1	1.0E-100/	2.28	34588	27076	9633
wis (שיביא ו אינ) בעאר ביר בא momo sapiens culva cione IMAGE:2488920 3: elimilar to contains element MER22 repetitive element ;	EST_HUMAN	1.0E-100 AI972388.1	1.0E-100	1.65			9510
Tion of NO COAD Prof. 1400 protein, partial cos	2	1,0E*100/ADV#0810.1	1,00	3.00	300,0	1000	97.00
AUTIOSS I DEMEAT DOMO SAPISAS CONA CIGNE HEMBATQUUSAS S	NAMORI	1.0E-100 AO 10901.1	1.00	0.4	36073	Т	0/22
AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 6		1.0E-100/AU116951.1	1.05-100	0.4/	35030	Т	3210
Homo saplens chromosome 21 segment HS21C003	┖	1.0E-100 AL163203.2	1.06-100	5.59		Т	8766
601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'	THUMAN	1.0E-100 BF103853.1	1.0€-100	3.53	35346	Г	8729
Human mRNA for kidney epidermal growth factor (EGF) precursor	NT	X04571.1	1.0E-100 X04571.1	6.2			7033
MR1-TN0048-060900-004-b05 TN0048 Homo sapiens cDNA	EST_HUMAN	1.0E-100 BF376478.1	1.0E-100	1.18		20162	7026
MR1-TN0046-060900-004-b05 TN0046 Hamo sapiens cDNA	EST_HUMAN	1.0E-100 BF376478.1	1.0E-100	1.18	33583	П	7026
ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418 G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.	EST_HUMAN	1.0E-100 AA496841.1	1.0E-100	1.02	33639	20210	6982
G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;	EST_HUMAN	1.0E-100 AA496841.1	1.0E-100	1.02	33638	20210	0982
seasons of Cost for Williams transported to the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Con		10001				Т	
Home seniors Rho OTDese activation and ARHGARD tensor desire university of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Co	<u> </u>	7382479	1.0E-100	177	33653		888
v38c08.s1 Spares fetal liver spieen 1NFLS Homo sapisns cDNA clone IMAGE:122134.31	EST HUMAN	R10887.1	1.0E-100 R10887	1.36	33384	T	6824
AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5	EST HUMAN	1.0E-100 AU140214.1	1.0E-100	5.62			6626
Homo saplens ER to nucleus signelling 1 (ERN1) mRNA	NT	4557568 NT	1.0E-100	0.9	32818	19465	6292
Homo saplens ER to rucleus signalling 1 (ERN1) mRNA	NT	4557568 NT	1.0E-100	0.9	32817	19465	6292
Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)	NT	X14690.1	1.0E-100 X14690.	0.85	32461		6960
Hamo sepiens NF-E2-related factor 3 gene, complete cds	NT	1.0E-100 AF1351 6.1	1.0⊑-100	1.78	32361	19054	5864
AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'	EST_HUMAN	1.0E-100 AU118182.1	1.0E-100	1.45	32314	Г	5818
xa82701.x1 NCI_CGAP_CML1 Homo septens cDNA clone IMAGE:2573305 3' striller to gb:X12433 PROTEIN PHPS1-2 (HUMAN);	EST_HUMAN	1.0E-100 AW075583.1	1.0E-100	0.76	31893	18819	5625
601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'	EST_HUMAN	1.0E-100 BF244218.1	1.0E-100	1.74	31578	18806	5404
Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA		5032104 NT	1.0E-100	3.01	31292	П	5202
Hamo sapiens small optic labes (Drosophila) homolog (SOLH) mRNA	NT	5032104 NT	1.0Ε-100	3.01	31291		6202
Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA	NT	4503792 NT	1.0Ε-100	2.28			4351
Homo sapiens myotubularin-related protein 1a mRNA, partial cds	TIN	1.0E-100 AF057354.1	1.0E-100	1.67	30456	17469	4326
Homo sapiens RGH2 gene, retrovinus-like element	NT	D11078.1	1.0E-100 D11078!	6.55		16259	388
Homo sapiens KIAA0957 protein (KIAA0957), mRNA	NT	11418976	1.0E-100	2.5	28996	15886	2771
H.sapiens mRNA for IPN-gamma (pKC-0)	NT	X62468.1	1.0E-100 X62468.1	1.41	28754	15634	2507
Ret mRNA for short type PB-cadherin, complete cds	TN	D83349.1	1.0E-100 D83349:1	1.14		15447	2315
Top Hit Descriptor	Top Hit Database Source	Top Hit/Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exam SEQ (D NO:	Probe SEQ ID NO:
						1	7

			1.44 1.05-101		A787 27849		
Homo sapiens butyrophilin, subtaining 4, mention 11 (2)	5021460 NT	7			43 27299	77 14243	1077
qg99e09.x1 Scares_NFL_I_GBC_OT number A1 (F	EST HUMAN	OE 101 A1221878.1	T			09 14180	1009
	EST HUMAN	1.0E-101 BERR121B.1	Τ			948 14121	<b>@</b>
Homo septens of cardiac eigha-myosin heavy chain gene Homo septens of cardiac eigha-myosin heavy chain gene	4503914 NT	١.				876 14052	
Homo saplens phosphonbosygyxulatilika iviinisaania			Ţ	23	71 27023	792 13971	7
Homo sepiens pescedillo (zebrefish) nomolog i, colimining o	7657454 NT		2 1.0E-101			П	7
Homo sapiens ventral anterior homeobox 2 (VXXX), in the BRCT domain (PES1), mRNA	7110734 NT		ا.		)4 26945	٦	722
Homo sapiens ventral anterior homeobox 2 (VAXX), mrNA	7110734 NT	ADOOLA			7 26919	П	704
Homo sapiens mRNA for KIAA0446 protein, parual cus	NT.	2002018 3	Ι.	0.92		П	
Homo sapiens SEC14 (S. cerevistee) like 2 (SEC14L2), mRNA	7110714 NT					79 13315	79
Homo sapiens SEC14 (S. carevislae)-like 2 (SEC14L2), mRNA	11417974 NI		1.0E-100		1	1	3107
Homo sapiens transcobalemin II; macrocytio anemia ( ICNZ), IIIVVV	11410123141		1, 1.0E-100	3 1.31		1	
Homo sapiens KIAA0063 gene product (KIAA0063), ITTAVA	11040102 NT			3 4.97	32063	П	12493
Homo saplens SH3-domain binding protein 1 (SH3BP1), mRNA	EST_HUMAN	BF4465		1.78	<u> </u>	26037	12312
genes, complete cas genes, complete cas 7q88h03.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE: 3' similar to TR:Q21997 Q21997	3	1.0E-100 AF240786.1	1	7.59	38832	25137	12177
rase meta 2 (GG114)		1.00-100 101007	T	1.83	38812	П	12128
Homo sapiens class gene, exon 12	NT	0E 100 A 1131034 1	T			24962	11977
18	Z	1.0E-100 AE 100271.E	T		26241	13241	11665
Homo sapiens chromosome 21 segment HSZ1VV47	NT.	1.0E-100 AF 11110.5	Τ			_ [	11635
Homo sapiens 14q32 Jagged2 gene, complete cus, and all all all all all all all all all al	3	1.UE-100/AF 111170 3	1.05-100		38406	24715	11635
Homo sapiens 14q32 Jagged2 gene, complete cas, and cincioning series	Z	1.0E-100 X84033.1	1.05-100				11564
H. sepiens CD97 gene exon 4	Z	1.0E-100 X84033.	1.05-100		38300	24619	11564
H.saplens CD97 gene exon 4	NT TOWN	1.0E-100 BF327292-1	1.0E-100		37708	24076	10996
MRQ-BN0070-270300-008-h11 BN0070 Homo sapians cDNA	TOT LINAN	1.0E-100 Y10391.1	1.0E-100	1.35	١	23815	1078
Human endogenous retrovirus HERV-K, pol gene	EOI DOWERS	1.0E-100 BF347518.1	1.0E-100	0.64	37327	23721	
602020554F1 NCI_CGAP_Brn67 Hamo septens cDNA clane IMAGE:4156165 5	1	1.0E-100 AW630487.1	1.0E-100	1.81	36688	23086	3 2 2
GI 11 Homo sepiens cDNA clone	L	1.0E-100 AW 630487.1	1.0E-100	181	2007		70/8
Homo saplens mittha for next local promise CDNA clone IMAGE::2969396 6		1.0E-100 AB046846.1	1.0E-100	2.17	36401	22822	0782
Homo sapiens mRNA for KIAA1620 protein, partial cols	1	1.0E-100 AB046846.1	1.05-100	0.84		22736	9687
AU127720 NT2RP2 Homo sepiens cDNA clone NT2RP2001918 5	EST HUMAN	N1407700 1	Value			, ,	O
	Database Source	No.	m =	Expression Signal	ORF SEQ	_0_	0 0
Top Hit Descriptor	Top Hit	Ton Lik Ar ession					

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601764686F1 NIH_MGC_53 Homo septens cDNA clane IMAGE:3996837 5'	EST_HUMAN	1.0E-101 BF029174.1	1.0E-101	1.6	34843	21327	8245
601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'	EST_HUMAN	1.0E-101 BE275821.1	1.0Ε-101	0.74	34697	21179	8097
801121621F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3345869 5	EST_HUMAN	.0E-101 BE275821.1	1.0E-101	0.74	34698	21179	8097
RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA	EST_HUMAN	.0E-101 BF330759.1	1.0E-101	6.64	34469	20952	7900
601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3348901 5'	EST_HUMAN	.0E-101 BE257384.1	1.0E-101	1.99	_	20809	7749
wv55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'	EST_HUMAN	.0E-101 AW008475.1	1.0€-101	7.65	34192	20714	7645
Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds	NT	.0E-101 AF208970.1	1.0E-101	4.22	34020	20548	7473
Homo sepiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds	NT	1.0E-101 AF208970.1	1.0E-101	4.22	34019	20548	7473
Homo sepiens hypothetical protein FLJ22087 (FLJ22087), mRNA	NT	11545780 NT	1.0E-101	1.26		20500	7423
Homo sapiens carbonic anhydrase VII (CA7), mRNA	NT	11430734 NT	1.0E-101	0.96	33398	19987	6834
Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA	NT	7427612 NT	1.0∈-101	4.07	32646	19305	6126
Homo sapiens cytopiasmic linker 2 (CYLN2), mRNA	NT	7427512 NT	1.0E-101	4.07	32645	19305	6126
EST377212 MAGE resequences, MAGI Homo saplens cDNA	EST_HUMAN	1.0E-101 AW965139.1	1.0E-101	1.94	31611	18633	5433
601452067F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3855761 5'	EST_HUMAN	1.0E-101 BE612554.1	1.0E-101	0.6	31337	18369	5248
601452067F1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:3855761 5	EST_HUMAN	1.0E-101 BE612554.1	1.0E-101	0.6	31336	18369	5248
Homo saplens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	NT	5921460	1.0E-101	1.14	31240	18269	5147
	NT	5921460	1.0E-101	1.14	31239	18269	6147
Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene	NT	1.0E-101 AB022785.1	1.0E-101	3.81	30142	17138	3981
Homo saplens RIBIIR gene (partial), exon 12	NT	1.0E-101 AJ237744.1	1.0E-101	3.59	29026	15916	3487
Homo espiens RIBIIR gene (pertiel), exon 12	NT	1.0E-101 AJ237744.1	1.0E-101	3.69	29025	15916	3487
EST377629 MAGE resequences, MAGI Homo sapiens cDNA	EST_HUMAN	1.0E-101 AW965556.1	1.0E-101	1.82	29654	16635	3468
601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'	EST_HUMAN	1.0E-101 BF035327.1	1.0E-101	23		16486	3313
Homo sapiens gamma-glutamy/transferase 1 (GGT1) mRNA	NT	4885270	1.0E-101	2.97	29467	16447	3273
Homo sepiens genomic downstream Rhesus box	NT	1.0E-101 AJ252312.1	1.0E-101	20.16		16186	3020
Homo sepiens RIBIIR gene (pertiel), exon 12	TN	.0E-101 AJ237744.1	1.0E-101	9.27	29026	15916	2802
Homo saplens RIBIIR gene (partial), exon 12	T	.0E-101 AJ237744.1	1.0€-101	9.27	29025	15916	2802
H.sapiens EWS gene, exon 5	NT	X72993.1	1.0E-101 X72933.	4.62	28917	15800	2680
Homo septens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA	NT	5729892	1.05-101	1.2	28680	16062	2425
RC3-9T0281-160600-016-h09 ST0281 Homo sapiens cDNA	EST_HUMAN	1.0E-101 BE843070.1	1.0E-101	2.70	28373	15254	2116
Homo sepiens cerboxypeptidese A1 (pencreatio) (CPA1) mRNA	NT	4502996 NT	1.0E-101	2.07	28247	15140	1999
Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	TN	7662183 NT	1.0E-101	1.57	28029	14934	1785
Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	NT	7662183 NT	1.0E-101	1.57	28028	14934	1785
Homo sapiens butyrophilin, subfemily 2, member A1 (BTN2A1), mRNA	NT	5921460 NT	1.0E-101	1.44	27850	14767	1614
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:
			Most Similer			1	,
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Table 4

Single Exon Probes Expressed in Placenta

601299982F1 NIH_MGC_21 Homo seplens cDNA clone IMAGE:3629901 5'	EST_HUMAN	.0E-102 BE408447.1	1.0E-102	355.9	27681	14603	1450
Homo seplens solute carrier family 2 (facilitated glucose transporter), member 8 (SLC2A8), mRNA	6 NT	11437146 NT	1.0E-102	2.06	27519	14453	1297
Homo saplens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	BINT	11437146 NT	1.0E-102	2.05	27518	14453	1297
Human endogenous retroviral DNA (4-1), complete retroviral segment	NT	M10976 1	1.0E-102 M1097611	1.9	27362	14308	1141
Homo sapiens down-regulated in adenoma (DRA) mRNA	4 NT	4557534 NT	1.0∈-102	1.06	27028	13975	796
601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'	EST_HUMAN	1.0E-102 BE252470.1	1.0E-102	0.61	26844	13820	635
Homo sepiens chromosome 21 segment HS21C103	NT	1.0E-102 AL163303.2	1.0E-102	4.57	26589	13562	351
Homo sepiens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds	NT	1.0E-102 AF012872.1	1.0E-102	0.61	26284	13278	6
QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA	EST_HUMAN	1.0E-101 AW939051.1	1.0E-101	12.79		25529	12793
QV3-HT0460-230200-101-d03 HT0460 Homo sapiens cDNA	EST_HUMAN	1.0E-101 BE163557.1	1.0E-101	2.24		25489	12738
RC-BT183-290499-085 BT163 Homo sapiens cDNA	EST_HUMAN	1.0E-101 AISO8168.1	1.0∈-101	1.85	38749	25040	12059
RC-BT163-290499-085 BT163 Homo sapiens cDNA	EST_HUMAN	1.0E-101 AI908168.1	1.0E-101	1.85	38748	25040	12059
Homo saplens mRNA for KIAA0819 protein, partial cds	NT	1.0E-101 AB020626.1	1.0E-101	1.31	38089	24432	11371
601680825F1 NIH_MGC_B3 Hamo sapiens cDNA clone IMAGE:3950887 5'	EST_HUMAN	1.0E-101 BE973648.1	1.0E-101	0.83	37427	23804	10771
601680825F1 NIH_MGC_83 Hamo sapiens cDNA clone IMAGE:3950887 5'	EST_HUMAN	1.0E-101 BE973648.1	1.0E-101	0.83	37426	23804	10771
to77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M28326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	EST_HUMAN	1.0E-101 Al570263.1	1.0E-101	4.37	37300	23690	10656
to77d11.x1 NCI_CGAP_Gas4 Horno saplens cDNA clone IMAGE:2184309 3' similar to gb:M26328 KERATIN, TYPE   CYTOSKELETAL 18 (HUMAN);	EST_HUMAN	1.0E-101 AI5702£3.1	1.0€-101	4.37	37299	23680	10656
Homo saplens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	7 NT	11429127 NT	1.0E-101	1.94	37264	23654	10620
Homo septens potassium chemnet, subfamily K, member 10 (KCNK10), mRNA	NT	10863960 NT	1.0E-101	0.68	36737	23136	10098
601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE;3875953 3'	EST_HUMAN	1.0E-101 BE616667.1	1.0E-101	3.36	36594	22998	9959
601472808T1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3875953 3'	EST_HUMAN	1.0E-101 BE619687.1	1.0E-101	3.36	36593	22998	9359
Homo saplens gamme-glutamytransferase 1 (GGT1), transcript variant 3, mRNA	2 NT	9845492 NT	1.0E-101	19.41	36209	22638	9876
Human mRNA for pancreatic gamma-glutamytransferase	NT	X60069,1	1.0E-101 X60069;1	17.36	34620	21103	8661
Human mRNA for pancreatic gamma-glutarnytransferase	NT	X60069 1	1.0E-101 X60069[1	17.36	34619	21103	9661
Homo saplens mRNA for KIAA1351 protein, partial cds	NT	1.0E-101 AB037772.1	1.0E-101	0.99	36168	22596	8531
Homo septens mRNA for KIAA1351 protein, pertiel ods	NT	1.0E-101 AB037772.1	1.0E-101	0.99	36167	22696	9531
zk29g08.r1 Soares_pregnant_uterus_NbHPU Homo saplens cDNA clone IMAGE:471998 5' similar to PIR:S54840 S54640 YD9335.03c protein - yeast ;	EST_HUMAN	1.0E-101 AA036800.1	1.0E-101	1.1	35832	22290	9212
hh74g10.y1 NCL_CGAP_GU1 Homo sapiens oDNA clono IMAGE:2968578 5' similar to gb.J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);	EST_HUMAN	1.0E-101 AW630370.1	1.0E-101	0.71	35133	21598	8517
hh74g10.y1 NCL_CGAP_GU1 Homo saplens cDNA clone IMAGE::2888578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);	EST_HUMAN	1.0E-101 AW630070.1	1.0E-101	0.71	35132	21598	8517
Top Hit Descriptor	Top Hit Database Source	Top Hil: Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signed	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:

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Table 4
Single Exon Probes Expressed in Placenta

				Si igi		- Lyrossou III raverna
SEQ D	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
15514	28642	1.91	1.0E-102	VI124669.1	EST_HUMAN	am50c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.;
16614	28643	1.91	1.0E-102	VI124669.1	EST HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA done IMAGE:16399543' similar to SW:GG96_HUMAN Q08379 GOLGIN-96.;
16266		0.74	1.0E-102	/13932.1	NT	Hamo sepiens PRKY exan 7
16309	29322	1.47	1.0E-102	1979	NT	Homo sepiens KIAA0187 gene product (KIAA0187), m≂NA
16378	29387	3.73	1.0E-102	\U141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
16378	29388	3.73	1.0E-102	\U141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
17490	30472	1.74	1.0E-102	\L163207.2	NT	Homo saplens chromosome 21 segment HS21C007
17871	30655	2.57	1.0E-102	3E251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3343882 5'
18346	31316	1.28	1.0E-102	₹66488.1	EST_HUMAN	y/32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 6
18686	31704	1.6	1.0E-102/		NT	Homo saplens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
19057		6.87	1.0E-102		NT	
18094	32408	3,25	1.0E-102	7705398	Z	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
10100	22/1/2	0.40	105-102	11/220/0	1	Linna saplens have domain and BI D 2 (HEBC2), HIDNA
						ar82/09 x1 Barstand colon HDI RB7 Homo saplans cDNA done IMAGE 2151785 3' similar to TR-013137
19591	32956	281	1.0E-102	1459825.1	EST_HUMAN	
20090	33507	0.7	1.0E-102 /	\W451343.1	EST_HUMAN	UI-H-BI3-alj-d-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'
20369	33823	0.91	1.0E-102	3E729323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
20396	33858	1.02	1.0E-102	3E386106.1	EST HUMAN	601277215F1 NIH_MGC_20 Harno sepiens cDNA clone IMAGE:3618243 51
20500	33977	1.5	1.0E-102 /		NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
20584	34057	8.03	1.0E-102		NT	Homo septens mRNA for Centaurin-alpha2 protein
20858	34350	261	1.0E-102		EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
21499	35031	3.85	1.0E-102	3E763051.1	EST_HUMAN	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA
21771	35301	1.71	1.0E-102 /		EST_HUMAN	AV694817 GKC Homo sapiens aDNA clone GKCEEE11 5'
21771	35302	1.71	1.0E-102/		EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
21881	35419	0.81	1.0E-102/		NT	Homo sepiens mRNA for KIAA0454 protein, partial cds
22210	35754	1.2	1.0E-102 E		EST_HUMAN	601283770F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3605536 5'
22210	35755	1.2	1.0E-102 E		EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5
22538	36102	0.84	1.0E-102 /		EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
22587	36155	2	1.0E-102	70393 1	EST_HUMAN	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
22587	36156	2	1.0E-102	70393 1	EST_HUMAN	yd13d07.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE;67021 5'
22666	36237	3.11	1.0E-102/	U124629.1	EST_HUMAN	AU124629 NT2RM4 Home saplens cDNA clone NT2RM4000309 5'
	Exon SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		ORF SEQ Express ID NO: Signa 28642 28643 29327 29327 29387 29388 30472 31704 31704 32408 32408 32408 32408 32408 32408 32575 33858 33977 33858 33977 33858 33977 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 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34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 34057 3	ORF SEQ Expression (Top) Hit ID NO: Signal Value 28642 1.91 1.0E-102 28643 1.91 1.0E-102 28643 1.91 1.0E-102 28643 1.91 1.0E-102 28649 3.73 1.0E-102 28689 3.73 1.0E-102 28689 3.73 1.0E-102 30655 2.57 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.9 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 1.2 1.0E-102 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 31704 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6015/311311 NIH_MCC_9 Homo sapiens cDNA clone IMAGE:3834315 5' UI-H-BW0-ajt-h-11-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733165 3'	EST_HUMAN	1.0E-103 AW298245.1	1.0E-103	5.33	29853	16634	3467
			1.0E-103 N32770.1	2 1	28921	15805	2685
Homo sepiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds			1.0E-103	1.84	28772	15648	2523
AU134991 PLACE1 Hamo sepiens cDNA clane PLACE1000965 5'	NAWOH_TSB	1.0E-103 AU134991.1	1.01-103	1.95	28638	15510	2379
Horno saplens bane marphogenetic protein 8 (asteogenic protein 2) (BMP8) mRNA		4502428 NT	1.0E-103	0.95	28281	15172	2031
Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	NT	4502428	1.0E-103	0.95	28280	15172	2031
Homo saplens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA		7657592 NT	1.0E-103	1.02	28207	15107	1964
Homo sapiens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds	NT	٠	1.0E-103	3.51	27863	14778	1626
801485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'	EST_HUMAN		1.0E-103	. 7.08	27500	14429	1272
Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)	TN	1.0E-103 AJ278348.1	1.0E-103	74.34	27234	14176	1004
Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA		5453793 NT	1.0E-103	0.84	26466	13436	213
Homo saplens mRNA for KIAA0235 protein, partial cds	IN		1.0E-103	8.24	26365	13338	102
801500405F1 NIH_MGC_70 Hamo sapiens cDNA clone IMAGE:3902305 5'		.0E-103 BE908158.1	1.0E-103	0.85	26332	13308	71
601500405F1 NIH_MGC_70 Hamo sapiens cDNA clone IMAGE:3902305 5'	EST HUMAN	.0E-103 BE908158.1	1.0E-103	0.85	26331	13308	71
Homo sepiens myeloid/lymphoid or mixed-lineage leukernia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA		11419159 NT	1.0E-102	1.25	32015	25553	12831
xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'	EST_HUMAN	1.0E-102 AW300862.1	1.0∈-102	5.67	32000	25517	12775
Homo saplens chromosome 21 segment HS21C080			1.0E-102	5.69			12182
Humen chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds	NT		1.0E-102 U41302.1	2.83	38699	24994	12009
RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA	EST_HUMAN	1.0E-102 BF359243.1	1.0E-102	2.47	38378	24688	11690
ak49h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408347 3'	EST_HUMAN	1.0E-102 AA868675.1	1.0E-102	1.47	38337	24653	11600
Homo saplens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA		4507822 NT	1.0E-102	2.44	38036	Т	11327
Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA		4507822 NT	1.0E-102	2.44	38035	24390	11327
601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'		1.0E-102 BE897488.1	1.0E-102	1.37	38030	24386	11323
on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15608223 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2. [1] ;	EST_HUMAN	1.0E-102 AA970786.1	1.0E-102	1.5	37394	23781	10748
RC-BT074-260499-014 BT074 Homo sapiens cDNA	EST_HUMAN	.0E-102 AIS05037.1	1.0E-102	3.26	37326	23720	10687
RC-BT074-260489-014 BT074 Homo sepiens cDNA	EST_HUMAN	1.0E-102 AI805037.1	1.0E-102	3.26	37325	23720	10887
Homo sapiens myomesin (M-protein) 2 (165kD) (MYOWZ), mRNA	NT		1.0E-102	0.67	37292		10647
Home sapiens myomesin (M-protein) 2 (165kD) (MYON2), mRNA	T	11425430 NT	1.0E-102	0.67	37291	23681	10847
Homo saplens phospholipid scramblase 1 gene, exon 1 and 5 flanking region	NT	1.0E-102 AF153715.1	1.0E-102	0.64		23628	10593
Top Hit Descriptor	Top Hit Database Source	Top Hi! Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exan SEQ (D NO:	Probe SEQ ID NO:
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Single Exon Probes Expressed in Placenta

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7951	7951	7488	7375	7178	7108	6987			6987		685 <u>9</u>	6859	_	6768 8	67 <u>25</u>	68 7	6887	8397	8397 1		88	5325	4110	3933	3894	3850	3526	-		$\dashv$
21001	21001	20563	20454	20310	18535	90081			18506		20011	20011		19924	25831	19748	19748	19566	1056	19245	19238	18438	17264	17092	17053	17010	16691		SEQ ID	
01 34512	34511	34032				Γ			8 31521		33423	33.422		33318	٦	33131	33130		٦	П	32563		30264	30090	30053		00/62	20720	ORF SEQ ID NO:	
12	==													8 0.91	3 1.15	0.84				1.67	0.9	. 0.63	4.63		6.0	0.40			Expression Signal	
4 1.0E-	4 1.0E-	3.6		Τ.	T	Ţ	77 1 OF-103		1.77 1.0E-103		1.66 1.0E-1	1.02-1		Γ		Г	Γ		0.8 1.0E-103	П	Γ		Π	Γ		Т	Ţ	T	(Top) Hit BLAST E Value	, Most Similar
1.0E-103 AI590071.1	1.0E-103 AI590071.1	1.0E-100 DE/ 40 100.1	OF 100 DE 7/81 58 1	1.0E-103 AW 085778 1	12000				03 5032282 NT		1.0E-103 A1590071.1	1.0E-103 Alasouri.	1500074 4	1.0E-103 AF053490.1	1.0E-103 AA781442.1	1.0E-103 AW 954565.T	1.0E-103 AW 954555.1	3 11435063 N		AF1798	.0E-103 BF569527.1	1.0E-103 AA451615.1	1.0E-103   Z3003.	1,14308/6	AA4856	1.0E-100 Lt. 07000 (1.	AEDZARA: 1	1 0E-103 AB040892.1	Top Hit Acession Nc.	
EST HUMAN	EST_HUMAN	10	FST HUMAN	EST HUMAN	3	OO NT	5032282 NT		82 NT		EST_HUMAN	1.	FST HUMAN	2	EST_HUMAN	TOTAL TOTAL	EGT HIMAN	S Z Z	1	Z	EO TONS	EST_HUMAN	1,000	EST LIMAN	EST_HUMAN		,	NT		Top Hit
Q13/69 ANONT MOCO.	Q13769 ANONYMOUS.; Im58b05.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2162289 3' similar to TR:Q13769	tm58b06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162269 3 similar to TN:210700	601571537F1 NIH_MGC_55 Home sapiens cDNA clone IMAGE: 3030043 3	EST377849 MAGE resequences, MAGI Homo saplens cDNA	Homo sepiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene		mana	DXS206, DXS230, DXS239, DXS269, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m,	mRNA i.a. destrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,	DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Up42/m,	Q13769 ANONYMOUS: ;  Lump comions distrophin (muscular dystrophy, Duchenne and Backer types), includes DXS142, DXS164,	tm58b05.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2182289 3 similar to In. 3 1970	Q13769 ANONYMOUS.;	m-58h06 x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to IR:Q13769	Homo saplens divoline receptor alpha 2 subunit (GLRA2) gene, exon 4	JORGA ST Scarce feetls NHT Homo sapiens cDNA clone 1391452 3	EST366838 MAGE resequences, MAGC Homo capiens cDNA	EST365636 MAGE resequences, MAGC Homo sapiens cDNA	Homo seriens KIAA0440 protein (KIAA0440), mRNA	Homo sepiens KJAA0440 protein (KIAA0440), mRNA	Home sentin 2 (SEP2) mRNA, partial cds	TR:G292352 G292352 COLLAGEN CHAIN RH;	2x43b04.r1 Scares total fetus Nb2HF8_9w Home sepiens cDNA clone IMAGE:/89T89 3 simula to	sec340 b4HB3MA-Cot108+10-Bio Homo sapiens cDNA done b4HB3MA-Cot109+10-Bio-7-3	clement LTR10 repetitive etainest.  Homo septemb reuropilin 1 (NRP1), mRNA	ab10d12.s1 Strategene lung (#937210) Homo sepiens CUNA Glone INVACE CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIAN CONTROL OF CHILLIA	Maceca mulatta cyclophilin A mRNA, compisie cus	Homo sapiens mRNA for KIAA1459 protein, perual cus	Top Hit Descriptor.	

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Single Exon Probes Expressed in Placenta

					Ç	2011	Ciligio Exciti i Deserva III i facetina
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top HI! Acession No.	Top Hit Database Source	Top Hit Descriptor
8484	21565	35101	0.59	1.0E-103 T3108C.1	T3108C.1	EST_HUMAN	EST27183 Human Brain Homo sapiens cDNA 5' end similar to None
8822	21901	35440	1.05	1.0E-103	1.0E-103 AU140344.1	NAMOH_TS3	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5
8822	21901	35441	1.05	1.0Ε-103	1.0E-103 AU140344.1	EST HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
			<u>.</u>				7160e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sablens cDNA clone IMAGE:3525964 3' similar to
8900	Т	35518	1.34	1.0E-103	1.0E-103 BF109244.1	EST_HUMAN	SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1:
830/	Г	35934	3.18	1.0E-103	6005921 N I	2	Homo sapiens triple functional domain (FTPRF interacting) (TRIO), mRNA
8307	22383	35935	3.18	1.0E-103	6005921 NT	NT	Homo sepiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9349	22425	35980	0.97	1.0E-103	1.0E-103 AA581086.1	EST_HUMAN	nd13c02.s1 NCI_CGAP_Ov1 Homo septens cDNA clone IMAGE:800162 3' similer to gb:L02426 26S   PROTEASE SUBUNIT 4 (HUMAN);
10263	23298	36896	2.04	1.0E-103 Z37976.1		NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10304	23339	36944	2.07	1.0E-103	.0E-103 AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10443	23478	37083	10.79	1.0E-103	1.0E-103 AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518328 5' cimilar to TR: O15046 O15046 KIAA0338 ;
10878	23963	37591	1.52	1.0E-103	1.0E-103 BE549:06.1	EST HUMAN	7b41f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb.M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10071	34054	77694	D	105-103	1 0E-103 A1702750 1	NVIVI IN LOS	002d06.y5 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084
11072		37785	2.45	1.0E-103	11424061 NT	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11072	24147	. 37786	2.45	1.0E-103	11424061 NT	TN	Homo sepiens AXL receptor tyrosine kinase (AXL), mRNA
11083	24157	37794	2.4	1.0E-103		NT	Homo septens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11083	Г	37795	2.4	1.0E-103		NT	Hamo saplens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11656	Г	38426	2.67	1.0E-103	3.1	EST_HUMAN.	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11731	23917	37642	4.1	1.0E-103 L43610.1		NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11968	24963		1.71	1.0E-103	1.0E-103 AB024759.1	3	Homo sapiens TSA305 gene, exon 16
12044	25025	38730	2.26	1.0E-103	1.0E-103 BE644611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element;
12178	25138		3.4	1.0E-103	1.0E-103 AF224669.1	NT	Homo sepiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12209	25182		1.22	1.0E-103	11526291 NT	NT .	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12414		32083	1.71	1.0Ε-103	1.0E-103 AB011889.1	NT	Hamo saplens gene for AF-6, camplete cds
243	П	26494	2.46	1.0E-104		EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5
243	Г	26495	2.48	1.0€-104	1.0E-104 AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo saplens cDNA clone DKFZp564H1072 5
1937	15080	28182	1.92	1.0E-104	4502428 NT	NT	Homo saplens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA

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Homo sepiens I rio isoform mRNA, complete cds	NT	1.0E-104 AF091395.1	1.0E-104	5	36147	22580	9515
Homo saplens Trio isoform mRNA, complete cds	NT	1.0E-104 AF091385.1	1.0E-104		36146	22580	9515
yc83f02.r1 Soares inferrt brein 1NIB Homo sapiens cDNA clone IMAGE:22440 5'	EST_HUMAN	T74219.1	1.0E-104 T74219.1	1.03		22541	9484
zB8b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Hamo septens cDNA clone IMACE:462897 3'	EST_HUMAN	1.0E-104 AA682308.1	1.0E-104	0.46	36082	22520	9463
nad18g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3*	EST_HUMAN	1.0E-104 BF448230.1	1.0E-104	2.41	36004		9368
UI-H-BI4-Bow-b-09-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'	EST_HUMAN	1.0E-104 BF509244.1	1.0E-104	0.87	35414	21875	8798
Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	Y,	11425572	1.0E-104	2.01	33917	20452	7373
601150451F1 NIH_MGC_19 Hamo sapiens cDNA clane IMAGE:3503220 5'	EST_HUMAN	1.0E-104 BE314182.1	1.0E-104	3.39	33693	20255	6942
601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'	EST_HUMAN	1.0E-104 BE314182.1	1.0E-104	3.39	33692	20255	6942
Homo sapiens PDZ domain-containing guanine nucleotide exchange factor i (LOC51735), mRNA	NT	7706512	1.0E-104	0.74	33339	18941	6786
wj03b12x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN. ;contains element LTR7 repetitive element;	EST_HUMAN	I.0E-104 AI768797.1	1.0E-104	8.6	. 33143	19756	6596
MOSDIZXI NU_CGAY_NGIZ HOMO septens CUNA Gorb IMAGE;2401/2/3 similar to IR;Q14145 Q14145 KIAA0132 PROTEIN.;contains element LTR7 repetitive element;	EST_HUMAN	1.0E-104 AI768797.1	1.0E-104	8.5	33142	19756	0598
Homo sapiens ali3 mRNA for Aurora/lp11-related kinase 3, complete cds	NT	1.0E-104 AB017332.1	1.0E-104	0.93	32623	19288	6108
Human Down Syndrome region of chromosome 21 DNA	N T	1.0E-104 U43379.1	1.0E-104	1.05	32568		6061
Human Down Syndrome region of chromosome 21 DNA	NT	.0E-104 U43379.1	1.0E-104	1.05	32567	18243	6061
Homo sapiens chromosome 21 unknown mRNA	NT	1.0E-104 AF231920.1	1.0∈-104	1.2	30850	17867	4732
Homo sapiens chromosome 21 unknown mRNA	TN	1.0E-104 AF231920.1	1.0E-104	1.2	30849		4732
Human mRNA for fibronectin (FN precursor)	NT	X02761.1	1.0E-104 X02761.1	33.85	30618	17636	4496
HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07	EST_HUMAN	1.0E-104]F11745.1	1.0E-104	0.71	30383		4248
Homo sapiens mRNA for KIAA1172 protein, partial cds	NT	1.0E-104 AB032998.1	1.0E-104	0.71	30218	17209	4053
Harno saplens mRNA for KIAA1276 protein, partial cds	NT	1.0E-104 AB033102.1	1.0E-104	0.65			3690
Homo sapiens mRNA for KIAA1276 protein, partial cds	NT	1.0E-104 AB033102.1	1.0E-104	0.65	29860		3690
EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end	EST_HUMAN	1.0E-104 AA318436.1	1.0E-104	2.33			3478
AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000936 5	EST_HUMAN	1.0E-104 AU133926.1	1.0E-104	66.0	29526	16510	3337
H. sapiens gene encoding phenylpyruvate tautomerase II	NT	Y11151.1	1.0E-104 Y11151.1	2.15		16159	2983
Human lymphocytic antigen CD59/MEM43 mRNA, complete cds	NT	1.0E-104 M346711	1.0E-104	17.99	29125		2934
Hamo sapiens ARP2 (actin-related protein 2, yeast) hamolog (ACTR2), mRNA	NT	31570	1.0E-104	2	28753	15633	2505
RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA	EST_HUMAN	.0E-104 BF334221.1	1.0E-104	9.73	28699	15570	2442
RC1-CT0249-110900-214-f12 CT0249 Hamo septens cDNA	EST_HUMAN	.0E-104 BF334221.1	1.0E-104	9.73	28698	15570	2442
601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5	EST_HUMAN	.0E-104 BE744628.1	1.0E-104	4.55	28540	16409	2277
zo22c06.s1 Stratagene colon (#937204) Homo sapians cDNA clone IMAGE:587626 3' similar to gb:Z14116_ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);	EST_HUMAN	1.0E-104 AA132975.1	1.0E-104	33,29	28528	15400	2267
Top Hit Descriptor	Top Hit Database Source	Top HI! Acession	Most Similar (Top) Hit BLAST E Value	Expression Signel	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:
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Page 443 of 550 Table 4 Single Exon Probes Expressed in Placenta

ES1373761 MAGE resequences, MAGG France September 201	1 EST HUMAN	0F-105 AW 961688.1	_		T	Т	3
Inditio sapiets promoving the Company can be	7304922 NT		1.0E-105		1	Ţ	
Harmonian adjacent to zinc finger domain, 2B (BAZ2B), mRNA	73049ZZ N I		1.0E-105	0.86	29618	╗	3432
Library series bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA	2	AJZZ804		2.79	17	16247	3071
Homo saplens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3		.0E-105 AA0848UG.		0.88	8	4 15900	2784
no10d05.s1 NCI CGAP Phen Homo sapiens cDNA cione IMAGE: 1100265 3		.UE-105 BE09 1700.		1.18	8	8 15529	2398
601434491F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3919611 3		OF 405 BE 901768 1	T.		28524	Г	2263
EST20609 Spleen I Homo saplens cDNA 5' end similar to autoimmune anugen ku, prorped subunit		1.UE-105 DO01010	1.00-103			Γ.	1979
1		1.0E-106 AL 102COL	T			Г	1865
Homp saptens chromosome 21 segment HS21C080		1.0E-105 AF 032697.1			Γ	Γ	607
Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	NT -	1.0E-105 AF032807 1	1.01-105			П	607
Homo sepiens potassium channel subunit (HERG-3) mRNA, complete cds	į	140	1.05-106		Γ	13238	438
Homo sapiens amyloid beta (A4) precursor protein (proteoso nexin-il, Alzheimer disease) (Arr), muxiva Homo sapiens Meist (mouse) homolog (MEIS1) mRNA	4502168 NT		1.0E-105		26541	15981	289
	EST_HOMEN	.0E-104 BE393892.1	1.0E-104	1.32	2	П	13073
A01312181F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3658676 5	4/29	114:	1.0E-104		38768		12082
Homo saniens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA	EGITOWAN	1.0E-104 BF684288.1	1.0E-104	4.1	38350	П	11611
RONA1215F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE:4302507 5',	EST HUMAN	1.0E-104 BE720191.1	1.0E-104	44.88	38311	24632	11577
BCn-HT0885-310700-021-509 HT0885 Homo sapiens cDNA	EOI TOWN	1.0E-104 BE720191.1	1.0E-104	44.86	38310	┑	11577
RCn-HT0885-310700-021-509 HT0885 Homo saplens cDNA	10427757 NI	1142	1.06-104	0.74		П	10791
Loron seriens KIAA0649 gene product (KIAA0649), mRNA	Z -	U66535.1	1.0E-104 U66535.1	5.4	37430	П	10774
Himan heha4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25	EG LOWNIN	1.0E-104 AA931321.1	1.0E-104			7	10757
CONGRATO AT Sources NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1666370 3	EST HUMAN	1.0E-104 AAB31321.1	1.0Ε-104	0.64		$\neg$	10757
anged of Sparce NEL T GBC S1 Homo septens cDNA clone IMAGE:1565370 3	EST HOWAY	1.0E-104 AU130/65.1	1.0E-104	4.47	37301	$\neg$	10857
ALI130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5	EST LINAN	.0E-104 AV728070.1	1.0E-104	1.49	37253		10611
AV729070 HTC Homo capiens cDNA clone HTCBYA07 5	TOT LOWN	.0E-104 BE /91 /13.1	1.0E-104	3,15	36938	╗	10298
R01581503F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3835977 5	EST HOWAN	.0E-104 BE791713.1	1.0E-104	3.16	. 36937	٦	10298
R01581503F1 NIH MGC 7 Homo sepiens cDNA clone IMAGE:3935977 5	201	.0E-104 AF113514.1	1.0⋶-104	0.49		$\neg$	10163
Q2416 HYPOTHETICAL 29.4 KD PROTEIN.	EST_HUMAN	.0E-104 AW103848.1	1.0E-104/	0.92	36590	22894	9955
Q24116 HYPOTHETICAL 29.4 KD PROTEIN.;  Q24116 HYPOTHETICAL 29.4 KD PROTEIN.;  LEZE-JOS A Secres NET T GRC S1 Homo septens cDNA clone IMAGE: 2603523 3' similar to TR: Q24116	EST_HUMAN	1.0E-104 AW103848.1	1.0E-104	0.92	36589	22994	888
WT9402 Y Scares NFI T GBC S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR.Q24116	ES   TOMPN	1.0E-104 BF352841.1	1.0E-104	4.14	34598	21084	9641
III 3-1170619-080900-249-F07 HT0619 Homo sepiens cDNA	EST HOMAN	1.0E-104 BF352841.1	1.0Ε-104 Ε	4.14	34697	21084	9841
II 2 LTDs40 080000-244-F07 HT0619 Homo sepiens cDNA			Value		į	Ö	Ö
Top Hit Descriptor		Top Hit Acession	Most Similar (Top) Hit BLAST E	Expression	ORF SEQ	Expa SEQ ID	Probe SEQ ID
				1			

11887

24875 24614

1.0E-105 AW027554.1

EST\_HUMAN

P87892 PROTEASE ;
7018010 M NCLOGAP\_Kid11 Homo sapiens cDNA cone IMAGE:3574291 3' similar to TR:P87680 P97880

wv74f07.x1 Soares\_thymus\_NHFTh Homo sepiens cDNA clone IMAGE:2535301.3' similar to TR:P87892

24957 26091 13380

38794 38659 38572

1.0E-105 AF218896.1 1.0E-106 AW503208.1 1.0E-106 AI565085.1 1.0E-106 AW965556. 1.0E-106 J00146.1 J00145.1

EST\_HUMAN

RN1.

EST\_HUMAN EST\_HUMAN

HUMAN

EST377629 MAGE resequences, MAGI Homo sapiens cDNA

Homo sapiens soluble neuropilin-1 mRNA, complete cds Human dihydrofolate reductase pseudogene (psl-hd1) Human dihydrofolate reductase pseudogene (psi-hd1)

UI-HF-BNO-ekt-9-07-0-UI.71 NIH\_MGC\_50 Homo sapiens cDNA clone IMAGE:3078348 5'

Homo sepiens attractin precursor (ATRN) gene, exon 8

<del>.</del> 2 8

13433 13748 13807 13807

26464 26774 26828 26828

1.89 1.13

22764 22764 24243 24564

36333 36334 37876 38241 38293

0.75 4.82 1.42

1.0E-105 1.0E-105

7705936 NT

Z

Homo sapiens COL4A6 gene for s6(IV) collagen, exon 31 Homo sapiens Ren binding protein 11 (LOC51184), mRNA

Single Exon Probes Expressed in Placenta Page 444 of 550 Table 4

Probe SEQ ID	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
	1		5.34	Ì	1.0E-105 AL163208.2	NT	Homo saplens chromosome 21 segment HS21C008
5053	18181		0.04	l			Homo sepiens mRNA for KIAA0866 protein, complete cds
5259	9 18378	31344	1.08				10010 Septembria de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l
7	Т	1	1.18		.0E-105 AF016704.1	NT	Homo sapiens Eo-Ar uniquini-piocennigeae (Cocco.) BEC.1) mSNA
n d		T	1.12		1,1420134 NT		Homo sapiens Retina-derived POU-domain ractor - (NTT-1), 1114 CE: 4430334 5
7048	1	33513		٦	1.0E-105 BF314302.1	T HUMAN	
7045	1		1.44		1.0E-105 BF314302.1	EST_HUMAN	601901028F1 NIT WOOL 19 notify septiate cutting (GAPI ) mBNA
7121	7	31458	3.78	1.0E-106	11419186 N I	Z	Companies CTPass activating proteh-like (GAPL), mRNA
7121	1 18547	31459	3.78		11419196 N I		ECTROSESO MAGE resentiences. MAGB Homo sapiens cDNA
7167	7 20300	33743	0.72		1.0E-105 AW851634.1		E3133737051 NIH MGC 21 Home saplens cDNA clone IMAGE:3960019 5
7436	20513	33986	0.72		1.0E-105 BE802616.1	HOMAN	do lo / 27 al la la la concomene
8043 2043	٦	34647	0.93		1.0E-105 X12556.	NT.	FOTOMOTE Eat-1 brain Straturone (certifo36206) Homo sapiens cDNA clone HFBCR32
8217	1	34820	11.05		1.0E-106 T05087.;	EST_HUMAN	EG 1025 O 1 Stall Mail 1, County September 20NA come IMAGE:2500626 3' similar to
989			1.63		1.0E-105 AW007194.1	EST_HUMAN_	SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE;
9128	-1	7 35750	0.82		1.0E-105 AW 840817.1	EST_HUMAN	RC1-CN0000-070 100-0 11-200 CRAP Sub2 Homo sapiens cDNA clone IMAGE:27117823
9250	0 22327	7 35874	2.51		1.0E-105 AW016879.1	EST HUMAN	OV2-OTIORS2-140300-083-d09 OT0062 Homo sapiens cDNA
9404	) <del>4</del> 22478	8 36041	0.83	Γ.	1.0E-105 AW 882372.1	EST HOWAN	OV2 OT0082-40300-083-d09 OT0082 Homo sapiens cDNA
9404	22478	8 36042			1.0E-105 AW 882: /2.1	EOT TOWAN	GRAMANTESET NIH MGC 65 Homo sapiens cDNA clone IMAGE:3847884 5
9767	_	4 36333	0.75		1.0E-105 BE867793.1	EST HOMAN	GOYAA3755E3 NIH MGC 65 Homo sapiens cDNA clore IMAGE:3847884 5
9767	37 22764	4 36334	0.75		1.0E-105 BE887793.1	EST HOMAN	Lorgo serviens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively opticed
11173	73 24243	3 37876	4.82		1.0E-105 AF254822.1	2	Light captions COI 446 game for a6(IV) collagen, exon 31
	I	l		1		27	IHomo sabiens COC+AO geno id ec/i*/ concessi control

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Table 4
Single Exon Probes Expressed in Placenta

			7				7				ٳ	3	ω	اړ	ابو	اي	ω	2	ري	2	اي	2	2	26	23	2	<del>18</del>	100		17	1		Probe SEQ ID	}.
6227	6116	6116	6026	5976	5976	5485	4	4723	4149	41 46	3527	3527	٦	╗	$\neg$	П	Т	٦	7		7	П	П	2674	2391	П	1846	1846	$\neg$	╗	1736			
19402	19266	19296	19209	19161	19161	18684		17858	73 73 94	17301 1301	16692	16692	16628	16422	16422	16182	16182	16116	14617	14617	15929	15790	16788	15699	15522	15326	14892	14992		14906	14885 5		SEO D	
2 32762	32632	32631	32528	32481	32480	31701			30294	30293	29702			29439		29205		29128	27701	27700	29041	28906	28904	28821	28651	28461	28094	28093		28000	27978		ORF SEQ ID NO:	
	2	-						0 2.27			1.07	1.07	1.04			5.7		1.18	1.84	1.84	8.05		1.83	2.19	3.62	1,94	6.51	5.51		1.33	7.83		Expression Signal	
8.39	╞	-	0.61	38.0	0.95	2.95		27	8.2	9.2	12	37	4	25	26		7	Г							T	T		1			Г	١,	~ E 3 8	1
1.0E-10	1.0E-10	1.0E-10	1.02-10	1.01-10	1.06-106	1.0E-100	i	1.0E-106	1.06-106	1.06-106	1.0E-106	1.0E-106	1.0E-106	1.02-106	1.0E-106	1.0E-108	1.0E-106	1.0E-106	1.0E-108	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.02-108	1.0E-106	1.0E-106	1.05-100	3	1.0E-106 U04510.1	1.0E-106 U48724.1		Most Similar (Top) Hit BLAST E	
.0E-106 BF679574.1	1.0E-106 AU143,728.1	1.0E-106 AU143.728.1	1.0E-106 AA434168.1	1.0E-106 AU130113.1	1.0E-106 AU130113.1	1.0E-106 AA781 : 55.1		1.0E-106 BE144286.1	1.0E-106 AW974550.1	1.0E-106 AW974550.1	1.0E-106 AB033104.1	1.0E-106 AB033104.1	.0E-106 AB008681.1	8922965 N		AB03774	1.0E-106 AB0377,47.1	1.0E-106 BE384298.1	4504184 NI	4504184 NI	1.0E-106 A1276526.1	1.0E-106 BE260201.1	1.0E-106 U64675.2	1.0E-106 AF003528.1	101100	1.0E-106 BE144206.1	1.0E-106 AA527448.1	1.02-100/2027 130.1	A N T 27 A J B 4	J04510.1	J48724.1		Top Hit Acession No.	
EST HOWEN	EO LICINAN	TO TOWN	EO L TOWN	EGI LI JAAN	EGI HUMAN	EU TOMAN	TOT LINAN	EST HOMAN	EST HUMAN	EST TOWAR	N-	Z	Z	02	5 N	2	Z	EST HOMEN	4	- N	EG! HOWEN	EST HUMAN	Z	Z		CO I POWER	EST HUMAN	1	FOT HIMAN	2			Top Hit Database Source	
	R02154012F1 NIH MGC 83 Homb sapiens cDNA done IMAGE:4295067 6	AII143228 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5	Al 143478 Y79AA1 Homo sepiens cDNA clone Y79AA1001912 5	w28d12 s1 Spares overy tumor NbHOT Homo septens cDNA clone IMAGE:770615 3'	ALI 130/13 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'	ALI130113 NT2RP3 Homo saplens cDNA clone NT2RP3000274 5	BLPS1-2 (HUMAN)	ANALON A Server hearts NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN	NEO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA	ESTREBYS MAGE resequences, MAGN Homo sepiens cDNA	EST388875 MAGE resequences, MAGN Homo sapiens cDNA	Homo septions mRNA for KIAA1278 protein, partial cds	The project ment for KIAA1278 projein, partiel cds	Homo contens name for activin receptor type IIB, complete cds	Homo septions hypothetical protein FLJ11273 (FLJ11273), mRNA	Line and the protein FL 111273 (FL.11273), mRNA	Long seriens mRNA for KIAA1326 protein, partial cds	100 187 - DANA for KlaA1326 protein partial cds	a l			- 178410 x1 Sparses NhHMPii S1 Homo sapiens cDNA clone IMAGE: 1878307 31	POLICE SPECIE SPECIE NIEL MGC 18 Homo Saplens cDNA clone IMAGE:3502461 6	regions	Homo sapiens X-linked arhidrojijo ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	Homo saniens glutathione S-transferase thete 1 (GSTT1), mRNA	LTR3 repetitive element : IMB0.HT0165-140200-008-d10 HT0165 Homo sepiens cDNA	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element	LTR3 repetitive element;	THE COAP Co3 Homo sapiens cDNA clone IMAGE:937352 3' Similar to contains element	The content the World and shall (COL4A5) gene, exon 41	Uman enthammel arough factor receptor (EGFR) precursor-mRNA, exon 4, partial cds	Top Hit Descriptor	

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Single Exon Probes Expressed in Placenta

36108 0.77 1.0E-106 AI750447.1 EST_HUMAN cn03e04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03e04 random Im4102.x1 NGL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.63 1.94 1.0E-106 AI479569.1 EST_HUMAN TAR1 PTR5 repetitive element:  36256 1.94 1.0E-106 AI479569.1 EST_HUMAN TAR1 PTR5 repetitive element:  36267 0.6 1.0E-106 BE380234.1 EST_HUMAN TAR1 PTR5 repetitive element:  36268 1.99 1.0E-106 BF027310.1 EST_HUMAN B0128267F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.63 1.0E-106 BF027310.1 EST_HUMAN B0128267F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3804217 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054403 5' S16040417.1 EST_HUMAN B01671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:30604217.1 S16040417.	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1.0E-106   11545913 NT   1.0E-106   11545913 NT   1.0E-106   11545913 NT   1.0E-106   AA8837/78.1   EST_HUMAN   1.0E-106   BE292722.1   EST_HUMAN   1.0E-106   BE292721   EST_HUMAN   1.0E-106   BE741408.1   EST_HUMAN   1.0E-106   BE741408.1   EST_HUMAN   1.0E-106   BE387950.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA825307.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   EST_HUMAN   1.0E-106   AA80447.1   E	Exam ORF SEQ Express SEQ ID ID NO: Signa 19507 32864 19507 32864	ORF SEQ Express ID NO: Signa 32864	Expressk Signal	8 8	Most Similar (Top) Hit BLAST E Value 1.0E-106 1.0E-106	ssion	Top Hit Database Source EST_HUMAN	01439670F1 NIH 01439670F1 NIH
1.0E-108   11545913   NT   1.0E-108   AAB837/8.1   EST_HUMAN   1.0E-108   BE2B2722.1   EST_HUMAN   1.0E-106   BE2B2722.1   EST_HUMAN   1.0E-106   BE2B2722.1   EST_HUMAN   1.0E-106   BE741408.1   EST_HUMAN   1.0E-106   BE741408.1   EST_HUMAN   1.0E-106   AB824723.1   EST_HUMAN   1.0E-106   AB824723.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0E-106   AAB25307.1   EST_HUMAN   1.0	19507 19711			0.68	1.0E-106	45913		201439670F1 NIH_MGC Tomo sapiens xylosyltran
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1.94 1.0E-106 BE292722.1 EST_HUMAN   8.06 1.0E-106 11425503 NT   8.06 1.0E-106 11425503 NT   9.06 1.0E-106 ALP116850.1 EST_HUMAN   3.62 1.0E-106 BE741408.1 EST_HUMAN   3.62 1.0E-106 BE741408.1 EST_HUMAN   3.62 1.0E-106 BE397950.1 EST_HUMAN   9.64 1.0E-106 BE397950.1 EST_HUMAN   9.64 1.0E-106 AI654123.1 EST_HUMAN   9.64 1.0E-106 AA825307.1 EST_HUMAN   9.83 1.0E-106 AA825307.1 EST_HUMAN   9.83 1.0E-106 AA825307.1 EST_HUMAN   9.34 1.0E-106 AA825307.1 EST_HUMAN   9.34 1.0E-106 AA825307.1 EST_HUMAN   9.35 1.0E-106 AA825307.1 EST_HUMAN   9.36 1.0E-106 BE389234.1 EST_HUMAN   9.37 1.0E-106 BE389234.1 EST_HUMAN   9.38 1.0E-106 BE389234.1 EST_HUMAN   9.39 1.0E-106 BE389234.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.31 1.0E-106 BF927310.1 EST_HUMAN   9.32 1.0E-106 BF927310.1 EST_HUMAN   9.33 1.0E-106 BF927310.1 EST_HUMAN   9.34 1.0E-106 BF927310.1 EST_HUMAN   9.35 1.0E-106 BF927310.1 EST_HUMAN   9.36 1.0E-106 BF927310.1 EST_HUMAN   9.37 1.0E-106 BF927310.1 EST_HUMAN   9.38 1.0E-106 BF927310.1 EST_HUMAN   9.39 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST_HUMAN   9.30 1.0E-106 BF927310.1 EST	П	П	છ	4.17	1.0E-106	11429617	NT	omo saplens XPMC2
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3.82 1.0E-106 BE741408.1 EST_HUMAN 3.62 1.0E-106 BE741408.1 EST_HUMAN 2.21 1.0E-106 BE741408.1 EST_HUMAN 2.21 1.0E-106 AI523066.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.83 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 1.94 1.0E-106 AI750447.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.95 1.0E-106 BF027310.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN			34556	0.6	1.0E-106	AU116850.1	EST_HUMAN	U116850 HEMBA1 H
3.62 1.0E-106 BE741408.1 EST_HUMAN 2.21 1.0E-108 AI523066.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.83 1.0E-106 AV838331.1 EST_HUMAN 0.83 1.0E-106 AA825307.1 EST_HUMAN 0.77 1.0E-106 AA825307.1 EST_HUMAN 0.77 1.0E-106 AI750447.1 EST_HUMAN 1.94 1.0E-106 AI750447.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 0.6 1.0E-106 BE389234.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.07 1.0E-106 AA604477.1 EST_HUMAN 1.07 1.0E-106 AA604477.1 EST_HUMAN 1.07 1.0E-106 AA604477.1 EST_HUMAN	21255		34778	3.62	1.0E-106		EST_HUMAN	101594331F1 NIH_MG
2.21 1.0E-106 AI523066.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.64 1.0E-106 BE387950.1 EST_HUMAN 0.64 1.0E-106 AI664123.1 EST_HUMAN 2.77 1.0E-106 AA825307.1 EST_HUMAN 0.83 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 1.94 1.0E-106 AI750447.1 EST_HUMAN 1.94 1.0E-106 AI479569.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.95 1.0E-106 BF927310.1 EST_HUMAN 1.06 1.0E-106 BF927310.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN			34///	3.62	1.05-106	BE741408.1	EST_HUMAN	v68e07.x1 Barstead ao
0.64 1.0E-106 BE387950.1 EST_HUMAN 2.77 1.0E-106 AI654123.1 EST_HUMAN 0.83 1.0E-106 AW838831.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 0.77 1.0E-106 AI75047.1 EST_HUMAN 1.94 1.0E-106 AI479569.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.94 1.0E-106 BE389234.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN	21909		34972	0.64	1.0E-106	AI5Z3066.1	EST_HUMAN	DI282717F1 NIH MG
2.77 1.0E-106 AI654123.1 EST_HUMAN 0.83 1.0E-106 AW836831.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 0.77 1.0E-106 AI750447.1 EST_HUMAN 1.94 1.0E-106 AI479569.1 EST_HUMAN 0.6 1.0E-106 BE389234.1 EST_HUMAN 1.09 1.0E-106 BF927310.1 EST_HUMAN 1.09 1.0E-106 BF927310.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN	21909	Ť	35448	0.64	1.0E-106	BE387950.1	EST_HUMAN	101282717F1 NIH_MGC
0.83 1.0E-106 AW838831.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 2.34 1.0E-106 AA825307.1 EST_HUMAN 0.77 1.0E-106 AI750447.1 EST_HUMAN 1.94 1.0E-106 AI479569.1 EST_HUMAN 1.94 1.0E-106 AI479569.1 EST_HUMAN 0.6 1.0E-106 BE389234.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN 1.07 1.0E-106 AA604417.1 EST_HUMAN	21882		35522	2.77	1.0∈-108	AI664123.1	EST_HUMAN	y62a05x1 NCI_CGAP_ 105084 69 KD ISLET C
2.34 1.0E-106   AA825307.1   EST_HUMAN   2.34 1.0E-106   AA825307.1   EST_HUMAN   0.77 1.0E-106   A175047.1   EST_HUMAN   1.94 1.0E-106   A479569.1   EST_HUMAN   1.94 1.0E-106   A479569.1   EST_HUMAN   0.6 1.0E-106   BE389234.1   EST_HUMAN   1.09 1.0E-106   BF027310.1   EST_HUMAN   1.09 1.0E-106   BF027310.1   EST_HUMAN   1.07 1.0E-106   AA604417.1   EST_HUMAN   10.7 1.0E-106   AA604417.1   EST_HUMAN		۳	35876	0.83	1.0E-108	AW838831.1	EST_HUMAN	3M4-LT0059-150200-00
2.34 1.0E-106 AA825307.1 EST_HUMAN  0.77 1.0E-106 AI750447.1 EST_HUMAN  1.94 1.0E-106 AI479569.1 EST_HUMAN  1.94 1.0E-106 AI479569.1 EST_HUMAN  0.6 1.0E-106 BE889234.1 EST_HUMAN  1.09 1.0E-106 BF027310.1 EST_HUMAN  1.09 1.0E-106 BF027310.1 EST_HUMAN  10.7 1.0E-106 AA604417.1 EST_HUMAN  10.7 1.0E-106 AA604417.1 EST_HUMAN	22424	Ť	35978	2.34	1.0E-108	AA825307.1	EST_HUMAN	x67e08.s1 NCI_CGAP
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1.94 1.0E-106 A479569.1 EST_HUMAN 0.6 1.0E-106 BE389234.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.09 1.0E-106 BF027310.1 EST_HUMAN 1.07 1.0E-106 BA604417.1 EST_HUMAN 10.7 1.0E-106 AA604417.1 EST_HUMAN	22684	-	36255	1.94	1.0E-108	AI479569.1	EST_HUMAN	m41f02x1 NCI_CGA AR1 PTR5 repetitive
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10.7 1.0E-106 BH027310.1 EST_HUMAN 10.7 1.0E-106 AA604417.1 EST_HUMAN 10.7 1.0E-106 AA604417.1 EST_HUMAN	23324	۲	36926	1.09	1.0Ε-106		EST_HUMAN	01671674F1 NIH_MG
10.7 1.0E-106 AA604417.1 EST_HUMAN	23481		37088	1.09	1.0E-108			9576/16/4F1 NIH_MG0
	23481	Н	37089	10.7	1.0E-106		EST_HUMAN	p57b10.s1 NCI_CGAF

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Table 4
Single Exon Probes Expressed in Placenta

IT Call to application of the control of the control of the call of the control of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the cal		7 5902087 N I	1.0E-107	2.9	29352	1634 1436	3169
Library Carloss CMT3 (cultural sector of military 3 (vess)) ha	ESI_HUMAN	AW 8424		6	3 29269	16248	3072
	EST HOMAN	AW842451.1	Γ	6.14	29268	16248	3072
L	EST HOMAN	1.0E-107 AW842451.1	Γ			Γ.	2435
PMI-CN0031-190100-001-003 CN0031 Homo septems CDNA	ESI_HUMAN	1.0E-107 AW842451.1	Γ		28691	16563	2435
	N	1.0E-107 U13729.1			4 28548	15414	2282
Homo sapiens mXNA for KIAAO455 protein, per var cas	3	1.0E-107 AB007922.2		1.52	28139		1887
Homo septems mRNA for KIPA0453 protein, partiel cas	N.T	.0E-107 AB007822.2					1887
Homo sapiens cathepsin 2 precursor (C132) gene, exon 3	Z	.0E-107 AF136275.1	1			٦	1791
QV2-HT0540-120900-368-e05 HT0540 Homo sapiens ci	EST_HUMAN	.0E-107 BF087405.1	_			П	1600
Homo sapiens BAZ18 mRNA for bromodomain adjacent	NT	.0E-107 AB032253.1		1.06			1307
	T	1.0E-107 AF154121.1	_	9.71	27223	14163	991
Human IFNAK gene for interferon alphaneta receptor	3	1.0E-107 X60459.1	Г	1.38	27149		606
Human IFNAK gene for interferon alphabeta receptor	NT	1.0E-107 X60459,1		1.02			888
Homo sapiens NY-REN-25 antigen mk/NA, peruar cas	NT	1.0E-107 AF165103.1		2.34	26858		227
Homo sapiens neuronal cell adhesion molecule (INCLAM) mixias	3 NT	4826863 NT		1.03		П	837
	Z	1.0E-107 X60459 1		0.9		П	275
Homo sapiens Xq pseudoautosomal region; segment 1/2	N	1.0E-107 AJ271735.1		4.52		T	244
RC1-CT0249-090800-024-d05 C 10249 Homo sapiens CUNA	EST_HUMAN	1.0E-106 BE695905.1		3.71		7	12717
601433087F1 NIH_MGC_72 Homo sapiens cDNA clone	EST_HUMAN	1.0E-106 BE894488.1	1.0E-108	1.97		П	12484
	EST_HUMAN	1.0E-106 BE8944B8.1	1.0E-106	1.97	32059		12484
	EST_HUMAN	1.0E-108 AW410405.1		4.3	٦	25946	12253
RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cUNA	EST HUMAN	1.0E-106 BE010832.1		1.89		24826	11837
RC5-BN0192-100500-021-B02 BN0192 Homo saplens c	EST_HUMAN	1.0E-106 BE010832.1		1.69		24828	11837
601109219F1 NIH_MGC_16 Homo septens cDNA clone	EST_HUMAN	1.0E-106 BE257385.1	1.0E-108	1.35		24692	11694
	NT	.0E-106 J05200.1	1.0E-106	206	1	24380	11317
Human ryanodine receptor mRNA, complete cds	NT	1.0E-108 J05200.1	1.0Ε-108	2.06	T	24380	11317
601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:385/366 5	EST_HUMAN	1.0E-106 BF032755.1	1.0E-106	4.81	T	24207	11135
	EST_HUMAN	1.0E-106 BF032755.1	1.0E-106	4.81	1	24207	11135
	NT.	1.0E-108 AL163202.2	1.0Ε-106	4.26		23840	10807
	EST_HUMAN	1.0E-106 AL039886.1	1.0圧-106	0.66		23712	10678
Homo sepiens multimerin (MMKN), mKNA	l '	11436432 NT	1.0E-106	0.66	37142	23532	10497
Homo sapiens multimerin (MMRN), mRNA	2 NT	11436432 NT	1.0E-106	0.66	37141	23532	10497
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	NO:	Probe SEQ ID NO:

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Table 4
Single Exon Probes Expressed in Placenta

Homo sepiens potassium charmet subunit (HERG-3) minuta, compress cas	<b>1</b>	1.0E-108 AF032897.1	1			16508	240
Homo sapiens poussuin chamino accumin (Lange of Lands	4	1 0E-108 AF032897.1	_				
The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	N	B 6000		0.64	)1 29224		3025
bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA cione IMAGE2905099 3 sunina 10 g070977 TELEMOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexakinase mRNA, complete cdc (MOUSE); RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexakinase mRNA, complete cdc (MOUSE); RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexakinase mRNA, complete cdc (MOUSE);	EST_HUMAN	BE20669		11.96	26 28746	15626	2499
PROTEOGLYCAN II PRECURSOR (HUMAN):	EST_HUMAN	1.0E-108 AI686040.1	1.0E-108	1211	28666	7 16538	2407
PROTEOGLYCAN II PRECURSOR (HUMAN);  191410.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb.M14219 BONE	EST_HUMAN	1.0E-108 AI686040.1	1.0E-108	1211	8 28665	7 15538	2407
#91e10 x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE	EST FORMAN	1.0E-108 BF026/28.1	1.0E-108	1.02	8 28398	15278	2140
Ro1671914F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:3954939 5'	NT	.0E-108 Y18000.1	1.0E-108		0 27516		1294
OUT 170 OF 1 WILL AND CO. T. T. T. T. T. T. T. T. T. T. T. T. T.	EST HUMAN	1.0E-108 BE286042.1	1.0E-108	1.72	27210	7	977
CO13020321 NR UNCC. 17 Homo sections oDNA clore IMAGE:3532348 5	EST_HUMAN	.0E-107 BE798189.1	1.0E-107	1.24	31920	T	13211
THR repetitive element;	EST_HUMAN	1.0E-107 AA001415.1	1.0E-107	7.14	<u>.                                    </u>	26100	12322
2645e01.s1 Soares retina N254HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1	2	11418/01 NI	1.0E-107	4.29	37527	23904	11676
Homo saniens HSPC049 protein (HSPC049), mRNA	2		1.0E-107			П	11676
Use a control of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property	EST HUMAN	BE5405	1.0E-107	3.91	38341	24656	11603
MOTORBREATET NIH MGC 10 Homo septems cDNA clone IMAGE:3452829 5		1.0E-107 BF666511.1	1.0€-107	2.3	37907		11202
En24270653E1 NIH MGC 56 Home septems cDNA clone IMAGE:4281039 5'		1.0E-107 L49141.1	1.0E-107	1.58	37894	٦	11189
PO5095 ALPHA-ACTINU 3, NON MUSCULAR;	EST_HUMAN	1.0E-107 Al392850.1	1.0E-107	2.96	37662		10944
CATAMARS VI NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI	EST_HOMAN	1.0E-107 BE168723.1	1.0€-107	1.92	37604	П	10889
OV1-HT0516-140300-107-c10 HT0516 Homo sapiens cDNA	EVI HOMAN	1.0E-107 AU122469.1	1.0E-107	. 0.99	36299	22729	9587
ALI 1777ARQ MAMMA1 Homo saplens cDNA clone MAMMA1002433 5	2	1.0E-107 AJ404488.1	1.0E-107	0.59	34468	20981	7809
Holiz septems milker for drugen heavy chain (DNAH9 gene)	Z	.0E-107 AJ404468.1	1.0E-107	0.59		П	7909
whoshore mBNA for dynein heavy chain (DNAH9 gene)	EST_HUMAN	.0E-107 AI785078.1	1.0E-107	1.36	П		7698
OF-PROPERTY OF THE WAY A LAND SERVICE OF THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND THE WAY AND T	EST_HUMAN	0E-107 AW 503913.1	1.0E-107	1.33	1	1	7520
CI-HF-BNO-81-0-00-0-11-11-11-11-10-0-0-0-11-11-11-1	EST_HUMAN	.DE-107 AW 503913.1	1.0E-107	1.33	7	20593	7620
601442336F I NIFL MCC 60 Home saders cDNA done IMAGE:3079310 5	EST_HUMAN	.0E-107 BE867469.1	1.0E-107	271	٦	19171	5986
23 (30) 113 WAR AND SANIES CON CONE MAGE:3946494 5	EST HOMAN	1.0E-107 AW968038.1	1.0E-107	0.64		18935	5742
ECT 21115 MAGE recommences WAGK Homo sapiens cDNA	Z	1.0E-107 AF020671.1	1.0E-107	4.89	30087	17090	3931
Lisens contens muntiphiliprin (MTM1) gene, expn 9	1		Value			Z C	Ö
Top Hit Descriptor	Top Hit Database Source	Top Hit Apession	Most Similar (Top) Hit BLAST E	Expression   N	ORF SEQ	Exan SEQ ID	Probe SEQ ID

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Homo sepiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sepiens) (LOC83446), mRNA	NT	11428165 NT	1.0∈-108	1.08	37500	23880	10847
yy35h10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone iMAGE:273283 6' similar to PIR:A45773 A45773 kelch protein, long form - fruit fly ;	EST_HUMAN	V44974.1	1.0E-108 N44974.1	0.46	35912	22363	9287
Homo saplens ETS-family transcription factor EHF (EHF) mRNA, complete cds	NT	1.0E-108 AF203977.1	1.0E-108 /	0.77	35869	22324	9247
ULHF-BM0-ade-e-12-0-Ul.:1 NIH_MGC_38 Homo septens cDNA clone IMAGE:3062878 5'	EST_HUMAN	1.0E-108 AW 408694.1	1.0E-108/	0.61	34911	21388	8306
UHHF-BM0-eds-6-12-0-UI.r1 NIH_MGC_38 Homo sepiens cDNA done IMAGE:3062878 5	EST_HUMAN	1.0E-108 AW 408694.1	1.0E-108	0.61	34910	21388	8306
	NT		1.05-108	1.72		21336	8254
602043384F1 NCI_CGAP_Bm67 Homo sepiens cDNA clone IMAGE:4181037 5	EST_HUMAN	1.0E-108 BF5289; 2.1	1.0E-108	0.73	34219	20739	7674
602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5	EST_HUMAN	1.0E-108 BF5289;2.1	1.0E-108 I	0.73	34218	20739	7674
601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'	EST_HUMAN	1.0E-108 BE252607.1	1.0E-108	1.32	34193	20715	7646
Homo sapiens delta-6 fatty acid desaturase (FADSD6) mRNA	TN	4758333	1.0E-108	212	34143	20667	7597
Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA	NT	31857	1.0E-108	4.52	33850	20390	7308
Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4	NT	1.0E-108 AF016706.1	1.0E-108	0.64	33303	19809	6753
Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4	NT	1.0E-108 AF016708.1	1.0E-108	0.64	33302	19909	6753
PM4-CT0403-240700-001-c10 CT0403 Homo saplens cDNA	EST_HUMAN	1.0E-108 BF334851.1	1.0E-108	1.09	32644	19304	6489
Homo saptens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)	N	1.0E-108 AJ133269.1	1.0E-108	1.22	32921	19561	6392
Homo saplens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds	Z	1.0E-108 AF264717.1	1.0E-108	6.14	32790	19441	6287
Homo sapiens FTVE domain-containing dual specificity protein phosphatase FTVE-DSP2 mRNA, complete	NT	1.0E-108 AF264717.1	1.0E-108	6.14	32789	19441	6287
PM4-CT0403-240700-001-c10 CT0403 Homo septens cDNA	EST_HUMAN	1.0E-108 BF334851.1	1.0E-108	0.74	32644	19304	6125
Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20	NT	1.0E-108 AF012623.1	1.0E-108	0.66		Г	6049
601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5	EST_HUMAN	1.0E-108 BE869016.1	1.0E-108	2.56	31917	18838	5644
601444922F1 NIH_MGC_65 Homo sapiens cDNA cione IMAGE:3848980 5	EST_HUMAN	1.0E-108 BE869016.1	1.0E-108	2.56	31916	18838	5644
RC0-HT0372-241199-031-c03 HT0372 Homo saplens cDNA	EST_HUMAN	1.0E-108 AW384094.1	1.0E-108	1.24	31839	18791	5598
Homo sapiens PSN1 gene, alternative transcript	NT	1.0E-108 AJ008005.1	1.0E-108	3.18	31166	18191	6063
UI-HF-BN0-ain-e-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'	EST_HUMAN	1.0E-108 AW504799.1	1.0E-108	0.63	31141	Γ	5037
Homo sepiens KIAA0187 gene product (KIAA0187), mRNA	NT	7661979 NT	1.0E-108	3.37	31040	18057	4927
Human hepatocyte nuclear factor 4-alpha gene, exon 2	NT	U72961.1	1.0E-108 U72961.1	2.62	30766	17783	4647
Human hepatocyte nuclear factor 4-alpha gene, exon 2	NT	U72961:1	1.0E-108 U72961:1	2.62	30765	17783	4647
h12a11x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2972050 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1.;	EST_HUMAN	1.0E-108 AW664,138.1	1.0E-108	1.67	30406	17418	4273
Top Hit Descriptor	Top Hit Database Source	Top Hil Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
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Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hii Descriptor
10904	Г	34549	2.09	1.0E-108	1.0E-108 BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA cicne IMAGE:3445361 5
11066	18501	31537	2.67	1.0E-108 Y12490.1	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
2		38037				i	sapiens calcium channel alpha1E subunit (CAC
11318	Т	3802/	1.35	1.0E-108	1.0E-108 AFZZ3391.1		spliced
11048	Т	38283	3.46	1.0E-108		EST_HUMAN	EST378258 MAGE resequences, MAGI Homo capiens cDNA
11605	Г	38343	1.71	1.0E-108		EST_HUMAN	AV708780 ADC Homo sapiens cDNA clone ADCAEE03 5'
11606	П	38344	1.71	1.0E-108	1.0E-108 AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11652	24731		2.77	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
1168B	15538	28665	2.99	1.0E-108	1.0E-108 A16860-10.1	EST_HÚMAN	tt91e10.x1 NCI_CGAP_P/28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11688	16538	28666	2.99	1.0E-108	1.0E-108 AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_P/23 Home sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11712	1	38446	1.72	1.0E-108 D63539.1		NT	Homo septens COL4A6 gene for a6(IV) collagen, exon 23
12499	П	32064	4.15	1.0E-108		N	Homo saplens mRNA for FLJ00037 protein, partial cds
12940	25018		5.09	1.0E-108	1.0E-108 BF346356.1	EST_HUMAN	602018571F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4154297 5
£	13281	26287	1.01	1.0E-109	1.0E-109 AW803,116.1	EST HUMAN	IL2-UM0077-260400-079-D06 UM0077 Homo sapiens cDNA
8 8	13303	26328	1.17	1.0E-109 D86974.1		NT	Human mRNA for KIAA0220 gene, partial cds
3 6	1344/	204/0	3.34	1.0E-109	11422486 NT	NT .	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
200	10400	20407	2.11	1.05-108	11438391 N	NT	Homo sepiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
2 4	130/4	20/05	2.28	1.0E-109	4507712 NT	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
617	13800	26820	14.77	1.0E-109	1.0E-109 AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
61.	13800	26821	14.77	1.0≅-109		NT	Homo sapiene mRNA for KIAA0999 protein, partial cds
1037	14205	27262	1.62	1.0E-109	2	NT	Homo sepiens chromosome 21 segment HS21C049
1228	14389	27451	8.5	1.0E-109 M28699.1		NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1230	14389	27451	6.38	1.0E-109 M28699.1		NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1673	14728	27806	0.99	1.0E-109	1.0E-109 BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 51
1673	14726	27807	0.89	1.0E-109 t	.0E-109 BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE::2959636 5
1923	15066	28170	23	1.0E-109 D13643/2		NT	Homo sapiene mRNA for KIAA0018 protein, partial cds
2314	15446	28580	5.46	1.0E-109 /	.0E-109 AL163284.2	NT	Homo sepiens chromosome 21 segment HS21C084
2326	16467	28589	3.65	1.0E-109 Y17123:1		NT	Homo sapiens SNF5/INI1 gene, exon 6
2687	15807	28923	19.35	1.0E-109 Al022328.1		EST_HUMAN	ow95801.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplans cDNA clone IMAGE:1654636 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.
2687	15807	28924	19.35	1.0E-109 AI022328.1		EST_HUMAN	ow95e01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IN/AGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.
2687	15807	28924	19.35	1.0E-109		Ľ.	TR:002197 0021

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Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2688	15808	28925	2.68	1.0E-109	4504206 NT	TN	Homo sapiens guanylate cyclase activator 1A (retina) (GÜCA1A) mRNA
3125	16301	28314	3.37	1.0E-109 N85190.1	N86190.1	NAWNH_LSB	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3475	_	29661	2.08	1.0E-109	1.0E-109 AW893192.1	NAMUH_TS3	CM3-NN0009-190400-150-f10 NN0009 Homo septems cDNA
3475		29662	2.08	1.0E-109	1.0E-109 AW893192.1	NAMUH_TSE	CM3-NN0009-190400-150-f10 NN0009 Homo seplens cDNA
3606	16770	29785	1.1	1.0E-109	1.0E-109 AF240598.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3945	17104		1.31	1.0Ε-109	1.0E-109 BE146144.1	EST_HUMAN	MR0-HT0209-110400-108-e04 HT0209 Homo sepiens cDNA
4264	17409	30395	4.35	1.0E-109	1.0E-109 AI655417.1	EST_HUMAN	ts98e06.x1 NCI_CGAP_GC6 Homo septens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100 ;
4524	17663	30650	2.67	1.0E-109	4504206 NT	NT	Homo sapisns guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4722	17857	30838	1.7	1.0E-109	7662083 NT	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5165	18287	31252	0.72		1.0E-109 BE293873.1	EST_HUMAN	801186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859836 5
5165	18287	31263	0.72		1.0E-109 BE283873.1	NAMOH_TSE	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858636 5'
5361	18564	31480	0.67	l	1.0E-109 AU137282.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1006169 6'
5374	П	31445	0.92	1.0E-109	1.0E-109 BF673;18.1	EST_HUMAN	602135445F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922.5
5428	10020	31604	2.92	1.0E-109	1.0E-109 51/4622 N1	NOT LINAN	Homo sapiens piecental protein 11 (serine proteinase) (F11) mr.VA
6050	T	32556	1.23	1.0E-109	1.0E-109 BF379688.1	EST HUMAN	CM1-UT0038-060900-399-h07 UT0038 Homo sapiens cDNA
6119	18917		1.41	1.0E-108	1.0E-108 BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6721	П	33269	0.85	1.0Ё-109	1.0E-109 AI221385.1	EST_HUMAN	qg85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 31
6907	20222	33651	0.69	1.0E-109	11024711 NT	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6907	20222	33652	0.69	1.0E-109	11024711 NT	NT	Homo sapiens myosin, heavy polypeptide 4, skeletel muscle (MYH4), mRNA
7389	Г	33933	0.67	1.0Ε-109	1.0E-109 AB046911.1	3	Homo sepiens mRNA for KIAA1591 protein, partial cds
7738	20799	34288	3.75	1.0Ё-109	11432574 NT	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7740	20801	34290	4.91	1.0E-109	1.0E-109 BF1827,07.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7740	20801	34291	4.91	1.0E-109	1.0E-109 BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8366	1	34970	1.35	1.0E-109	1.0E-109 AL049784.1	NT	Novel human gene mapping to chomosome 13
8480	Π	35098	1.39	1.0E-109	1.0E-109 AW749130.1	EST_HUMAN	PM0-BT0340-091299-002-e05 BT0340 Homo saptens cDNA
8867	7		2.84	1.0E-109	1.0E-109 AA077498.1	EST_HUMAN	7818H01 Chromosome 7 Felal Brain cDNA Library Homo septens cDNA clone 7818H01
8932	Т	35549	4.36	1.0E-109	1.0E-109 BE787540.1	EST_HUMAN	6014/941/F1 NIH _MGC_68 Homo sapiens cUNA cione IMAGE:3582124 5
8932	Γ	35550	4.36	1.0E-109	1.0E-109 BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo septens cDNA done IMAGE:3882124 5'
9177	22255	35797	0.57	1.0E-109	1.0E-109 BE145672.1	EST_HUMAN	IL0+HT0205-071199-142-g01 HT0205 Homo sapiens cDNA
9439	22513	36077	1.65	1.0E-109 H84860.1	H84860.1	EST HUMAN	ys90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5 similar to SP:A53491 ,A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINY ;
	I						

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Table 4

Single Exon Probes Expressed in Placenta

numan autominimure amagen smaii nuceau riponuciaoprotein E pseudogene	2	MIDEID.I	1.0E-110[M1011.1	AO' I	Repor	1/403	4320
Homo sapiens pregnency-zone protein (PZP), mRNA		11436041 NT	1.0至-110	2.66	29458	Т	3264
Homo sapiens pregnancy-zone protein (PZP), mRNA		11436041 NT	1.0€-110	2.66	29457	1	3264
Homo sepiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	NΤ		1.0E-110 U78027.1	1.48		16331	3156
Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA		4503088 NT	1.0Ε-110	7.10		16081	2903
UI-H-BI4-acs-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:3085784 3'	EST_HUMAN	1.0E-110 BF508896.1	1.0E-110	1.66		15256	2118
801237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'	EST_HUMAN	1.0E-110 BE379477.1	1.0E-110	1.51	28217	16116	1973
Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds	NT	1.0E-110 AB032253.1	1.0≘-110	1.02	27532	14464	1308
Homo sapiens calcitonin receptor-like (CALCRL) mRNA		5031620 NT	1.0E-110	0.89	27429	14369	1207
Human dystrobrevin (DTN) gene, exon 20	NT		1.0E-110 U84550.1	1.04	20757	13733	548
Human mRNA for inward rectifier potassium channel, complete cds	NT		1.0E-110 D87291.1	1.31	26656	13621	306
Homo sapiens deiodinasa, iodothyronina, typa II (DIO2), transcript variant 2, mRNA		7549804 NT	1.0E-110	1.83	26242	13242	112
Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA		5803073 NT	1.0E-110	3.96	26282	13276	38
Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA		5803073 NT	1.0€-110	3,96	26281	13276	38
Homo sepiens deloclinese, iodothyronine, type II (DIO2), transcript varient 2, mRNA		7549804 NT	1.0E-110	1.4	26242	13242	3
Homo sapiens gene for AF-6, complete cds	NT	1.0E-109 AB011399.1	1.0E-109	8.36	32036	25508	12762
Homo sepiens SNF5/INI1 gene, exon 6	NT		1.0E-109 Y17125.1	3.2	28589	15457	12636
Homo sapiens SNF5/INI1 gene, exon 6	NT		1.0E-109 Y17123.1	2.32	28589	15457	12397
Homo saplens mRNA for KIAA0463 protein, partial cds	NT	1.0E-109 AB007832.1	1.0E-109	2.26	38810	25106	12126
Homo sapiens single-minded (Drosophile) homolog 1 (SIM1), mRNA		11418618	1.0E-109	1.31	38673	24969	11984
DKFZp76111124_r1 761 (s/monym: hamy2) Homo sapiens cDNA clone DKFZp76111124 5'	EST_HUMAN	1.0E-109 AL118824.1	1.0E-109	1.6	38636	24934	11948
hh23f05.x1 NGI_CGAP_Lu24 Homo septens cDNA clone IMAGE:2855869 3' similar to TR:Q9Z124 Q9Z124 YGR163W MRNA HOMOLOGUE, COMPLETE CDS.;	EST_HUMAN	1.0E-109 BE045560.1	1.0E-109	1.64	38569	24872	11884
zb08b12.r1 Scares_fetal_tung_NbHL19W Homo saptens cDNA clone IMAGE:301439 5' simitar to PIR:S43989 S43989 p54-beta stress-activated protein kinases - rat ;	EST_HUMAN	W16510.1	1.0E-109 W16510.1	4.5	38382	24691	11693
Homo sapiens Chedlak-Higashi syndrome 1 (CHS1) mRNA	NT	4502838	1.0E-109	2.18	38422	24730	11651
AU121370 HEMBB1 Home suplens cDNA clone HEMBB1002690 5'	EST_HUMAN	1.0E-109 AU121370.1	1.0E-109	1.57	38109	24448	11387
602080724F2 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4245341 5'		1.0E-109 BF694831.1	1.0E-109	19.68	37757		11046
601063030F1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:3449599 5'		1.0E-109 BE540909.1	1.0E-109	1.8	37731	24092	11013
601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'		1.0E-109 BE540909.1	1.0€-109	1.8	37730		11013
HSC1EC121 normalized thfant brain cDNA Homo saplens cDNA clone c-1ec12	EST_HUMAN	F06604.1	1:0E-109 F06604.1	1.37	36304	22734	9885
601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'	EST_HUMAN	1.0E-109 BE397088.1	1.0E-109	0.64	36185	22615	9550
601289760F1 NJH_MGC_8 Homo septens cDNA clone IMAGE:3620030 5'	EST_HUMAN	1.0E-109 BE397068.1	1.0E-109	0.64	36184	22615	9550
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	Exon SEQ ID NO:	Probe SEQ ID NO:

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Single Exon Probes Expressed in Placenta

Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslan No.	Top Hit Database Source	Тор Hit Descriptor
	30872	204	1.0E-110	Al017213.1	EST_HUMAN	ou32b10.xt Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1627863 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121;
$\neg$	30897	3.01	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Hamo sapiens cDNA clone HEMBA1002241 5
		2.28	1.0E-110	7662441	NT	Homo sepiens KIAA1002 protein (KIAA1002), mRNA
	31583	2.23	1.0E-110	BE289436.1	EST_HUMAN	801118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
	32339	0.78	1.0E-110	BE621059.1	EST_HUMAN	6014S3677F1 NIH_MGC_70 Homo sepiens cDNA clone IMAGE:3895785 5'
	32358	8.61	1.0€-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
19050	32357	8.61	1.0E-110	11419323	ZT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
	33421	5.43	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
20311	33764	0.59		BE251436.1	EST_HUMAN	601109388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
20334	33782	0.85	1.0E-110	U08888 1	4	Human GS2 gene, expn 2
20334	33783	0.85			N.T	Human GS2 gene, exon 2
	34025	0.78	1.0E-110	AI560289.1	EST_HUMAN	\$12408.x1 NCI_CGAP_Bm25 Home ceptene cDNA cone IMAGE:2167407 3' similar to SW :E I V1_HUMAN P50549 ETS TRANSLOCATION VARIANT 1;
20655	34131	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sepiers cDNA clone DCBCGE01 5'
	34132	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Hamo sapiers cDNA dane DCBCGE01 5'
20683	34159	2.87	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
20804	34293	0.96	1.0E-110	AU137923.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
	36174	1.09	1.0E-110	BE302594.1	EST HUMAN	ba68f01.y1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:2905561 5" similar to TR:O77258 O77258 EG:114D9.2 PROTEIN. ;
	36395	2.46	1.0€-110	AW838394.1	EST_HUMAN	QV2-LT0053-020400-119-c04 LT0053 Hamo sapiens cDNA
	37171	3.38	1.0⊱-110	1432732	NT	Homo septens galactokinase 2 (GALK2), mRNA
	37700	3.2		Y12337 1	NT .	H. sepiens mRNA for myotonic dystrophy protein kinase like protein
	37916	3.64	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3840433 5".
24278	37917	3.64	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_2: Horno sapiens cDNA clone IMAGE.3840433 5
24661	38347	1.89	1.0E-110	M1005111	NT	
	37539	1.7	1.0E-110	AA446529.1	EST_HUMAN	zw67g02:1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:781298 5 similar to TR:G1145816 G1145816 FKBP54;
		2.47		BE897218.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3924548 5
		286		AW062258.1	EST_HUMAN	ILD-BT0163-040899-094-g10 BT0163 Homo sepiens cDNA
		2.98		AB011399.1	NT	Homo sepiens gene for AF-6, complete cds
		6.01		BF364546.1	EST_HUMAN	PM3-NN1082-140800-006-f12 NN1082 Harno sepiens cDNA
		1.16		BF608898.1	EST_HUMAN	UI-H-BI4-aos-b-05-0-UI:s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30857843
		11.92		U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
Probe SEQ ID NO: 1758 4778 5088 5409 5860 6860 6860 6860 6860 6860 7778 7783 7783 7783 7783 7783 7783 778		EXON ORI SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID	Exon ORF SEQ Expres SEQ ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO:	Exon SEQ ID NO:         ORF SEQ ID NO:         Expression Signal Signal ID NO:         Mos Signal Signal ID NO:         Mos Signal Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID NO:         Mos Signal ID 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     7662441           1 18216         30887         3.01         1.0E-110         AU1172612.1         7662441         7662441         1.0E-110         AU1172612.1         7662441         1.0E-110         AU1172612.1         7662441         1.0E-110         AU1172612.1         7662441         1.0E-110         BE28406.1         1.0E-110         BE28406.1         1.0E-110         BE28406.1         1.0E-110         BE28406.1         1.0E-110         BE28406.1         1.1419323         1.0E-110         BE28406.1         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.0E-110         M55112.1         1.1419323         1.1419323         1.0E-110         M714276.1         1.0E-110	Expr   ORF SEQ   Expression   CTop Hit Accession   Database NO.   DNO.   Signal   Signal   Database   NO.   Signal   Signal   Signal   Database   NO.   Signal   Signal   Signal   Database   NO.   Signal   Signal   NO.   Signal   NO.   Signal   NO.   Signal   No.   Source   NO.   Signal   No.   Source   NO.   Signal   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Source   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal   No.   Signal

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	FO: 1 10188 11.	7.02-11101000200.1		0.54	36162	22583	9518
OV2-BT0817-270900-398-606 BT0817 Homo sepiens cDNA	EST HIMAN		Τ			22365	9289
Homo sepiens Trio iscform mRNA, complete cds	4	AE001305 1	J			T	8085
Human mRNA for Integrin alpha-2 subunit	NT.	0E-111 X17033.1	Ţ		T	T	8000
Human minux for integral advise a course	Z	LOE-111 X17033.1			35708	T	
	EST_HUMAN	1.0E-111 BF214902.1		8.43	7	- 1	9008
SA184733254 NIH MGC 55 Home saplens cDNA clone IMAGE: 4078303 5		1.0E-111 AK0Z4453.1	Γ.	0.64	4 35597	22054	8975
Home springs mRNA for Ft. 100045 protein, partial cds		1 1420010	١.	0.96	7 35492	21057	8878
Homo septens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA	27	000000				21518	8435
Human beta4-integrin (ITG34) gene, exon 13	NTI	100533	. _			Γ	8383
Homo sapiens protein x 0001 (LOC51185), mRNA	BNT	11431896 NT	١		Ī	Т	8020
G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR;	EST_HUMAN	1.0E-111 AA278838.1		0	3.4890		3
G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR;	EST_HUMAN	1.0E-111 AA278868.1		0.8	8 34888	21368	8286
zs78g03.r1 NCI_CGAP_GCB1 Homo septens cDNA cione IMAGE:/03/32 5 similar to Int. G12504 fo			1		245	14007	1/61
protein (naip) and survival motor neuron protein (smn) genes, complete cds	Z-1	1 0E-111 U80017.1					
Homo saniens basic transcribition factor 2 p44 (bt/2p44) gene, partial cds, neuronal apoptosis inhibitory	EGILTOMAN	1.0E-111 AI761223.1	Π	0.7	34254	20769	7704
WIBSGOTLXT NCL_CGAP_Not is Foliate september 2012 and control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t	1,				$\neg$		
11.2-N.10101-200700-11-E03141010-1000000000000000000000000000000	EST HUMAN	1.0E-111 BF366228.1				П	7605
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UNTZDASAC IS 12 1 NCT CGAP Sub6 Homo septens cDNA clone IMAGE:2729525 3	EST HUMAN	1.0E-111 AL0407621	Г	0.96		T	6818
DEED LO LIVE LENGTH AS A 634 (Symposym: https://doi.org/10.100/10.000 DKFZp434C1815.5)	EST_HUMAN	.0E-111 Al344679.1	1.0E-111	2.09	32678	19332	6156
GET ATEN DROTTEIN RAL-A (HUMAN):		-					
TABILITY WILL CARD WILE Up and sortions of NA clone IMAGE: 1917574 3' similar to gb:M29893 RAS-	Z	.0E-111 U19969.1	1.0E-111	0.66	32360	19052	5882
Limes the handed zinc finger protein ZEB mRNA, partial cds	EGITHOWAIN	.0E-111 BE867909.1	1.0E-111	0.88	32242	18941	5749
gbM23575 PREGNANCY-SPECIFIC BE IA-1 OLT COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTAC TERN COTA		1.0E-111 AA151017.1	1.0E-111	0.75	31836	18788	6693
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gbM23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);	EST_HUMAN	1.0E-111 AA151017.1	1.0E-111	0.75	31835	18788	5593
HA7Ko7 rt Sogres pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to	2	1.0E-111 K02268.1	1.除-111	4.59	30570	17589	4449
U. The carbonholin B (ankB) none exprit 4 and 3' flank and complete ods		7881569 N	1.0E-111	1.15	30419	17431	4286
Using senient OKEZP434D156 protein (DKFZP434D156), mRNA			1.0E-111 M25142	25	27185	14123	950
Human cardiar sinha-mosin neaw chain (MYH8) gene, expns 32 to 34		1N 780888	1.0E-111	4.13	26989	13843	762
Homo saniens cat eve syndrome critical region gene 1 (CECR1), mRNA	HOMAN	BF03532/.1		1.99		13934	753
601459631F1 NIH MGC 66 Homo sepiens cDNA clone IMAGE:3862086 5	T CHANN	1N 708001		1.64	26455	13424	201
Homo saplens ras GTPase activating protein-like (NGAP) mRNA		475007					
Top Hit Descriptor	Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	NO:	SEQ ID
	Top Hit	•	Most Stmiler				<u>'</u>
	On Grant Cook	On Grand				i	

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Table 4

Single Exon Probes Expressed in Placenta

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	EST HOWAIN	1.0E-112 BE741666.1	Г	0.93	18 32904	9 19548	6379
Ign1504717F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3948557 5	EO TOWAN	1.0E-112 AW502437.1	Г	0.66	17 32796	3 19447	6273
II ILLE BROD-air-o-06-0-ULTI NIH MGC 52 Homo sapiens cDNA clone IMAGE:3075658 5	EST HOMEN	1.0E-112 AW 50Z437.1	Γ		17 32795	3 19447	6273
111.HE BROD-als-0-06-0-ULTI NIH MGC 52 Homo sapiens cDNA clone IMAGE:3075658 5	NT	1.0E-112 AF149773.1	Γ	7 1.33			6201
Work and and in (NOD1) game exons 1. 2 and 3	ESI_HOMEN	1.0E-112 N460461		2 36.7	6 32282	18976	5784
AGENOT 1 Soarce melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5	201	1.0E-112 AB037832.1			30991		4876
Homo seriene mRNA for KIAA1411 protein, partial cds	Z	1.0E-112 AB037832.1		5.87		٦	4876
Homo serviens mRNA for KIAA1411 protein, partial cds		2 4504176	Γ		30843	6 17861	4726
Homo septens clutemate receptor, ionotropic, keinete 1 (GRIK1) mRNA	EST HOWEN	BE0/60/	Ι.		7 30153	0 17147	3990
MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA	TOT LINAN	1.0E-112 VIOZGO III.			2 28630	4 16612	3444
SEMENOGELIN 1 PROTEIN PRECURSOR (HUMAN);	EST HUMAN	0 0 1806511 1				$\neg$	
Informo sapirata giutani ano icorper, carriens cDNA clone IMAGE:2418335 3' similar to gb:M81650_rna1	6 NI	2 4504116 NT	1.0E-112	0.76	٦	П	3147
and larger of the company in mittanic kalnate 1 (GRIK1) mRNA	EST HUMAN	1.0E-112 BE888859.1		2.83	7	П	2577
ENALAZETAET NIH MICC. 65 Homo sapiens cDNA clone IMAGE:3846858 5	Z	1.0E-112 AF248540.1		1.11	28115	٦	1883
Homo saniens intersectin 2 (SH3D1B) mRNA, complete cds	2 -	2 /6521280 N	Ι.	7.1	В 27959		1718
Homo senions KIAA0440 protein (KIAA0440), mRNA	DN			7.1	B 27958		1718
Homo saniens KIAA0440 protein (KIAA0440), mRNA	- NATION TO STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE	P52/42	Γ		27308	14263	1087
TINC FINGER PROTEIN 135	CWICCODOT	1.0E-112 AF 10/023.1	Γ			14197	1026
Homo sapiens HTRA serine protease (PRSS11) gene, complete cds	LO LICHOLIA	1.0E-112 BF000000.1	T		Γ	13834	649
III.H.BI4-pot-0-04-0-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086023 3	EST LIMAN	1.0E-112 BF500004.1			26860	13834	649
I II-H-BI4-apt-q-04-0-UI,S1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3	ECT LIMAN	1.0E-112 U29103.1	Γ			13810	625
Human steroldogenio acute regulatory protein (StAR) gens, exon 5		1.0E-172 UZ9103.	Γ		26831	13810	62
Human steroidogenic acute regulatory protein (SIAR) gene, exon 5	21	4001001 NT	Τ		Γ	Γ	623
Homo sablens acetyl-Coenzyme A carboxylese beta (ACACB), mRNA	1	AB03535	1.0E-111			18504	13041
Libro sariens mRNA for neurodin I-alpha protein, complete cds	100000	1.0E-111 W ZZ50Z.1	1.05-111		31855	25888	12881
72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo saplens cDNA not directional	TOT LINAN	1.UE-111 AV (00402-1	1.00-11			25492	12741
AV708482 ADC Homo sapiens cDNA clone ADCAOB08,5"	EST HUMAN	11/708/871 ES	1.05-111	4.07	Ι	Г	12167
Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	21	ACT 890	1.05-111	3.29	Γ	24366	11299
Human thromboboletin receptor (MPL) gene, exons 1,2,3,4,5 and 6	TOWER	0E-111 AW 296467.1	1.0E-111	1.34	37707	24074	10995
TILLERWIN-aig-d-07-0-UI ST NCI COAP Sub6 Homo expiens cDNA clone IMAGE:2730276 3		.0E-111 AA131245.1	1.0E-111	5.58	37127	23514	10479
H31m1 of Spaces pregnant uterus NbHPU Homo saptens cDNA clone IMAGE:503545 5	1.	1.0E-111 D10083.1	1.0E-111	1.04		٦	10383
VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);	T HUMAN	1.0E-111 AA504160.1	1.0E-111	1.56	37000	23390	10355
aa58g02.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:825170 3' similar to gb:L09235							
	Source	No.	Value	Signal	D NO:	S	S S
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	<u> </u>	ORF SEQ	SEXON EXON	Probe
Single Exon Probes Expressed in Placental	e Exon Probes	Singl					

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Single Exon Probes Expressed in Placenta

ad95i01.x1 Schiller meningicma Homo sapiens cDNA clone IMAGE:1953625 3'	EST_HUMAN	1.0E-113 Al365586.1	1.0E-113	3.23	27805	14725	1572
Human X-linked phosphoglycerate kinase gene, exon 8	Ŋ	M11965.1	1.0E-113 M11965.1	283	27199	14138	965
ace5701.x1 Schiller meningicma Homo sapiens cDNA clone IMAGE:19536253'	EST_HUMAN	.0E-113 Al365586.1	1.0E-113	6.82	26988	13942	761
ao95f01.x1 Schiller meningicma Homo sapiens cDNA clone IMAGE:1853625 3	EST_HUMAN	.0E-113 Al365586.1	1.0E-113	6.82	26987	13942	761
Homo sapiens adenylosuccinate lyase gene, complete odo	TN	1.0E-112 AF106656.1	1.0⊑-112	1.31		25484	12727
qk24c08.y5 NCI_CGAP_Kkd3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR-Q64362 Q64362貸貨FUSED TOES ;	EST_HUMAN	1.0E-112 AI792603.1	1.0E-112	1.66	38784	25076	12096
qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clane IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES :	EST_HUMAN	1.0E-112 AI792603.1	1.0E-112	1.66	38783	25076	12096
PMD-CT0237-141099-001-h02 CT0237 Homo sepiens cDNA	EST HUMAN	1.0E-112 AW377670.1	1.0E-112	4.78	38188	24519	11460
qk24c08.y5 NCI_CGAP_Kid3 Homo septens cDNA clane IMAGE:1868902 5' similar to TR:Q64362 Q64362, FUSED TOES;	EST_HUMAN	1.0E-112 AI792603.1	1.0E-112	2.28	38154	24489	11428
qk24c08.y5 NCi_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;	EST_HUMAN	1.0E-112 AI792603.1	1.0E-112	2.28	38153	24489	11428
601155323F1 NIH_MGC_21 Homo saptens cDNA clone IMAGE:3138989 5	EST_HUMAN	.0E-112 BE280479.1	1.0E-112	224	38077	24421	11359
Homo sapiens mRNA for secreted modular calcium-binding protein (smo	NT	1.0E-112 AJ249900.1	1.0E-112	3.14	37896	24260	11191
yd56d10.s1 Soares fetal liver spieen 1NFLS Homo septens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;	EST_HUMAN	T93967.1	1.0E-112 T93967.1	1.31	37811	24176	11103
yd56d10.s1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN;	EST_HUMAN	T93967.1	1.0E-112 T93967.1	1.31	37810	24175	11103
MR3-SN0009-100400-108-b12 SN0009 Homo saptens cDNA	EST_HUMAN	.0E-112 AW863327.1	1.0E-112	16.73	37735	24096	11017
7130g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saptens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CG8743 PROTEIN.;	EST_HUMAN	1.0E-112 BF1114/3.1	1.0E-112	237	36736	23135	10097
601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5	EST_HUMAN	1.0E-112 BE867635.1	1.0E-112	264	35782	22236	9158
601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5	EST_HUMAN	1.0E-112 BE867635.1	1.0E-112	264	35781	22236	9158
AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5	EST_HUMAN	1.0E-112 AU118051.1	1.0E-112	1.79	34895	21468	8387
Homo sepiens solute cerrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	NT	11416777 NT	1.0E-112	1.49	34038	20566	7491
Homo septens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	NT .	11416777 NT	1.0E-112	1.49	34037	20566	7491
DKFZp434M0523_r1 434 (synonym: htes3) Homo saptens cDNA clone DKFZp434M0523 5"	EST_HUMAN	1.0E-112 AL043299.1	1.0E-112	0.68	33847	20387	7305
602131405F1 NIH_MGC_81 Homo septens cDNA clone IMAGE:4270921 5	EST_HUMAN	1.0E-112 BF574235.1	1.0E-112	1.51	33637	20209	6981
601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508508 5	EST_HUMAN	1.0E-112 BE273103.1	1.0E-112	0.83	33324	19928	6773
601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5	EST_HUMAN	1.0E-112 BE273103.1	1.0E-112	0.83	33323	19928	6773
Top Hit Descriptor	Top Hit Database Source	Top HII Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:
		9.0					ŀ

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Table 4

Single Exon Probes Expressed in Placenta

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	13207	24457	24457	24446	238/6	23291	23291	23074	22656	22372	22372	22172	20549	20549	19613	19613	19458	19458	19371	19264	19228	18805	25930	18300	888	16375	15297	15994	NO.		
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1	٦	Т			T		Τ		Γ	П						1.0E-113	1.0E-113	1.0E-113	1.0E-113	T	T	Γ	Ι.		1.0E-113		1.0E-113	1.0E-113	BLAST E Value	Most Similar (Top) Hit	
	1.0E-114 Y17151.2	1.0E-113 AW 630281.1	1.0E-113 AW630291.1		3 AWS00519 1	AW6005	5453007 NT		BE7725	1.0E-113 BE382842.1	1.0E-113 BE382842.1	8922819 N I	1.0E-113 BE282161.1	1.0E-113 BE262161.1	6006002 NT			· 9961249 NT	11525737 NT	1.0E-113 Aro 10333.1	1.0E-113 AU140291.1	1.0E-113 AU12/214.1	1.0E-113 BE /80858.1	5453562 N	5453562 NI	1.0E-113 AJ223948.1	1.0E-113 BF515218.1	1.0E-113 AF240775.1	) 2	Top Hit Acession	
	NT	EST_HUMAN	EST_HUMAN		EST HUMAN	EST HUMAN	NT	7 NT	ESI_HOMAN	EST HUMAN	EST HOMAN	N I	EOI TOWAN	'h	1	ZNI	NT	3	NT	1	NT LONG	EGT HIMAN	EST LINAN	N.	Z	NT	EO L TOIVINIA		Source	Top Hit Database	
		601105529F1 NIH_MGC_15 Homo saptens cDNA clone IMAGE:2988366 5	similer to TR:060327 0603	hh81e09.y1 NCI_CGAP_GU1 Homo septens cDNA clone IMAGE:2868176 9 simile w 17. Course, Course, Access BBOTEN:	UI-HF-BNO-BN-b-12-0-UI-H NIH MGC 50 Homo sapiens curve civile invocation invocation in TB-050327 O60327	UI-HF-BN0-akj-b-10-0-UI.r1 NIH_MGC_50 Homo capiens cDNA clone (MAGE::07/7328.5)	Homo sapiens RAN binding protein 7 (RANBP7), mRNA	Homo sapiens RAN binding protein 7 (RANBP7), mRNA	Homo seplens transmembrane protein 2 (TMEM2), mRNA	DOI FT0134-280600-021-d02 FT0134 Homo sapiens cDNA	GRADOTZAGET NIH MIGG. 19 Homo sapiens cDNA clone IMAGE:3627554 5	GRIT 2077 705E1 NIH MGC 19 Homo sepiene cDNA clone IMAGE:3627554 5	Homo saniens hypothetical protein FLJ11006 (FLJ11008), mRNA	COLLEGE NIII MGC 19 Homo sapiens cDNA clcre IMAGE:3508362 5	ENTIS STREET NIH MGC 19 Homo sepiens cDNA clone IMAGE:3508362 5		mRNA Lucros seriens el tamata receptor, lonotropic, N-methyl D-espertata 2A (GRIN2A) mRNA	mRNA Homo sabiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), trenscript variant B,	(GalNAc-T8) (GALNT9), mRNA Homo appiene ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B.	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyiransicrase o	Homo sepiens P-glycoprotein (mdr1) mRNA, complete cds	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5	ALI127214 NT2RP2 Homo sepiens cDNA clone NT2RP2000807 5	R014/69465F1 NIH MGC 67 Homo sapiens cDNA clone IMAGE:3872536 5	Tomo serios estivation franscription factor B (B-ATF), mRNA	Home socions activating transcription factor 8 (B-ATF), mRNA	The series and for nutritive RNA helicase, 3' end	HUILU SEPTICIO SCI. TE STATE CONTROL SUBTRACTION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICION SEPTICI	Lean series of FAF transporter mRNA, complete cds	Top Hit Descriptor	

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Table 4
Single Exon Probes Expressed in Placenta

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yd15c01.c1 Soares fetal liver spleen 1NFLS Homo sapiens gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR 8923087 NT Homo sapiens hypothetical protein FLJ20080 (FLJ20080) Homo sapiens habdoid tumor deletion region protein 1 (R 6831094 NT Homo sapiens miniohromosome maintenance deficient (S. 6879073 NT Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA 4.1 EST_HUMAN WRO-HT0559-250200-002-d07 HT0559 Homo sapiens cu		I	Ī
yd15c01.c1 Soares fetal liver spleen 1NFLS Homo sapieni gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR 8923087 NT Homo sapiens hypothetical protein FLJ20080 (FLJ20080), 7857529 NT Homo sapiens maintenance deficient (S. 6831094 NT Homo sapiens minichromosome maintenance deficient (S. 6879073 NT Homo sapiens nucleopodin-like protein 1 (NLP_1), mRNA 8679073 NT Homo sapiens nucleopodin-like protein 1 (NLP_1), mRNA 8579073 NT Homo sapiens nucleopodin-like protein 1 (NLP_1), mRNA 8579073 NT Homo sapiens control protein 1 (NLP_1), mRNA	0.89		T
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yd15c01.c1 Soares fetal liver spleen 1NFLS Homo sapient gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR 8023087 NT Homo sapiens hypothetical probsin FLJ20080 (FLJ20080) Homo sapiens habdoid tumor defeition region protein 1 (R 7857529 NT Homo sapiens minichromosome maintenance deficient (S. 6831084 NT Homo sapiens minichromosome maintenance deficient (S.	5.08		
yd15c01.c1 Soares fetal liver spleen 1NFLS Homo sapieni EST_HUMAN gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR 8023087 NT Homo septens hypothetical probsin FL/20080 (FL/20080). Homo septens that doctor unar deletion region protein 1 (R7 7657529 NT Homo septens that doctor unar deletion region protein 1 (R7).	1.9		٦
yd15c01.p1 Soares fetal liver spleen 1NFLS Homo sapiani EST_HUMAN gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR 8923087 NT Homo sapiens hypothetical protein FLJ20080 (FLJ20080).	4.65		T
yd15c01.c1 Soares felal liver spleen 1NFLS Homo sapisni EST_HUMAN gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR	264	61 27318	
	7.46	48 26876	662 13848
1.0E-114 Y17151.2   NT   Homo sapiens mixing to multiple deliberation of Property	0.75	П	
NT Homo saplens mkwa tor munding resistance protein 3 (a	0.75	97 26315	59 13297
Most Similar (Top) Hit Accession Database BLASTE No. Source Value	Expression Signal	ORF SEQ	Probe Exan SEQ ID SEQ ID NO: NO:

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Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9384	22459	36022	0.87	1.0E-114	1.0E-114 BF109832.1	EST_HUMAN	7169g12.x1 Scares_NSF_FB_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3526847 3' similar to TR.Q9UHN6 Q9UHN6 TRANSMEMBRANE PROTEIN 2. ;
9614	П		1.3	1.0E-114	1.0E-114 AW327,455.1	EST_HUMAN	dq03f05.x1 NIH_MGC_2 Homo sepiens cDNA clone IMAGE:2846744 51
9662	21104	34621	2.67	1.0E-114	1.0E-114 AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9748	22812		1.36	1.0E-114	1.0E-114 M13535.1	NT	Human ceruloplasmin mRNA
10343	23378	36989	1.02	1.0E-114	1.0E-114 BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10364	23399	37010	1.11	1.0E-114	1.0E-114 AL163227.2	NT	Homo sepiens chromosome 21 segment HS21C027
10762	23795	37415	1.18	1.0≅-114	1.0E-114 BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-d07 HT0559 Homo septens cDNA
							ba73g12.y1 NIH_MGC_20 Homo sepiens, cDNA clone IMAGE:2906086 6' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gBM20632 Mouse LLRep3 protein mRNA from a repetitive element,
11027	T		4.31	1.0E-114	1.0E-114 BE302666.1	EST_HUMAN	comptete (MOUSE);
11466	Г	38197	8.11	1.0€-114	1.0E-114 AV733454.1	EST_HUMAN	AV733454 cdA Homo sepiens cDNA clone cdABA08 5'
11466	Г	38108	8.11	1.0E-114	1.0E-114 AV733464.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
11842	24831	38522	6.28	1.0E-114	1.0E-114 AV733454.1	EST_HUMAN	AV733454 cdA Hamo sepiens cDNA clone cdABA08 5'
11842	Г	38523	6.28	1.0E-114	1.0E-114 AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
12643	Г		4.63	1.0E-114	11418041 NT	Z	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12936	Γ	31975	2.75	1.0E-114	11034850 NT	Z	Homo saplens hypothetical protein (DJ1042K10.2), mRNA
12836	Γ	31976	2.78	1.0E-114	11034850 NT	NT	
24	13262	26284	3.06	1.0E-115	4758111 NT	NT	Homo sepiens HLA-B associated transcript-1 (D6S81E) mRNA
132	13358	26391	1.09	1.0E-115	4505938 NT	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	Г		18.42	1.0E-115	4557887 NT	NT	Homo saplens keratin 18 (KRT18) mRNA
38	13519	26552	2.02	1.0E-115	1.0E-115 AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
549	13742	26766	1.68	1.0E-115	1.0E-115 Al339208.1	EST_HUMAN	qt06f01.x1 NCI_CGAP_GC4 Homo septens cDNA done IMAGE:1946809 3' similar to TR:000536 000536. TTF-I INTERACTING PEPTIDE 6;
649	13742	26767	1.68	1.0E-115	Al339206.1	EST_HUMAN	qt08f01.x1 NCI_CGAP_GC4 Homo sepiens cDNA clone IMAGE:1946809 3' striller to TR:000536 000536 TTF-I INTERACTING PEPTIDE 6 ;
809	П	27041	3	1.0E-115	5174702 NT	NT	Homo saptens transforming growth factor beta-ectivated kinase-binding protein 1 (TAB1), mRNA
809	13988	27042	3	1.0E-115	5174702 NT	TN	Homo sapiens trensforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
811	Г	27044	15.24	1.0E-116	4503794 NT	NT	Homo saplens ferritin, heavy polypeptide 1 (FTH1) mRNA
1590	Г	27823	1.15	1.0E-115	1.0E-115 AF229180.1	FN	Homo sepiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1590	14742	27824	1.15	1,0E-115	1,0E-115 AF229180.1	ZT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
_		}	:			i	Homo saplens Brutan's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
2142	15278	28400	1.13	1.0E-116 076027.1	RF745469 1	TOT HIMAN	MAGE:3928832 5'
2142	ı	28400	1.13	1.05-116	1.UE-116 BE/45469.1	EGI HOMAN	OUIS/8630F I NIT MIGC_8 Homo Sapiens CDNA Glone IMAGE:3828832 3

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Table 4
Single Exon Probes Expressed in Placenta

oz31a08.x1 Soeres_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914.3'	EST_HUMAN	1.0E-115 AI076598,1	1.0E-115	1.24	33976	20505	7428
ens cDNA clone IMAGE:1676914 3'	EST_HUMAN	1.0E-115 AI076598.1	1.0E-115	1.24	33975	20506	7428
yd86b08.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115085 5' similar to SP.DPOG_YEAST P15801 DNA POLYMERASE GAMMA;	EST_HUMAN	1.0E-115 T86774.1	1.0E-115	0.75	33543	20127	7074
Homo capienc KIAA0054 geno product Holicaso (KIAA0064), mRNA		7661883 NT	1.0⊑-116	1.68	33206	19817	6668
Homo sapiens KIAA0054 gene product Helicase (KIAA0054), mRNA		7661883 NT	1.0E-115	1.68	33204	19817	6858
Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA		11426038 NT	1.0E-115	9.49	33064	19690	6525
Homo sapiens sperm surface protein (HSS), mRNA		11426786 NT	1.0E-115	0.68	32920	19560	6391
Homo sapiens sperm surface protein (HSS), mRNA	NT	11426786 NT	1.0E-115	0.68	32919	Г	6391
ans aDNA clone IMAGE:2519568 3' similar to gb:L0780	EST_HUMAN	1.0E-115 Al928799.1	1.0E-115	1.15	32305	18998	5808
au84g01.x/ Schneider tetal brain 00004 Homo sepiems cDNA clone IMAGE:2518568 3' similar to gb:L0/802.4 DYNAMIN-1 (HUMAN);	EST HUMAN	1.0E-115 AI928769.1	1.0E-115	1.15	32304	18998	5808
Homo saplens similar to ER to nucleus signalling 1 (H. saplens) (LOC63433), mRNA		11425128 NT	1.0E-115	1.74	32137	18853	5659
Homo saplens similar to ER to nucleus signalling 1 (H. saplens) (LOC83433), mRNA		11425128 NT	1.0E-115	1.74	32136	18853	5659
602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'	EST_HUMAN	BF665387.1	1.0E-115	0.97	31754	П	5540
	EST_HUMAN	1.0E-115 AW970335.1	1.0E-115	2.8	31642		5463
Homo saplens mRNA for KIAA0768 protein, partial cds	NT	1.0E-115 AB018311.1	1.0E-115	0.92	31425	18460	5347
Homo saplens Interleukin 1 receptor, type i (IL1R1) mRNA	NT	4504658	1.0E-115	1.23	31391	18421	5304
Homo saplens putative psihHbC pseudogene for hair keratin, exons 1 to 9	NT	1.0E-115 Y19215.1	1.0E-115	1.01	31149	18172	5044
Homo sapiens chromosome 21 segment HS21C068	NT	1.0E-115 AL 163268.2	1.0E-115	2.99	31133		5026
Homo sapiens chromosome 21 segment HS21C068	NT	1.0E-116 AL163268.2	1.0E-116	2.99	31132	18166	6026
Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	NT	1.0E-115 AL096857.1	1.0E-115	2.86	30919		4797
Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	NT	1.0E-115 AL096857.1	1.0E-115	2.86	30918		4797
Homo saplens EphA4 (EPHA4) mRNA	NT	4758279 NT	1.0E-115	4.28	30674		4557
Homo saplens sir2-like 3 (SIRT3), mRNA	NT	6912659	1.0E-115	2,49	30847	17660	4521
Homo saplens mRNA for KIAA0350 protein, partial cds	NT	1.0E-115 AB002348.2	1.0E-115	4.2	30299		4153
Homo sapiens partial TTN gene for titin	NT	1.0E-115 AJ277892.1	1.0E-115	1.8	29742	16726	3561
Homo sapiens mRNA for a'pha-tubulin 8 (TUBA8 gene)	NT	1.0E-115 AJ245922.1	1.0E-115	2.88	29368		3184
Homo saplens mRNA for alpha-tubulin 8 (TUBA8 gene)	NT	1.0E-115 AJ245922.1	1.0E-115	288	29365	16359	3184
QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA	EST_HUMAN	1.0E-115 AW804759.1	1.0E-115	1.03			2912
Homo saplens testican-1 mRNA, complete cds	NT .	1.0E-115 AF231124.1	1.0E-115	1.11	28631	15505	2374
Homo sapians KIAA0442 mRNA, partial cds	NT	1.0E-115 AB007902.1	1.0E-115	1.1	28411	15286	2150
601579838F1 NIH_MGC_9 Horno sapiens cDNA clone IMAGE:3928832 5'	EST_HUMAN	1.0E-115 BE745489.1	1.0E-115	1.13	28401	15278	2142
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exxon SEQ ID NO:	Probe SEQ ID NO:
							7

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
7246	20329	33775	1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_/1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127 5'
7776	20833	34324	4.7	1.0E-118	11431050 NT	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7790	20846	34339	0.72	1.0E-118 L46590.1	_46590.1	NT	Homo saplens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8159	21241	34761	1.95	1.0E-118	1.0E-118 BE78(223.1	EST HUMAN	601469169F1 NIH_MGC_67 Hamo sapiens cDNA clone IMAGE:3872247 5'
8577	21658	35198	7	1.0E-118	1.0E-118 BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Horno saplens cDNA
8577	21658	35199	7	1.0E-118	1.0E-118 BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo saplens cDNA
8683	21684	35204	1.1	1.0€-118	1.0E-118 AA443024.1	EST_HUMAN	2x98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5
8583	21664	35205	1.1	1.0E-118	1.0E-118 AA443024.1	EST_HUMAN	298d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5
8873		35488	0.84	1.0E-118	1.0E-118 AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8873	Г	35489	0.94	1.0E-118	1.0E-118 AB002381.1	T	Human mRNA for KIAA0383 gene, partial cds
8918	21997	35536	1.94	1.0E-118	4557732 NT	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8918	21997	35537	1.94	1.0E-118	4557732 NT	NT	Homo saplens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9236	22313	35855	5.15	1.0E-118	1.0E-118 BE263134.1	EST_HUMAN	801144863F2 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3160502 5'
9266	22343	35894	0.55	1.0E-118	1.0E-118 AL048474.2	EST_HUMAN	DKFZp586K1824_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586K1824
9792	22832	38411	1.07	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
10541	23576	37184	1.23	1.0E-118	1.0E-118 BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10541	23576	37185	1.23	1.0E-118	1.0E-118 BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10586	23621	37228	1.75	1.0臣-118	1.0E-118 BF185,407.1	EST HUMAN	7n17e09x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:35647853' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;
10752	23785	37399	0.59	1.0E-118	1.0E-118 AW286351.1	EST_HUMAN	UI-H-BW0-ato-a-07-0-UI.s1 NCI_CGAP_Sub6 Homo saptens cDNA clone IMAGE:27297723'
11555	24610	38290	3.75	1.0E-118	1.0E-118 AA315007.1	EST HUMAN	EST186814 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light in chain 1. cytoplasmic
11855		38539	2.92	1.0E-118	1.0E-118 BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Horno seplens cDNA clone IMAGE:3901563 5'
11855	24843	38540	2.92	· 1.0E-118	1.0E-118 BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901663 5'
12071	25052	38761	1.81	1.0E-118	1.0E-118 BE218235.1	EST_HUMAN	hx36s06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q9Z2H4 (J)
776	13956	27007	2.46	1.0E-119	1.0E-119 AF170492.1	NT	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds
1062	16029	27284	0.93	1.0E-119	7705607	TN	Homo sepiens CGI-105 protein (LOC81011), mRNA
1987		28232	2.86	1.0E-119	1.0E-119 AB023147.1	NT	Homo saplens mRNA for KIAA0930 protein, partial cds
3171	16346	29353	1.01	1.0E-119	8922205	TN	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3312	16485		2.17	1.0E-119	1.0E-119 AA916760.1	EST_HUMAN	on 10b05.e1 NCI_CGAP_Lu5 Homo capiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2
4063	Г	30227	1.22	1.0E-119	4504116	Z	(GRIK1) mRNA
5453	18653	31632	3.86	1.0E-118	1.0E-118 AU133389.1	EST_HUMAN	AUT33399 N I 2RP4 Homo sapiens cDNA clone NT 2RP4001881 5

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associated factor 1 (TRAF1) mRNA	Homo sapiens TNF receptor-associated factor 1 (TRA)	NT	5032192 NT	1.05-121	1.31	20904	10020	74.7
E1000899 5	AC 134803 FLACE I Florid Septens CUNA Cione FLAC	EST HOWKIN	.VE-121 A0134303.1	1.00-121	1.00	3 2		
	N 1134083 DI ACE4 Uses ser			105434	1 35	26831	13595	380
	Homo saniena NEO cene	NT.	Y18000 1		0.62	26337	13311	75
ding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330)	NT	17862	. 1.0E-120	1.42	32049	25436	12657
801443135F1 NIH_MGC_65 Homo septens cDNA clone IMAGE:3847281 5	601443135F1 NIH_MGC_65 F	EST_HUMAN	.0E-120 BE867819.1	1.0E-120	2.12	38398	24705	11625
801443135F1 NIH_MGC_55 Homo sapiens cDNA cione IMAGE:3847281 51	801443135F1 NIH_MGC_65 F	EST_HUMAN	.0E-120 BE867619.1	1.0E-120	2.12	38397	24705	11625
601176727F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3532015 5	601176727F1 NIH_MGC_17 F	EST_HUMAN	1.0E-120 BE296387.1	1.0E-120	8.66	38115	24452	11391
A1077 protein, partial cdc	Homo saplens mRNA for KIAA1077 protein, partial cds	NT		1.0E-120	3.4	36916	23316	10281
	CM-BT043-090289-075 BT043 Homo saplens cDNA	EST_HUMAN	1.0E-120 AI904151.1	1.0E-120	0.65		23134	10096
o chomosome 13, similar to rat RhoGAP	Novel human gene mapping to chomosome 13, similar	TN	1.0E-120 AL049801.1	1.0E-120	1.02	36612	23018	9978
AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'	AU133205 NT2RP4 Homo sap	EST_HUMAN	1.0E-120 AU133205.1	1.0E-120	6.7	36597	23001	9862
601888956F1 NIH_MGC_17 Homo sapiens cDNA cione IMAGE:4122876 5'	601888956F1 NIH_MGC_17 F	EST_HUMAN	1.0E-120 BF306541.1	1.0E-120	3.54	36578	22985	9946
601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626544 5'	601307739F1 NIH_MGC_44 F	EST_HUMAN	1.0E-120 BE392102.1	1.0E-120	4.67	36320	22750	9701
Homo sapiens cDNA clone IMAGE:3825544 5"	601307739F1 NIH_MGC_44 Homo sepiens cDNA clor	EST_HUMAN	1.0E-120 BE392102.1	1.0E-120	4.87	36319	22750	9701
A0465 protein, partial ods	Homo sepiens mRNA for KIAA0465 protein, partial ods	TN	1.0E-120 AB007934.1	1.0E-120	1.31	35264	21727	8847
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485	Homo sapiens mRNA, chromo	NT	1.0E-120 AB007964.1	1.0E-120	1.94	35222	21684	8603
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495	Homo sapiens mRNA, chromo	NT	1.0E-120 AB007,964.1	1.0€-120	1.94	36221	21684	8603
A1231 protein, partial cds	Homo sapiens mRNA for KIAA1231 protein, partial cds	NT	1.0E-120 AB033057.1	1.0E-120	0.9	35219	21680	858
A1231 protein, partial cds	Homo sapiens mRNA for KIAA1231 protein, partial cds	NT	1.0E-120 AB033057.1	1.0E-120	6.0	35218	21680	Bece
rn64 Homo sapiens cDNA clone IMAGE:4183333 5'	602036352F1 NCI_CGAP_Brn64 Hamo sapiens cDN	EST_HUMAN	1.0E-120 BF337,599.1	1.0E-120	2.31	35147	21608	8527
nt subunit M (NF-M)	Human gene for neurofilament subunit M (NF-M)	NT	1.0E-120 Y00067.1	1.0E-120	1.38	34678	21160	8078
nt subunit M (NF-M)	Human gene for neurofilament subunit M (NF-M)	NT	1.0E-120 Y00067.1	1.0E-120	1.38	34677	21160	8078
omboxane synthase, exon 7	Human TBXAS1 gene for thromboxane synthase, exon	NT	1.0E-120 D34619.1	1.0E-120	1.84	34295	20806	7748
602183994F1 NIH_MGC_42 Homo sapiens cDNA done IMAGE:4300174 5	602183994F1 NIH_MGC_421	EST_HUMAN	1.0E-120 BF-568222.1	1.0E-120	16.08	32350	19043	5853
602183994F1 NIH_MGC_42 Homo sapiens cDNA done IMAGE:4300174 5'	602183994F1 NIH_MGC_421	EST_HUMAN	1.0E-120 BF568222.1	1.0E-120	16.08	32349	19043	5853
(STC) gene, partial cds	Homo sepiens stanniocalcin (STC) gene, partial cds	NT	1.0E-120 AF098463.1	1.0E-120	3.11	30907	17919	4784
(STC) gene, partial cds	Homo sapiens stanniocalcin (STC) gene, partial cds	NT	1.0E-120 AF098463.1	1.0E-120	3.11	30906	17919	4784
Homo saplens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo saplens cAMP-specific	NT	1.0E-120 AF055490.1	1.0E-120	2.05	30599	17617	4477
phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo sapiens cAMP-specific phosphodiesterase 8A (F	NT	1.0E-120 AF056480.1	1.0E-120	2.05	30598	17617	4477
(SYNJ1), mRNA	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	NT	4507334 NT	1.0E-120	1.61	26561	13528	3382
complete cds	Homo sapiens gene for AF-6, complete cds	NT	1.0E-120 AB011399.1	1.0E-120	1.83	28438	15309	2174
	Homo saplens gene for AF-6, complete cds	NT	1.0E-120 AB011399.1	1.0E-120	1.83	28437	16309	2174
	Homo sapiens disintegrin and metalloprotease domain	NT	4557250	1.0E-120	6.58	28098	14995	1848
epeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens cysteine-rich repeat-containing protein	TN	1.0E-120 AF167706.1	1.0E-120	11.19	27869	14783	183
Top Hit Descriptor		Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:

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Homo sapiens intersecun snort (solorii (115N) mwwx, complete cas	2	1.0E-122 AF114488.1	1.05-122	2,33	26565	1335/	48
Homo sapiens T-cell lymphoma Invasion and metastasis 1 (TIAM1), mRNA	ZT	11526176 NT	1.0E-122	2.64	26526	13498	278
yv74c01.s1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:2484483'	EST_HUMAN	N59624.1	1.0E-121 N59624	1.93		24312	11243
Homo sepiens chloride intracellular channel 4 like (CLIC4L), mRNA	3	7330334 NT	1.0E-121	5.74	37919	24280	11211
Homo sepiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4°E458 allele, complete cds	<u>Z</u>	1.0E-121 AF084200.1	1.0E-121	1.94	37740	24102	11023
Homo saplens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA	NT	11427788	1.0E-121	3.45	37733	24094	11015
ia05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 O75457 CYTOSOLIC LPHOSPHOLIPASE A2-CAMMA.;	EST_HUMAN .	1.0E-121 AW 56:3858.1	1.0E-121	1.02	36703	23100	10082
le05g05.y/ Human Pencreatic Islets Homo sepiens cDNA 5' similar to TR:075457 076457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.;	EST_HUMAN	1.0E-121 AW 58:858.1	1.0E-121	1.02	36702	23100	10062
Homo sapiens DNA for prostacyclin synthase, exon 8	TN	1.0E-121 D84122.1	1.0E-121	2.61	34730	21209	8127
Homo saplens DNA for prostacyclin synthase, exon 8	TN	.0E-121 D84122.1	1.0E-121	2.51	34729	21209	8127
Homo sepiens gamme-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA	Z	11436217	1.0E-121	1.07	34725		8123
RC3-NN0066-270400-011-f02 NN0066 Hamo sepiens cDNA	EST_HUMAN	.0E-121 AW 898088.1	1.0E-121	0.79	31484	18529	7102
RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA	EST_HUMAN	1.0E-121 AW898086.1	1.0E-121	0.79	31483	П	7102
Homo sapiens Xq pseudoautosomal region; segment 2/2	NT	1.0E-121 AJ271736.1	1.0E-121	0.98		20164	7028
Human glucose transporter (GLUT4) gene, complete ods	NT	1.0E-121 M91463.1	1.0E-121	0.64	33308	18913	6757
601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'	EST_HUMAN	1.0E-121 BE271424.1	1.0E-121	0.73	32161		5679
hu09f08.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3166119 31	EST_HUMAN	1.0E-121 BE222250.1	1.0E-121	0.84	31453		5382
H.sapiens ECE-1 gene (exon 17)	NT	.0E-121 X91937.1	1.0E-121	3.42	31189	18219	5091
qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'	NAMUH_TSE	.0E-121 Al263294.1	1.0E-121	1.76	30571	17690	4450
Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds	NT	.0E-121 AF155156.2	1.0E-121	8.25	29934	16929	3768
Homo saplens mRNA for KIAA1337 protein, partial cds	NT	1.0E-121 AB037758.1	1.0E-121	1.23	29808		3626
Hamo sapiens mRNA for KIAA1337 protein, partial cds	NT	1.0E-121 AB037758.1	1.0E-121	1.23	29807	16790	3626
Homo seplens hHb3 gene for heir keretin, exans 1 to 9	TN	1.0E-121 Y19203.1	1.0E-121	5.8	29337		3150
Homo sepiens hHb3 gene for heir keratin, exons 1 to 9	NT	1.0E-121 Y19203.1	1.0E-121	5.8	29336	16325	3150
602014759F1 NCI_CGAP_Brn64 Homo capiens cDNA done IMAGE:4160286 6'	EST_HUMAN	1.0E-121 BF344378.1	1.0E-121	1.07	28881	16768	2643
602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA done IMAGE:4150286 5	EST_HUMAN	1.0E-121 BF344378.1	1.0€-121	1.07	28880	15766	2643
Homo sepiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds	NT	.0E-121 L76631.1	1.0E-121	1.22	28431	15304	2169
Hamo sepiens inositol polyphospheto 4-phosphetese, type I, 107kD (INPP4A), splice varient e, mRNA	NT	4755139 NT	1.0E-121	-	28270	15164	2023
Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), spilce variant e, mRNA	NT .	4755139 NT	1.0E-121	1	28269	16164	2023
Top Hit Descriptor	Top Hit Database Source	Top Hit Acesslon No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Acession No.	Top Hit Database Source	Top Hit Descriptor
368	13577	26610	2.56	1.0E-122	11526176 NT	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
906	П	27146	3.34	1.0E-122	1.0E-122 AF114438.1	NI	Horro saptens intersectin short isoform (ITSN) mRNA, complete cds
1247	14406	27468	5.19	1.0E-122 M20707:1	M20707:1	N	Human kappa-immunogiobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1728	14878	27969	18.7	1.0E-122	AF167706.1	NT	Homo sapiens cystelne-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14899	27995	1.61	1.0E-122	11418424 NT	NT	Homo sapiens collagen, type XII, atpha 1 (COL12A1), mRNA
1750	14899	27996	1.61	1.0E-122	11418424 NT	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1857	15003	28110	6.92	1.0E-122	1.0E-122 BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo saplens cDNA clone IMAGE:3899358 5'
2560	15685	28810	7.43	1.0E-122	1.0E-122 BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo septens cDNA clone IMAGE:4125234 5'
2560	15685	28811	7.43	1.0E-122	1.0E-122 BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Home septens cDNA clone IMAGE:4125234 5
2901	16080	29096	4.87	1.0E-122	1.0E-122 AF284717.1	NT	cds
4971	18100	31076	3.81	1.0E-122	4502166 NT	NT	Homo sepiens amyloid beta (A4) procursor protein (protesse nexin-ll, Alzheimer disease) (APP), mRNA
5104	18232		1.41	1.0E-122	1.0E-122 AW504845.1	EST_HUMAN	UI-HF-BN0-all-a-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5
5681	18876	32164	1.2	1.0E-122	1.0E-122 BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Horno sepiens cDNA clone IMAGE:3354232 5
6896	18875	32164	6.8	1.0E-122	1.0E-122 BE266039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Hamo sepiens cDNA clone IMAGE:3354232 5
7363	П	33904	0.64	1.0E-122	1.0E-122 AA868671.1	EST_HUMAN	ak49h06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 31
8998	П	35614	0.6	1.0E-122	1.0E-122 AJ276801.1	NT	
9228	22306	35849	1.17	1.0E-122	11424216 NT	NT	Homo sapiens lethal giant larvas (Drosophila) homolog 2 (LLGL2), mRNA
9524	22589	36159	0.96	1.0E-122	1.0E-122 AI359618.1	EST_HUMAN	gyS2h07.x1 NCI_CGAP_Brn23 Homo sepiens cDNA done IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.
9524	22589	36160	. 0.96	1.0E-122	1.0E-122 Al359618.1	EST_HUMAN	qy32h07.x1 NGL_CGAP_Brn23 Homo sapiens cDNA done IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;
10338	23373	36983	0.64	1.0E-122	1.0E-122 AL117234.1	NT	Novel human gene mapping to chomosome X, isoform of dbl (proto-oncogene)
11233	24302	37939	2.12	1.0E-122	1.0E-122 AW955834.1	EST_HUMAN	EST367804 MAGE resequences, MAGD Homo sapiens cDNA
11667	24744	38436	1.83	1.0E-122	1.0E-122 AB024058.1	NT	Homo septens gene for B120, exon 10
12231	25178		5.28	1.0E-122	11418187 NT	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
789	13968	27019	1.53	1.0E-123	1.0E-123 BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4153670 5'
789	13968	27020	1.53	1.0E-123	1.0E-123 BF345274.1	EST HUMAN	602018058F1 NCI_CGAP_Brr67 Homo sapiens cDNA clone IMAGE:4153670 5
1038	14206	27263	6.18	1.0E-123	1.0E-123 AL163249.2	N.T	Homo saplens chromosome 21 segment HS21C049
1047	14213	27270	3.36	1.0E-123	5803114 NT	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1367	1	37404	۵ 2	100	4505848 NT	T	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP5K2B) mRNA, and translated
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Single Exon Probes Expressed in Placenta

UFH-BI3-ell-f-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2/3/291 3	EST_HUMAN	1.0E-123 AW 450931.1		2.71	38799	25094	12114
UFH-BI3-all-f-10-0-UI.s1 NCI_CGAP_Sub5 Homo captions cDNA clone IMAGE 2737291 3	EST_HUMAN	1.0E-123 AW450831.1	1.0E-123	2.71			12114
602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250878 5	EST_HUMAN	1.0E-123 BF677292.1	1.0E-123	4.91	38706	25004	12020
602089791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5	EST_HUMAN	1.0E-123 BF677292.1	1.0E-123	4.91			12020
Onyciolegus ouniquius New Zodland white elongation factor 1 alpha (Raberla2) mRNA, complete cds	NT	1.0E-123 U09823.1	1.0E-123	16.77	36325	22754	9705
Homo saplens mRNA for KIAA0454 protein, partial cds	NT	1.0E-123 AB007923.1	1.0E-123	2.07	36279		9569
RC4-BT0311-251189-012-e07 BT0311 Homo saplens cDNA	EST_HUMAN	1.0E-123 AW371924.1		0.7		21812	8732
AU131881 NT2RP3 Homo saplens cDNA clone NT2RP3003409 5	EST_HUMAN	1.0E-123 AU131881.1		0.79	34702	21182	8100
AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5	EST_HUMAN	1.0E-123 AU131851.1	1.0E-123	0.79	34701	21182	8100
yx88d11.r1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268817 5 cimilar to PiR:S48611 S48611 protein kinase PkpA - Phycomyces blakesieeanus ;	EST_HUMAN	1.0E-123 N35841.1	1.0E-123	0.6	34539	21025	7975
yx89d11.rl Soares melanocyte 2NbHM Homo saptens cDNA clone IMAGE: 268917 3 similar to PIR:S49611 S48611 protein kinase PkpA - Phycomyces blakesteeanus;	EST_HUMAN	1.0E-123 N35841.1	1.0E-123	0.6	34538	21025	7975
Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA	NT	11437202 NT	1.0E-123	0.8	34393	20891	7836
	EST_HUMAN	1.0E-123 BE263001.1	1.0E-123	2.22	34386	20884	7829
Homo sapiens 2'-5'cligoadenylate synthetase 2 (OAS2), mRNA	1	1/1436439 NT	1.0E-123	1.31	34374	20875	7820
Homo sapiens heparan sulfate (glucosamine) 3-0-sulfotransferase 2 (HS3ST2), mRNA	NT	1/1525833 NT	1.0E-123	0.83	34109		7662
Human hBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene, complete cds	NT	1.0E-123 U55258.1	1.0E-123	0.71			7344
Human growth hormone releasing hormone gene, exon 7	NT	1.0E-123 U42224.1	1.0E-123	1.39	33733	20290	7156
yq84e03.r1 Soeres fetel liver spicen 1NFLS Homo capiens cDNA clone IMAGE:202444 5' cimilar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;	EST_HUMAN	1.0E-123 H53188.1	1.0E-123	0.91	33718	20278	7143
AU118435 HEMBA1 Homo sepiens cDNA clone HEMBA1003591 5'	EST_HUMAN	1.0E-123 AU118435.1	1.0E-123	1.93	33146		6598
601591108F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3945433 5	EST_HUMAN	1.0E-123 BE799746.1	1.0E-123	1.76	32185	18893	5699
Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds	NT	1.0E-123 L34219.1	1.0E-123	1.62	31800		5563
Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds	NT	L34219.1	1.0E-123 L34218.	1.62			5563
Homo sepiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA	NT	6912617 NT	1.0E-123	0.71	29512	16495	3322
Homo sapiens RAB9-like protein (LOC51209), mRNA	NT	7705982 NT	1.0E-123	421			2389
Human amelogenin (AMELY) gene, 3' end of cds	NT	1.0E-123 M55419.1	1.0E-123	3.21			2166
Human amelogenin (AMELY) gene, 3' end of cds	NT	1.0E-123 M55419.1	1.0E-123	3.21			2166
Human amelogenin (AMELY) gene, 3' end of cds	NT	1.0E-123 M55418.1	1.0E-123	3.21	28427	15301	2168
Home sapiens similar to sex comb on midleg (Drosophila) Like 2 (H. sapiens) (LOC63782), mRNA	TN	11422479 NT	1.0E-123	0.94			2035
Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products	TN	4505818 NT	1.0E-123	3.83	27492	14424	1267
Top Hit Descriptor	Top Hit Database Source	Top Hit /\cession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	NO:	Probe SEQ ID NO:

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Acession No.	Top Hit Database Source	Top Hit Descriptor
279	13497	26527	1.02	1.0E-124	4507500 NT	NT	Homo sepiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279		28528	1.02	1.0E-124	4507500 NT	NT	Homo sepiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
285			1.49	1.0E-124 D87675.1	D87675.1	NT	Homo sepiens DNA for emyloid precursor protein, complete cds
498		26725	2.26	1.0E-124	1.0E-124 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
709	13891	26926	4	1.0E-124	1.0E-124 AA397551.1	EST HUMAN	231b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT];
					-		##81504.rd Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:C300482
777	13957	27008	3.72	1.0E-124	1.0E-124 AF155654.1	Z	
831	14009	27065	2.06	1.0E-124	4507500 NT	NT	Homo saplens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
927		27165	267	1.0E-124	7705446 NT	TN	Homo sepiens hypothetical protein (HSPC068), mRNA
1343	14499	27572	0.66	1.0E-124	11419092 NT	NT	
1377	14532	27605	6.42	1.0E-124	1.0E-124 AF274802.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1377	14532	27606	6.42	1.0E-124	1.0E-124 AF274892.1	N <sub>1</sub>	
1858	15004	28111	4.06	1.0E-124	1.0E-124 AJ131712.1		1 =
2123	15269	28379	2.16	1.0E-124	1.0E-124 BE879524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Hamo sepiens cDNA clane IMAGE:3893854 5
2528	1	28777	0.98	1.0E-124	1.0E-124 AB024069.1	NT	Homo septens gene for B120, exon 11
3679	Γ	29761	1.06	1.0E-124 S78684.1	S78684.1	NT T	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3579	Г	29762	1.06	1.0E-124 S78684.1	S78684.1	2	Homo septiens ATP-sensitive inwardly rectifying K-channel cubunit (KCNJ6/BIR1) gene, exon
3739	16900	29904	1.24	1.0E-124 X13794		NT	
4006		30170	0.64	1.0E-124	4507500 NT	NT	
4179	Ι.	30321	0.69	1.0E-124	4504116 NT	NT	1~
4187	17337	30330	0.98	1.0E-124	4504116 NT	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4866	17899	30983	251	1.0E-124	1.0E-124 AB024069.1	NT	Homo saplens gene for B120, exon 11
5050	18178		15.32	1.0E-124 M18178.1	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5205	18326	31296	0.74	1.0E-124	1.0E-124 AW863390.1	EST_HUMAN	EST375463 MAGE resequences, MAGH Homo sapiens cDNA
5412	18614	31588	10.49	1.0E-124	8922337 NT	NT	Homo sepiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6789	18981	32284	1.2	1.0E-124	4506786 NT	1	
6008	19183	32511	6.89	1.0E-124	.0E-124 BF696135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4281635 5'
6298	19471	32826	0.8	1.0E-124	1.0E-124 AV711263.1	EST_HUMAN	AV711263 Cu Homo sepiens cDNA clone CuAADF07 5'
6563	19725	33103	· 1.12	1.0E-124	11420654 NT	Ž T	Homo saplens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7152	20286	33728	3.15	1.0E-124 Y11717:1	Y11717.1	NT	
7287	20370	33824	0.94	1.0E-124	1.0E-124 BE271266.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5

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2K33c07 s1 Scares, pregnant, uterus, NbHPU Homo sapiens cDNA clone IMAGE: 486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);	EST_HUMAN	1.0E-125 AA042813.1	1.0E-125	1.45	27124	14059	883
Homo sapiens ALR-like protein mRNA, pertial cds	NT	1.0E-125 AF284750.1	1.0E-125	2.42	26988		746
HA0086 Human fetal liver cDNA library Homo sapiens cDNA	EST_HUMAN	1.0E-125 Al110656.1	1.0∈-125	2.02	26875		661
HA0086 Human fetal liver cDNA library Homo sapiens cDNA	EST_HUMAN	1.0E-126 All 10656.1	1.0E-126	2.02	26874	13847	661
601577881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5*	EST_HUMAN	1.0E-125 BE743922.1	1.0E-125	4.69	26239	13239	439
	NT	1.0E-125 AB032998.1	1.0E-125	7.32		13543	329
Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	NT	11417862 NT	1.0E-124	2.36	31681	26038	13080
	NT	11417862 NT	1.0E-124	2.36	31680	26038	13080
Homo saplens mRNA for KIAA1093 protein, partial cds	NT	1.0E-124 AB029016.1	1.0E-124	1,99	32004		12780
2/81b04.r1 Stratagene schize brain S11 Home septens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	EST_HUMAN	1.0E-124 AA397551.1	1.0E-124	4.6	26927	13891	12310
2/81b04.r1 Strategene schize brain S11 Homo septens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	EST_HUMAN	1.0E-124 AA397551.1	1.0E-124	4.6	26926	13891	12310
钦19e63次1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;	EST_HUMAN	1.0E-124 AI446456.1	1.0E-124	2.18	37576	23947	11761
til9e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA ctone IMAGE:2141980 3' stratter to TR:O31682 O31682 YKRS PROTEIN. ;	EST_HUMAN	1.0E-124 Al446455.1	1.0E-124	2.18	37676	23947	11761
hj05c08x1 Scares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:29809063	EST_HUMAN	1.0E-124 AW 665633.1	1.0E-124	3.9	38356	24668	11617
Human muscle glycogen phosphorylese (PYGM) gene, exons 6 through 17	NT	1.0E-124 U94776.1	1.0E-124	1.57	38009		11302
UI-HF-BNO-ekz-b-04-0-UI-M NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'	EST_HUMAN	1.0E-124 AW 503755.1	1.0E-124	1.46	36717	23113	10075
wi93f02x1 NCI_CGAP_Kld12 Homo sapiens cDNA clone IMAGE:2400891 3'	EST_HUMAN	1.0E-124 AI767133.1	1.0E-124	7.77	36427	22848	808
wi93f02x1 NCI_CGAP_KId12 Homo saplens cDNA clare IMAGE:2400891 3'	EST_HUMAN	1.0E-124 AI767133.1	1.0E-124	7.77	36426	22848	9808
AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'	EST_HUMAN	1.0E-124 AV645633.1	1.0E-124	1.72	36310	П	9691
AV645633 GLC Homo sapians cDNA clone GLCACE04 3'	EST_HUMAN	1.0E-124 AV645633.1	1.0E-124	1.72	36309		9691
wc43g03.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2321428 31	EST_HUMAN	1.0E-124 AI799864.1	1.0E-124	0.68	36997	П	9363
wc43g03.xt NCI_CGAP_Pr28 Homo sapiens cDNA done IMAGE:2321428 3*	EST_HUMAN	1.0E-124 A1799864.1	1.0E-124	0.68	96650	22438	9363
hg94a08.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE::2853240 3' similar to TR:095162 O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;	EST_HUMAN	1.0E-124 AW612106.1	1.0E-124	1.24	35278	21737	8657
hg94a09.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE: 2953240 3' similar to TR: 085182 095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. :	EST_HUMAN	1.0E-124 AW612106.1	1.0E-124	1.24	35277	21737	8657
Homo sapiens ribosomal protein L5 (RPL5) mRNA	NT	4506654 NT	1.0E-124	. 2.73	35064	21534	8453
ac08h05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3	EST_HUMAN	1.0E-124 AA6303\$1.1	1.0E-124	238	34278	20789	7726
600943771F1 NIH_MGC_8 Homo sepiens cDNA clone IMAGE:2966585 5	EST_HUMAN	1.0E-124 BE271295.1	1.0E-124	0.94	33825	20370	7287
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	Exan SEQ ID NO:	Probe SEQ ID NO:

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Inditio septetis ilitara ioi rana ison promiti periori vas	N	1.0E-126 AB03//13.1	1.0=-126	0.73	34663	21144	8062
TOTIO Sapiens in Nava 120+ process, parameters	2	1.0E-126 AB03//15.1	1.0≿-126	0.73	Γ	Г	8082
Homo sapiens clienty dynam ineavy chain e (CINATE) IIINNA, complete cas	Z	AF257737.1	1.0E-126	6.0		Г	7669
Homo sapiens ciliary dynain neavy chain 9 (UNAH9) mr.N.A. complete cos	NT	1.0E-126 AF257737.1	1.0E-126	6.0		Г	7669
Homo sapiens mRNA for KIAA 1525 protein, partial cds	NT	1.0E-126 AB040958.1	1.0E-126	4.33		19588	6419
Homo sapiens mRNA for KIAA 1525 protein, pertial cds	NT	1.0E-126 AB040958.1	1.0E-126	4.33	32951	19588	6419
TR:G1145880 G1145880 TITIN;	EST_HUMAN	1.0E-126 AA460075.1	1.0E-126	2.91	32891	19532	6362
2x66e03.r1 Soares_total_fecus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:798444 5" similar to						7	
ya52b12.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66527 3	EST_HUMAN	1.0E-126 T66998.1	1.0E-126	0.68			-5820
yx78c06.r1 Scares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:267850 5	EST_HUMAN	1.0E-126 N34078.1	1.0E-126	1.81	. 31082	18086	4956
Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63	NT	1.0E-126 AF101108.1	1.0E-126	1.08	31027		4908
Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63	NT	1.0E-126 AF101108.1	1.0E-126	1.08	31026		4908
Homo sapiens death receptor 6 (DR6), mRNA	NT	7657038 NT	1.0E-126	2.52	29910	16906	3745
H.sapiens DNA for liver cytochrome b5 pseudogene	NT	1.0E-126 X53941.1	1.0E-126	0.87	29885	16860	3719
2072c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5	EST_HUMAN	1.0E-126 AA160709.1	1.0E-126	8.12	29330		3140
zo72c03.r1 Strategene pancreas (#937208) Homo capiens cDNA clone IMAGE: 592420 5		1.0E-126 AA160709.1	1.0E-126	8.12		16316	3140
Homo sapiens RAN binding protein 2 (RANBP2), mRNA	NT	6382078	1.0E-126	4.65			2663
H. saplens gene for alpha1-antichymotypsin, exon 3	NT	X68735.1	1.0E-126 X58735.	1.53	27175	14116	942
Human laminin B1 chain gene, exon 20	NT	1.0E-126 M61938.1	1.0E-126	1.74	27030	13977	798
Homo saplens CDC-like kinese (CLK) mRNA	NT	4768007 NT	1.0E-126	2.16	27027	13974	795
QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA	EST_HUMAN	1.0E-125 BE074267.1	1.0E-125	4.71			11793
	EST_HUMAN	1.0E-125 BE074267.1	1.0E-125	4.71			11783
	EST_HUMAN	1.0E-125 AW812839.1	1.0E-125	2.27	38375		11686
	NT	1.0E-125 AF026029.1	1.0E-125	6.32			11575
Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA	NT	7669505 NT	1.0E-125	2.13	38303		11568
yh15a12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:37663 5	EST_HUMAN	1.0E-125 R61450.1	1.0E-125	1.63			11538
Homo sapiens mRNA for KIAA0667 protein, partial cds	NT	1.0E-125 AB014567.1	1.0E-125	3.35	38126	24462	11401
DKFZp434N2414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N2414 5	EST_HUMAN	1.0E-125 AL040655.1	1.0E-125	2.42			11357
Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA	NT	. 11425570	1.0E-126	1.34	37802		11091
Homo sapiens I-REL gene, exon 5	NT	1.0E-125 AF043458.1	1.0E-125	3.03	. 37639	┑	10921
Human mRNA for KIAA0300 gene, partial cds	NT	.0E-125 AB002298.1	1.0E-125	1.08	37351	23745	10712
601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5	EST_HUMAN	1.0E-125 BE794576.1	1.0E-125	0.72	37313		10670
th52b03.x1 NCI_CGAP_KId11 Homo sepiens cDNA done IMAGE:2171981 3' smilar to TR:Q14089 Q14089 HYPOTHETICAL PROTEIN ;	EST_HUMAN	1.0E-125 Al665993.1	1.0E-126	1.06	36293	22723	9581
	Source	N <sub>o</sub>	BLAST E Value	Signal	Ō NO:	NO C	NO. 0
To Hit Descriptor	Top Hit	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ		Probe

7/7/S/10 OM

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Single Exon Probes Expressed in Placenta

	4765	4725	4618	4368	4368	4232	3913		3781	2674	2418	2273	2127		2127	1726	939	804	284	284	177	177	176	176	12823	11808	11099	00001	8377	8177	Prabe SEQ ID S
	17890	17860	17765	17511	17511	17379	17072		16942	15794	16547	15408	15263		15263	14876	14113	14079	13502	13602	13400	13400	13400	13400	18500	24796	24172	23038	21458	21259	SEQ ID
		30842	30737	30492	30491	30368	30070		29948	28911	28675	28535	28383		28382	27887	27174	27145	26536	26535	26430	26429	26430	26429	31536	38494	37807	36629	34982	34781	ORF SEQ
	269	6.74	0.83	24.93	24.93	0.59	0.7		0.61	21.48	3.12	17.46	1.97		1.97	2.22	4.81	1.17	2.14	2.14	2.75	2.75	2.92	2,92	6.48	2.2	2.01	0.57	0.8	2.42	Expression Signal
Γ				1.0E-127	Г				Г	Γ	Γ	Γ	Ι.	ļ	1.0E-127	1.0E-127									Ι,		1.0E-126	1.0E-126			Most Similar (Top) Hit BLAST E Value
	AL16326	4506384 NT	1.0E-127 AF252297.1	7706239 NT		AF13518	1.0E-127 AW161297.1		1.0E-127 AF114488.1	1.0E-127 X12881.1	1.0E-127 AF245505.1	4506620 NT			5803085 NT	4827053 NT	1.0E-127 U72621.2	1.0E-127 AF114488.1	1.0E-127 D87675.1	1.0E-127 D87675.;	1.0E-127 AB024597.1	1.0E-127 AB024597.1	1.0E-127 AB024597.1	1.0E-127 AB024597.1	1.0E-126 BE743922.1	1.0E-126 BE261660.1	1.0E-126 BF683175.1	4505424 NT	1.0E-126 AA483368.1	1.0E-128 X16609.1	Top Hit Acession
	NT	NT	NŢ	NT	NT	N <sub>T</sub>	EST_HUMAN		2	21	Z	NT I	Z		NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	NT	Top Hit Database Source
	Homo seplens chromosome 21 segment HS21C068	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	18	Homo sapiens neuroblastoma-amplified protein (LOC51994), mRNA	Homo sapiens neuroblastoma-emplified protein (LOC51594), mRNA	Homo sapiens delayed rectifier potassium channel subunit IsK mKNA, complete cds		au80e06 yr Schneider fetai train 00004 Homo sepiens CUNA cione Invade 2762594 o similar to TR:015170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN contains element MER22	Homo saprens intersectin short isolorin (110N) mrink, complete cos	Human mRNA for cytokeraun 16	Homo sapiens adlican mRNA, complete cds	Homo sapiens ribosomai protein L26 (RPL26) mRNA	MRNA	Homo sapiens leukocyte immuroglobulin-like receptor, subfamily A (with TM domain), member 1 (LLRA1),	Homo sapiens leukocyte immunoglobulin-like receptor, subtamily A (with 1 M domain), member 1 (LILXA1), mRNA	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA	Homo sapiens lost on transformation LOT1 mRNA, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amyloid procursor protein, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase i epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	601577881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5	601149404F1 NIH_MGC_19 Homo capiens cDNA clore IMAGE:3502129 5	602139138F1 NIH_MGC_46 Homo sepiens cDNA clare IMAGE:4288240 5		ne/4b12.s1 NCI_CGAP_Ew1 Homo septens cDNA clone IMAGE:905983 similar to SW:TSG8_HUMAN P88066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-8 PRECURSOR;	Human mRNA for ankyrin (variant 2.1)	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

Human FAU1P pseudogene, trinucleotide repeat regions	NT	U02523.1	1.0E-128 U02523.1	18.07	28388		2132
Human FAU1P pseudogene, trinucleotide repeat regions	NT T	U02623.1	1.0E-128 U02623.1	18.07	28387		2132
Homo sapiens chondrottin sutfate proteoglycan 2 (versicen) (CSPG2) mRNA	NT	4758081 NT	1.0E-128	0.96	27397	14342	1179
Homo sapiens chondrollin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	NT	4758081 NT	1.0E-128	0.96	27396	14342	1179
601278127F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:3618822 5	EST_HUMAN	1.0E-128 BE385617.1	1.0E-128	1.66	26700	13667	472
Homo sapiens gene for AF-6, complete cds	NT	1.0E-127 AB011399.1	1.0E-127	1.64		26044	13170
Homo sapiens gene for AF-6, complete cds	NT	.0E-127 AB011399.1	1.0E-127	1.74	32037	25507	12763
Homo sapiens mRNA for casein kinase I epsilon, compl	NT.	1.0E-127 AB024597.1	1.0E-127	3.03	26430	13400	12539
Homo sapiens mRNA for caseln kinase I epsilon, compl	NT	1.0E-127 AB024597.1	1.0E-127	3.03	26429	13400	12539
601434784F1 NIH_MGC_72 Homo sapiens cDNA clon	EST_HUMAN	1.0E-127 BE895415.1	1.0∈-127	1.65	38615	24913	11927
601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 6'	EST_HUMAN	1.0E-127 BE895415.1	1.0E-127	1.65	38614	24913	11927
Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA	NT	11417339	1.0€-127	5.64	38151	24487	11426
Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA	NT	11417339 NT	1.0E-127	5.64	38150	24487	11426
Homo sapiens Chediak-Higashi syndrome 1 (CHS1), rr:RNA	NT	11427235 NT	1.0€-127	0.99	37194	23586	10551
qm94h09.x1 NCI_CGAP_Lu5 Homo sepiens cDNA clane IMAGE:1896449 3	EST_HUMAN	.0E-127 AI298932.1	1.0E-127	0.86	36718	23115	10077
Homo sapiens secretory pathway component Sec31B-1	<u> </u>	1.0E-127 AF274863.1	1.0E-127	3.73	38463	22880	9840
Homo sapiens secretory pathway component Sec31B-1	NT	1.0E-127 AF274863.1	1.0E-127	3.73	38462	22880	9840
Homo sapiens Chediak-Higashi syndrome 1 (CHS1), m	TN	11427235 NT	1.0E-127	0.81	35714	22167	9088
Homo sepiens Chedlak-Higashi syndrome 1 (CHS1), mi		11427235	1.0E-127	0.81	35713	22167	9088
602161232F1 NIH_MGC_8: Homo septens cDNA clone IMAGE:4292575 5'	EST_HUMAN	1.0E-127 BF671355.1	1.0E-127	0.63	34536	21023	. 7973
Homo sapiens Pendred syndrome (PDS), mRNA	NT	11421914 NT	1.0∈-127	1.31	34526	21014	7964
Homo sepiens Pendred syndrome (PDS), mRNA	NT	11421914 NT	1.0E-127	1.31	34525	21014	7864
Homo sepiens reciin (RELN) mRNA	NT	4826977 NT	1.0€-127	0.81	33485	20073	7208
Homo sepiens immunoglobulin superfamily, member 3	NT	11421595 NT	1.0E-127	1.09	33352	19952	6797
Homo seplens Integrin, beta 8 (ITGB8) mRNA	3 NT	4504778 NT	1.0E-127	5.73	32981	19818	6451
H.sapiens TCF11 gene, expn 3-6	NT	X84060.1	1.0E-127 X84060.1	223	32816	19464	6291
H. sapiens NOS2 gene, exon 6	NT	1.49298X	1.0E-127	4.18	32423	19110	5923
Homo sapiens neuronal cell adhesion molecule (NRCAN	3 NT	82686	1.0E-127	0.91	32351	19044	5854
DELTA 1;	EST_HUMAN	.0E-127 W03547.1	1.0E-127	1.57	32320	19014	5824
za01a10.r1 Soares melancoyte 2NbHM Homo sepiens cDNA clone IMAGE::291258 5' similar to SW::PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE							***************************************
Homo sapiens Ring1 and YY1 binding protein (RYBP),	TNE	6912639 NT	1.0E-127	4.36	30916	17930	4795
Top Hit D	Top Hit Database Source	Top HII/Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ.	SEQ ID	Probe SEQ ID NO:
							1

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Single Exon Probes Expressed in Placenta

4396	4279	3198	3198	3198	2838	2838	Į į		1761	1761		1766	426	124	12402	11210	10957		10949	10341		8745	8745	7070	6548	5662	4788	3481	2616	2283		Probe SEQ ID
6 17538	9 17424	8 16373	8 16373	Γ	Τ.	T,	Т	Ţ	14910	14910			13621	13621	25282	24279	24038		٦	23376		21824	21824	20123	19710	18856	17821	16648	15642	15415		SEQ ID
8 30517	30413	3 29382	Γ	Γ		T		T	28005	28004		27999	26663	26663		37918			37666	36987	٦		35360	33538	33086	•	30909	29664		28547		ORF SEQ
									÷.	1.66	: .·	,3.74	1.65	1.83	4.26				3.54	1.29			0.67			0.76	7.27	1.17	1.11	37.91		Expression Signal
2.32 1.0E-	2.37 1.0E-		Ţ	T	T	1	T	1	1.66 1.0E-1	T				Γ	Γ	Ī	T		1.0E-128					Γ	Т	Γ	Γ	Γ		1.05-120		Most Similar (Top) Hit BLAST E Value
1.0E-129 AW755254.1	.0E-129 AB040892.1	1.0E-128 W 14000	1.0E-128 CL 14000	1.0E-128 Q14585	•			29 11418522 NT	1.0E-129 AF240786.1	1.0E-128 AF 240 (00.1	20000	1.0E-129 AL095850.1	1.0E-128 S3//22	1.0E-129 S3//Z2	1.0E-128 AW 821-30.1	1.0E-128 BE88/304.1	DE 007E64 4	1 0F-128 AA926959.1	28 11425254 NI	AA6391		.0E-128 AB007923.1	1.0E-128 AB007923.1	1.0E-128 BFZZ4345.1	8 1,1420ao	REGRET	11420079 NT	AB0330	8 11437455 NT		1508718 NT	Top Hit Acession No.
EST_HUMAN	1	NT COLUMN	SWISSPROT	SWISSPROT	SWISSPROT	82 NT	4505682 NT	22 NT	ZT	-	<u>-</u>	2	1	12	ı٠	EST LIMAN	EST HIMAN	EST HUMAN	N	EST TOWN		N.	Z	11-		2	NT -	2 2 -	5NT	100	NT I	Top Hit Database Source
	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5	59 protein, partial cds	ZINC FINGER PROTEIN HZF10	ZINC FINGER PROTEIN HZF10	ZINC FINGER PROTEIN HZF10	Homo sapiens platelet-derived growth factor receptor, near polypepure (Figure 1997) instend		Homo sapiens zing inger protein of Courses the Section (PDGFRB) mRNA		Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)		Union content of transfer ase theta 2 (GSTT2) and glutathione S-transfer ase theta 1 (GSTT1)	mains	has like growth factor binding protein-2 (human, placenta, Genomio, 1019 nt, segment 2 or 4)	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 or 4]	EST367360 MAGE resequences, MAGC Homo sepiens cDNA	601511912F1 NIH MGC 71 Homo septens cDNA clone IMAGE:39133713	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);	COAP GC4 Homo sapiens cDNA clone IMAGE: 1552383 3' similar to gb:X54941 CYCLIN-	Homo sapiens clutamate receptor, lonotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA		Horno Sapielis IIIINNA TO TRIBE SADIENS CONA clone IMAGE:1182820 similar to TR:G951338 G951338	and the KIAA0454 protein partial cds	Home saniens mRNA for KIAA0454 protein, partial cds	7g86b10.x1 NCI CGAP_Lt/24 Homo sapiens cDNA clone IMAGE: 3'	Homo saplens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA	H sepiens gene for inter-alpha-trypsin inhibitor heavy chain H1, expn 12	31	Homo sapiens chromatin-apecific transcription elongation factor, 140 KDa subunit (FAC IF 140), IIINNA.  Homo sapiens mRNA for KIAA1247 protein, partial cds	•	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Top Hit Descriptor

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CM4-CN0045-180200-511-102 CN0045 Homo sapiens cDNA	EST_HUMAN	1.0E-130 AW843993.1		9.77			4660
Human T-cell receptor (V alpha 22.1, J alpha RPMI4265-variant, C alpha 1) mRNA	NT	1.0E-130 M97710.1		0.91		T	4184
UI-HF-BN0-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5	EST_HUMAN	1.0E-130 AW 503580.1		1.8		7	4047
601343016F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3685466 5'	EST_HUMAN	1.0E-130 BE5642 19.1	1.0E-130	6.31		16120	3864
601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'	EST_HUMAN	1.0E-130 BE564219.1	1.0E-130	6.31	29132		3864
Homo sepiens retinol dehydrogenese homolog isoform-1 (RDH) mRNA, complete cds	NT	1.0E-130 AF240698.1	1.0E-130	1.03			3668
I O	EST_HUMAN	1.0E-130 BE564219.1		1.36			2943
601343016F1 NIH_MGC_53 Homo sapiens cDNA clane IMAGE:3685466 5"	EST_HUMAN	1.0E-130 BE564219.1		1.36	29132		2943
Homo sepiens RET finger protein-like 1 antisense transcript, partial	NT	1.0E-130 AJ010230.1		7.23		16944	2830
Human gene for calalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13	NT	1.0E-130 X04092.1	1.0E-130	2.63			2040
	EST_HUMAN	1.0E-130 BE275192.1	1.0E-130	22.97	27940	14852	1700
601121995F1 NIH_MGC_20 Hamo sepians cDNA clane IMAGE:3346366 5'	L	1.0E-130 BE275192.1	1.0E-130	22.97	27939	14852	1700
Homo sapiens mRNA for KIAA1414 protein, partial cds	1_	I.0E-130 AB037835.1	1.0E-130	0.64	27418	14359	1197
Homo septens hypothetical protein (HSPC242), mRNA	NT	7705530	1.0E-130	1.01	26341	13314	78
DKFZp782K171_r1 762 (synonym: hmel2) Hamo septens cDNA clone DKFZp762K171 5'	EST_HUMAN	1.0E-129 AL120739.1	1.0E-129	1.97		25544	12817
yq48c05.r1 Socres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199112 5 similar to SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;	EST_HUMAN	1.0E-129 H83155.1	1.0E-129	4.28		25273	12387
Homo sapiens similar to ribosomal protein S26 (H. saptens) (LOC63694), mRNA	NT	11420850 NT	1.0E-129	5.01	33882	20420	11578
af72f07.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5	EST_HUMAN	.0E-129 AA625526.1	1.0E-129	3.32	38230	24555	11497
q140d08.x1 NCI_CGAP_Bm25 Homo saptens cDNA clone IMAGE:1658959 3' similar to TR:Q14840 Q14840 MTOGEN INDUCIBLE GENE MIG-2;	EST_HUMAN	1.0E-129 A1199117.1	1.0E-129	0.62	37371	23763	10730
qi40d08.xt NCI_CGAP_Bm25 Homo capieno cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840 MITOGEN INDUCIBLE GENE MIG-2;	EST_HUMAN	1.0E-129 Al199117.1	1.0E-129	0.52	37370	23763	10730
Homo sepiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA		11437282 NT	1.0E-129	1.03	36921	23319	10284
Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	NT	11437282 NT	1.0E-129	1.03	36920	$\neg$	10284
Homo sapiens mRNA for KIAA0634 protein, partial cds	NT	1.0E-129 AB014534.1	1.0E-129	3.57		21594	8513
Homo sapiens WSCR4 gene, exons 3 and 4	NT	1.0E-129 AF041056.1	1.0E-129	1.04	34246	20762	7697
Homo sapiens WSCR4 gene, exons 3 and 4	NT	1.0E-129 AF041056.1	1.0E-129	1.04	34245	20762	7697
Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA	NT	11420850	1.0E-129	4.03	33882	20420	7340
Homo sapiens KVLQT1 gene	NT	1.0E-129 AJ006345.1	1.0E-129	3.99	33814		7277
601513861F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3915350 5'	EST_HUMAN	1.0E-129 BE888334.1	1.0E-129	0.61	33201		238
Homo sapiens KVLQT1 gene	NT	1.0E-129 AJ006345.1	1.0€-129	3.77	32739	_	6216
CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5 Cardiomyopathy associated gene 5	EST_HUMAN	1.0E-129 AW755264.1	1.0E-129	232	30518	17538	4395
Тор Нії Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
			!				7

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					,		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
5208	18329	31300	1.49	1.0E-130	1.0E-130 AW363299.1	EST_HUMAN	RC0-CT0318-201189-031-a11 CT0318 Homo saplens cDNA
5208			1.49	1.0E-130	1.0E-130 AW363299.1	NAWOH_TSE	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6960			1.03	1.0E-130	1.0E-130 AW843375.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6960		33613	1.03	1.0Ε-130	I.0E-130 AW842875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sepiens cDNA
6975			0.85	1.0뜬-130	11425446 NT	TIN	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7404	20482	33849	1.85	1.0E-130	11416777	Z	Homo sepiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7506	7	7	0.63	1.0E-130	.0E-130 AF257737.1	NT	Homo sepiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7606			0.63	1.0E-130	.0E-130 AF257737.1	NT	Homo saplens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8881	21960		0.53	1.0E-130	I.0E-130 AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
9019	22098	35638	2.06	1.0E-130	1.0E-130 AW956242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
9415			1.82	1.0∈-130	1.0E-130 AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10137	23175		0.63	1.0E-130	1.0E-130 AW103454.1	EST_HUMAN	xd36e06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596874 31
4	13243	26243	2.52	0.01 +00	0.0E+00 AA228126.1	EST HUMAN	zr58c04.rl Soares_NhHMPu_S1 Homo capiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
	13243	26244	2.52	0.01	0.0E+00 AA228126.1	EST_HUMAN	2758c04.r1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
8	13246	26248	1.14	0.0€+00	4885136 NT	NT	_
16	13264	26254	3.34	0.0€+00	8923349 NT	NT	15
16	13254	26255	3.34	0.0E+00	8923349 NT	NT	Hamo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13201	20202	3.17	0.0E+00 D83327!1	D83327!1	NT	Homo sepieno DCRR1 mRNA, partial ods
23	Г		3.17	0.0E+00 D83327:1	D83327:1	NT	Homo sapiens DCRR1 mRNA, partial cds
27	Г		8	0.0E+00	0.0E+00 AF141349.1	NT	Hamo septens beta-tubulin mRNA, camplete cds
35		26277	0.62	0.0€+00	5802997	NT	Hamo sapiens Cdc42 effector protein 2 (CEP2), mRNA
37		26280	0.89	0.0E+00 M58600	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
41	13279	26285	4.6	0.0€+00	3857825	NT	
58	13296		1.77	0.0E+00 Y17181.2	Y17181!2	NT	Homo sapiens mRNA for multidrug resistance protein 9 (ABCC3)
58	13296		1.77	0.0E+00 Y17151.2	Y17151.2	NT	Hamo septens mRNA for multidrug resistance protein 3 (ABCC3)
60	13298	26317	1.45	0.0E+00 D7880411	D78804 1	EST_HUMAN	HUM516H08B Human placenta potyA+ (TFujiwara) Homo saplens cDNA clone GEN-516H08 5
න	13298	26318	1.45	0.0E+00 D78804 1	D78804!1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiwera) Homo sapiens cDNA clone GEN-516H08 5'
61	13299	26319	9.83	0.0E+00 L16558,1	16558,1	NT	
ස	13301	26322	16.36	0.0€+00	0.0E+00 AW069534.1	EST_HUMAN	
83	13301	28323	16.36	0.0E+00	0.0E+00 AW069534.1	EST_HUMAN	
67	13304	26327	2.48	0.0E+00	0.0E+00 M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34

7L7LS/I0 OM

NO: Probe 4 ස ଞ 23 SEQ ID 13350 19343 13332 13329 13318 13313 13313 13313 3313 13359 13353 16980 15980 13340 13320 13319 13367 13358 13350 13367 13382 ORF SEQ ID NO: 26340 26346 26339 28340 26347 26377 26371 26366 26367 26359 26356 26378 26379 26384 26377 26419 28416 26392 26393 Expression Signal 40.86 0.62 0.68 3.65 9 1.92 83 1.92 (Top) Hit BLAST E Most Similar Value 0.0E+00 0.05+00 0.0 = +00 0.0E+00 0.05+00 0.0€+00 0.0E+00 0.0E+00 N36040 0.0E+00 AI623701.1 0.0E+00 AB037784.1 0.0E+00 AI114743.1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 N36040 1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 X91213.1 AA953770.1 Top Hit Acession VI60676.1 AI623701.1 BF036881.1 AF111168.2 Z 4758977 4768977 NT 5016088 NT 4758977 NT 4505938 NT 4503680 NT 4504444 NT 4505458 NT 4501850 4505938 NT ż Ž ξ 3 EST\_HUMAN EST EST HUMAN EST\_HUMAN EST HUMAN Database Source Top Hit HUMAN HUMAN encoding mitochondrial protein, mRNA SW:TMOD\_HUMAN P28289 TROPOMODULIN.; cn89e04.s1 Scares\_NFL\_T\_GBC\_S1 Homo saplens cDNA clone IMAGE:1563870 3' similar to Homo sapiens protein tyrosine phosphatase, non-receptor type cubstrate 1 (PTPNS1) mRNA Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA Human von Willebrand factor pseudogene corresponding to exons 23 through 34 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. HA1347 Human fetal liver cDNA library Homo sapiens cDNA Human polyhomeotic 1 homolog (HPH1) mRNA, partial ods Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA Homo sapiens actin, beta (ACTB) mRNA Homo sapians amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene \$38b05.x1 NCI\_CGAP\_UM Homo saplens cDNA clone IMAGE:2230833 3' similar to TR:089551 Q9955 domo sepiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA ya83g04.r2 Stratagene fetal spieen (#837205) Homo sapiens cDNA clone IMAGE:68310 5 ya83g04.r2 Stratagene fetal spieen (#837205) Homo sapiens cDNA clone IMAGE:68310 5 yo1h09.r1 Soares melencoyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. H.saplens nox1 gene (exon domo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA 601174270F1 NIH\_MGC\_17 Homo sapiens 601460375F1 NIH\_MGC\_66 Homo septens cDNA clone IMAGE:3863803 5 Homo sapiens polymerase (RNA) ii (DNA directed) polypeptide A (220kD) (POLR2A) mRNA Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA y/01h09.r1 Soares melanocyte 2NbHM Homo capiens cDNA clone IMAGE:270017 5 1838b05.x1 NCI\_CGAP\_UI4 Homo septens cDNA clone IMAGE:2230833 3' similar to TR:099551 Q99551 Homo sapiens mRNA for KIAA1363 protein, partial cds Homo sepiens IgG Fc bincing protein (FC(GAMMA)BP) mRNA Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA domo sapiens neuropilin 2 (NRP2) mRNA Homo sapiens serine palmitoyi transferase, subunit il gene, complete cds; and unknown genes omo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA Top Hit Descriptor CDNA clone IMAGE:3529864 5

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Table 4
Single Exon Probes Expressed in Placenta

7L7LS/I0 OM

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Single Exon Probes Expressed in Placenta

			Γ	0.00	50404	7 13408	23/
cDNA clone TCBAP4466	EST HUMAN	o nE+00 BE246780.1					
cDNA cione TCBAP4466 TCBAP4466 Pediatric pre-B cell scute lymphoblestic leukernia Baylor-HGSC project=TCBA Homo sapiens	EST_HUMAN	0.0E+00 BE246780.1		3 0.89	9 26483	7 13459	237
TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens		00/0414	0.05+00	2.02	1 26479	13451	230
Man mucculus testis-specific protein, Y-encoded-like (Tspy), mRNA	212	ABOTOZO	Ī			Г	229
Homo seniens mRNA for KIAA0721 protein, partial cds	7	0.0E+00 AB016264.1	Γ				228
Homo seniens mRNA for KIAA0721 protein, partial cds	2	0.0E+00 AF132000.1	Τ			2 13444	222
Homo series TADA1 probin mRNA, complete cds		111200000		11.48	3	Γ.	221
	) N	Al-1956	Ī		0 26472	13440	218
Homo seniens DNA mismetch repair protein (MLH3) gene, complete cds	ESI HUMAN	0.0E+00 AI5873C8.1			7 28470	16007	216
NCI_CGAP_US Hamo sapietis coma civillo in	1					╗	
(HUMAN);	EST_HUMAN	0.0E+00 A1587308.1		12	7 26469	16007	216
mnama x1 NCI CGAP Ut3 Homo septens oDNA clone IMAGE:2207847 3' similer to gb:J03191 PROFILIN I	2	0.0E+00 AF16/1/4.1	Τ	7.71	26462	13429	206
Homo seniens chromosome X MSL3-2 protein mRNA, complete cds	2	0.0E+00 AF16/1/4.1	Γ		Γ	Γ	206
Homo seniens chromosome X MSL3-2 protein mRNA, complete cds	2	0.0E+00 AF2/3046.1			26459		204
Homo saniens CTCL tumor antigen se14-3 mRNA, complete cds	2	0.0E+00 AF2/3045.1			26458	13427	204
Homo seniene CTCL tumor antigen se14-3 mRNA, complete cds	77	0.0E+001D50659.3			26453		199
Human gamma-cytoplasmic actin (ACTGP9) pseudogene	2	0.0E+00[AB018327.1					191
Homo saniens mRNA for KIAA0784 protein, partial cds	1	0.0E+00 ABO 1832.7.1	l			13413	191
Homo septens mRNA for KIAA0784 protein, partial cds	2	0.0E+00 AB018327.1					190
Home seniers mRNA for KIAA0784 protein, partial cds	1 2	0.0E+00 AB018327.1			26439	13412	190
Homo seniens mRNA for KIAA0784 protein, pertiel ods	EST_HUMAN	0.0E+00 BE018970.1				13407	185
bb24e12.y1 NIH_MGC_14 Homo sapiens cunA cidile in/AGL/2000001 0 00000000000000000000000000000							
CE22831;	EST_HUMAN	0.0E+00 BE018970.1		6.75	26435	13407	185
bb24e12.y1 NIH MGC 14 Homo saplens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z	2	0.0E+00 AL163202.2		28.75	26428	13399	175
nomo sapiena chromosomo 21 segment HS21C002	Z	0.0E+00 AL163202.2	Γ	26.75	26427	13399	176
Homo septems chromosome 21 segment HS21C002	Z	0.0E+00 AF244088.1		4.73		7	172
QVO-110401-14220-000-001 mBNA complete cds	EST HUMAN	0.0E+00 BE162832.1	0.0€+00	0.79	26423	13395	171
CVS-ITIO457-142000000 HT0457 Homo saplens cDNA	EST_HUMAN	0.0E+00 BE162832.1		0.79		13395	171
200209,TI SOGRES_BUB_REAL(_NUTRITION TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR	EST_HUMAN	0.0E+00 W73973.1		24	28421	13394	170
ALL LANGUAGES STORE FOR STORE IMAGE:345201 5' similar to			Value			Ċ	Ö
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similer (Top) Hit BLAST E	Expression   Signal	ORF SEQ	Expn Expn Expn	Probe SEQ ID
	On Bio Cyclin 1990	i ging					

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Single Exon Probes Expressed in Placenta

	Ţ	_	Γ	Γ		П	Γ		Γ		П	П	Γ																		z m P
358	33	354	8	338	337	337	324	320	319	318	317	316	315	304	304	295	294	294	293	282	280	280	267	259	257	250	248	245	245	237	Probe SEQ ID 8 NO:
13569	13000	13565	13551	13551	13550	13550	13538	13534	13534	13533	16010	13532	13531	13520	13520	13512	13511	13511	13610	13500	13498	13498	13486	13478	13476	13471	13469	13467	13467	13450	Exen SEQ ID
26598	PAC07	26593	26581	26581	26580	26579	26570	26566	26566			26565	26564	26554	26553		26546	26545		26532	26530	26529		26510	26507		26501	26497	26496	26485	ORF SEQ ID NO:
4.58	0.74	4.38	1.82	4.14	1.15	1.15	1.59	24.65	18.55	1.42	8.13	4.28	6.16	5.65	5.65	1.41	1.2	1.2	0.96	1.9	1.37	1.37	5.95	1.22	4.65	3.79	7.54	1.17	1.17	0.89	Expression Signal
0.0m+00	0.05+00	0.0E+00	0.0E+00	0.0€+00	0.0E+00 O14867	0.0E+00 O14867	0.0€+00	0.0€+00	0.0E+00	0.0E+00	0.0E+00	0.0€+00	0.0€+00	0.0€+00	0.0€+00			0.0€+00	0.0E+00	0.0⊑+00	0.0E+00	0.0€+00					0.0E+00	0.0€+00	0.0E+00	0.0⊑+00	Most Similar (Top) Hit BLAST E Vatue
4827057	4505266	5174574 NT	7657213 NT	7657213 NT	O14867,	014867,	0.0E+00 AF114488.1	4507152	4507152	0.0E+00 AA480C02.1	4506728	0.0E+00 AB028942.1	0.0E+00 AB028942.1	4557029 NT	4557029 NT	0.0E+00 AW845293.1	0.0E+00 D83327.1	0.0E+00 D83327.1	0.0E+00 D83327.1	7706028	4507500 NT	. 4507500	0.0E+00 AF231919.1	0.0E+00 X89772.1	0.0E+00 AF231919.1	0.0E+00 AL163201.2	5453805	0.0E+00 AB018301.1	0.0E+00 AB018301.1	0.0E+00 BE246780.1	Tap HII Acessian
7 NT	2	Z Z	JNT	3 NT	SWISSPROT	SWISSPROT	TN	2 NT		EST_HUMAN	8 NT	NT	NT	TNE	NT	EST_HUMAN	N.	NT	N,	NT R	O NT		N.T	TN	NT.	NT	5 NT	NT	NT	EST_HUMAN	Top Hil Database Source
Homo sapiens X-box binding protein 1 (XBP1) mRNA		Homo saplens myeloidllymphold or mixed-lineage leukernia (trithorax (Drosophile) homolog); translocated to, 4 (MILLT4) mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)	Homo saplens intersectin short isoform (ITSN) mRNA, complete cds	Homo sepiens SON DNA binding protein (SON) mRNA	Homo sapiens SON DNA binding protein (SON) mRNA	zv18c06.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds		Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA	Homo saplens DCRR1 mRNA, partial cds	Homo sapiens DCRR1 mRNA, partial cds	Homo sapiens DCRR1 mRNA, partial cds	- 1	اد	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens chromosome 21 unknown mRNA	H.sapiens mRNA for interferon alpha/beta receptor (long form)	Homo sepiens chromosome 21 unknown mRNA	Homo saplens chromosome 21 segment HS21C001	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA	Homo saplens mRNA for KIAA0758 protein, partial cds	Homo sapiens mRNA for KIAA0758 protein, partial cds	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukernia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

444	444	443	442	441	433	419	415	415	414	414	413	412	411	410	410	409	408	408	407	404	399	398	387	376	374	373	372	369	367	366	366	Probe SEQ ID NO:
13640	13640	13639	13638	13637	19233	13614	13610	13610	13610	13610	13609	13608	13607	13606	13606	13605	13604	13604	13603	13601	13636	13635	13593	13584	13582	13582	13581	13578	16011	13576	13576	Exan SEQ ID
26678	26877	26676		26675	26233		26649	26648	26649	26648	26647	26846	26645	26644	26843	26642	26641	26840	26639	26636	26674	26873	26629	26818	26616	26616	26616	26611	26609	26608	26607	ORF SEQ ID NO:
17.7		2.82	3.85	1.39	1.49	18.46	1.07	1.07	98.0	0.96	214	2.55	1.98	1.42	1.42	2.18	2.34	2.34	2.24	1.32	1.08	7.56	3.37	. 0.68	1.43	2	1.50	1.01	2.53	2.75	2.75	Expression Signal
0.00+00	Γ	Г	0.0E+00	0.0Ё+00				Г				0.0€+00				0.0€+00	0.0€+00	0.0€+00								0.0€+00		0.0E+00	0.0⊑+00	0.0E+00	0.0€+00	Most Similar (Top) Hit BLAST E Value
4507152 NT		AB0286M	4508728 NT	4503914 NT	0.0E+00 R17795.1	4506608	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00 X74870:1	0.0E+00 X7487011		4503680 NT	4503680 NT			4503680 NT	4503680 NT	4503680 NT	4503680 NT	0.0E+00 AW754180.1	0.0E+00 Al363014.1	0.0E+00 AB028912.1	0.0E+00 AU134953.1	4507500 NT	0.0E+00 D80006.1	0.0E+00 D80006;1	4503854 NT	4507500	0.0E+00 AF2319;9.1	0.0E+00 AF2319;9.1	0.0E+00 AF2319;9.1	Top Hit Acession No.
2NT	2 NT	3	8 NT	NT NT	EST_HUMAN	BNT	4	3	즉	NT	TNI	NT	NT	TNIC	NT	NT	NT	NT	NT	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	NT	NT	NT	NT	NT	T	NT	NT	Top Hit Database Source
Homo sepiens SCN DNA binding protein (SCN) mixina		Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens ribosomal protein S5 (KPS5) mKNA	Homo capiens phosphoribosyglycinamide formytransferese, phosphoribosyglycinamide synthetase, phosphoribosyleminoimidezede synthetase (GART) mRNA	yg09a02r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31852 5	Homo sapiens ribosomal protein L19 (RPL19) mRNA	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiene gene for RNA pol II largest subunit, exons 23-29	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMWA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA		Homo septens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sepiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	RC2-CT0320-300100-016-209 CT0320 Homo capiens cDNA	qy61h05x1 NCL_CGAP_Bm25 Homo septens cDNA clone IMAGE:2018457 3: similar to gb:x54189 PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);	Homo saplens mRNA for KIAA1019 protein, partial cds	AU134963 PLACE1 Homo sapiens cDNA cione PLACE1000889 6			Human mRNA for KIAA0184 gene, partial cds	Homo saplens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens T-cell lymphoma invasion end metastasis 1 (TIAM1) mRNA	ı	Homo sepiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

co.			co.	CD CD	51		σ,	٥	۾	ابي	ق ا	5	91	ç;	ဥ	520	517	616	508	g	497	497	8	48	4g	8	4	<b>2</b>	459	457	£4.	Ž.	Probe SEQ ID	
599 13	680 13		562	557 13	$\neg$	7	$\neg$	٦	П	П	Т	╗	П	525 13718		7	П	П			T	T	T	T	П	П	П	П	П	7 13652	5 13841		<u> </u>	1
13789 260	13772	13762 26786	13754	13750 28777		13749 28775		13747 26772					25 26751	18	14 26741		14 26738	10 26737	02 26731	٦		T			٦		76 26706	59	34 28692	52	11 26679	<del></del>	ORF SEQ	
26810																			;			-			5 21.77	7 3.38		0.75	2 4.44	1.4	9 4.23		Expression Signal	
1.85 0.0E+00	5.31 0.0E	Γ	4.82 0.0E	0.63 0.0E+00	0.63 0.05+00	0.73 0.0E+00	4.53 0.0E+00	4.53 0.0E+00	8.39 0.0E+00		1.15 0.0⊑+	1.57 0.0E+	4.43 0.0E+	1.9 0.0E+	0.05+00	1.82 0.0E+	1.7 0.0E+			П				77 0.0E+00	77 0.0E+00	38 0.0E+00	Г		Г			Value	(Top) Hit BLAST E	
	0.0E+00 D10083.1	0.0E+00 AW 135324.1	0.0E+00 AF003528.1	100 89Z3831 N	Ţ.					0.0E+00 AB040909.1	0.0E+00 BF028005.1	0.0E+00 BE081527.1	0.0E+00 AL163210.2	0.0E+00 BF373403.1	8923955	0.0E+00 AL117233.1	0.0E+00 AW 938825.1	0.0E+00 BE385144.1	0.0E+00 AU132898.1	0.0E+00 AB033005.1	0.0E+00 AL163246.2	0.0E+00 AL163246.2	0.0E+00 AL163246.2	00 4557887 NT				BE25444	4557879	D AL 163201.2	0.0E+00 AF193607.1		Top Hit Acession	
5174742 NT	2	TO I TOWN		N	31 NT	31 N	36 NT	8 2	N N	3	EST_HUMAN	EST HUMAN	Z	EST HUMAN	Z	2	EST HUMAN	EST HUMAN	ESTHUMAN	NT	NT .	NT .	S	7 NT	7	2NT	NT	EST HOMAN	2	Z	Z		Top Hit Database Source	
encoding mitochondrial protein, mRNA	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQORFS1), nuclear gene	Harmo seniens RGH1 gene, retrovirus-like element	regions III.L.E11.ech-b-04.0-111.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2713951.3'	Homo sapiens X-linked anhidrottic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	Homo senions anillin (LOC54443), mRNA	Turis separate arimin (contact) mRNA	Homo septems smillin /I OC54443) mRNA	Tions sapirals guarante nucleatide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA	Homo septens deliscription productide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA	Homo sapiens mixika to NAS 11/0 processin, person of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of t	607/64838F1 NIT WOV_33 Hullo septical code	CVZ-0 10030-100100-1-12-100 00001-1000 CDNA clane IMAGE:399698 5	CV2 BTORSE 180400 142-h05 BTORSE Homo sapiens CDNA	Liza solve companie 21 segment HS21Q010	11 2 ETA150 A78800-120-F07 FT0159 Homo sapiens cDNA	Nove Hullian Borromerin (PC326) mRNA	New homes gene menning to champsome 1	DIA DTOORS 130400.002-006 DT0066 Home sapiens cDNA	RO1274651F1 NIH MGC 20 Home sapiens cDNA clone IMAGE:3615756 5	Home capiens mkNA for NAA 1209 protein, person vos	Homo saptens chromosorile 21 segiment nozi core	Hama saptens anomosome at segment 1921 0048	Homo sapiens chromosome 21 segment HS24C046	Homo sepiens Relatin 10 (NOT 10) III VIV	HOID SEPIETS NEIGHT TO (VICTOR) MENIA		Torro septers 31 journs of the draw front aming (Secretaria) receptor 1B (HTR1B) mRNA		norma septens mind conference of Homo septens cDNA clone IMAGE:3352348 5	Long series interferon gamma recentor 1 (IFNGR1) mRNA	vius linesculas autivaixo con premi HS21C001	Manager of Son protein (Son) mRNA, complete cds	Top Hit Descriptor	

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Homo sapiens potassium voltage-gated channel, isk-related family, member 1 (KCNE1) mRNA	NT	4557686 NT	0.0E+00	1.84	27088	П	850
Homo sapiens hormonally upregulated neu tumor-essociated kinase (HUNK), mRNA	TNT	7657213 NT	0.0E+00	2.46	27086	٦	848
Homo sapiens hormonally upregulated neu tumor-essociated kinase (HUNK), mRNA	TN	7657213 NT	0.0E+00	1.65	27085	14025	847
Homo sapiens T-ceil lymphoma invasion and metastasis 1 (TIAM1) mRNA	NT	4507500 NT	0.0€+00	11.09		14008	830
Homo sapiens pericentrin (PCNT) mRNA	NT	5174478 NT	0.0€+00	13.47	27064	14007	829
Homo sapiens mRNA for KIAA0910 protein, partial cds	NT	0.0E+00 AB0207,17.1	0.0€+00	3.26	27068	14003	824
Homo sapiens mRNA for KIAA0910 protein, partial cds	NT	0.0E+00 AB0207/17.1	0.0€+00	3.25	27057	14003	824
H.saplens mRNA for interferon alpha/beta receptor (long form)	NT	X89772 <sup>1</sup> 1	0.0E+00 X8977211	2.74	27063	13999	820
Human mRNA for KIAA0184 gene, partial cds	NT	0.0E+00 D80006.1	0.0€+00	1.24	27049	13994	815
Human mRNA for KIAA0184 gene, partial cds	NT	0.0E+00 D80006.1	0.0E+00	1.24	27048	13994	815
Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	NT	7661965 NT	0.0E+00	3.01	27035	13983	803
Homo sapiens gene for AF-6, complete cds	NT	0.0E+00 AB011399.1	0.0€+00	1.64	27031		800
Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA	NT	5032086 NT	0.0E+00	2.85	27022	13970	791
ฟฺ69g08.r1 Soares breast 2NbHBst Homo sapiens cDNA cione IMAGE:154046 5	EST_HUMAN	0.0E+00 R48915 1	0.0€+00	4.04	27021		790
601445647F1 NIH_MGC_65 Homo sepiens cDNA clone IMAGE:3849803 5	EST_HUMAN	0.0E+00 BE869735.1	0.0€+00	3.55	27015	13984	785
Homo saplens mRNA for repressor protein, pertial cds	N	D30612)1	0.0E+00 D30612	2.36	27014	16022	784
Homo saplens zinc finger protein 212 (ZNF212), mRNA	NT	6912749	0.0€+00	2.07	27012	13962	782
Homo saplens mRNA for KIAA1339 protein, partial cds	NT	0.0E+00 AB037730.1	0.0€+00	0.96	27011	13961	781
Human, plasminogen activator inhibitor-1 gene, exons 2 to 6	NT	0.0E+00 J03764.1	0.0E+00	8.92	27010	13958	778
Human, plasminogen ectivator inhibitor-1 gene, exons 2 to 9	N <sub>1</sub>	J03764.1	0.0E+00 J03764.1	8.92	27009	П	778
Homo saplens MHC class I antigen (HLA-G) mRNA, HLA-G1 alicle, complete cds	NT	0.0E+00 AF226990.2	0.0€+00	1.19	27008	13955	775
Homo sapiens MHC class I entigen (HLA-G) mRNA, HLA-G1 allds, complete eds	Ŋ	0.0E+00 AF226990.2	0.0€+00	1.19	27005	13966	776
TCAAP1D0779 Pediatric acuts myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sepiens cDNA clone TCAAP0779	EST_HUMAN	0.0E+00 BE241577.1	0.0E+00	2.26	26981	13936	755
Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA	N	11545800 NT	0.0E+00	9.17	26973	13930	749
Homo sapiens ALR-like protein mRNA, partial cds	Ŋ	0.0E+00 AF264750.1	0.0E+00	4.62	26970	13928	747
Homo sapiens ALR-like protein mRNA, partial cds	NT	0.0E+00 AF264750.1	0.0€+00	4.62	26969	13928	747
Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA	IN	5032182 NT	0.0€+00	1.35	26963		741
Human von Willebrand factor gene, exons 23 through 34	NT	0.0E+00 M60675;1	0.0E+00	6.4	26954	13913	731
Human von Willebrand factor gene, exons 23 through 34	NT	0.0E+00 M60675,1	0.0€+00	6.4	26953	13913	731
np46d01.81 NCI_CGAP_br?:1 Homo septens cUNA cione IMAGE:1128633 3' similar to gb:x5/352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);	EST_HUMAN	0.0E+00 AA614537.1	0.0€+00	13.13	26949	13809	727
Homo septens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	NT	7657468	0.0E+00	3.83	26935	13897	715
Homo sepiens mRNA for KIAA1089 protein, partial cds	NT	0.0E+00 AB029012.1	0.0E+00	4.94	26920	13888	705
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signel	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:
							]

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Single Exon Probes Expressed in Placenta

		1	т-	_	_		_	_	_	_	_			-	_	,	_		_			_	_		_	_	_		
1054 1056	1064	1051	1049	1045	1042	1041	1040	1039	1035	1034	1031	1030	1029	1017	1008	1008	1006	1008	1008	997	986	984	984	976	976	975	974	973	Probe SEQ ID NO:
14220 14221	14220	14217	14218	14211	14208	14207	14207	14207	14203	14203	14200	14200	14189	14188	14179	14179	14177	14177	14177	14168	14158	16027	16027	14149	14149	14148	14147	14146	Exon SEQ ID NO:
27278 27279	27277		27272	27268	27265	27264	27264	27264			27258	27258	27267	27249	27242	27241	27238	27237	27236	27229	27219	27217	27216	27209	27208	27207	27206	27206	ORF SEQ ID NO:
2.43 0.97	2.43	1.39	1.27	2.11	1.18	1.3	4.66	0.96	29.66	4	60'6	5.81	1.07	3.97	2.02	2.02	43.62		4	1.76	14.34	3.95			1.24	0.79	9.11		Expression Signal
			П																		0.0E+00				0.0E+00				Most Similar (Top) Hit BLAST E Value
0.0E+00 N43182.1 ES 0.0E+00 4759249 NT	0.0E+00 N43182.1	0.0E+00 AA458680.1		7661685 NT	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF111170.3	0.0E+00 AF198490.1	0.0E+00 AF198480.1	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 U83658.1	4757969	0.0E+00 X52207.1	0.0E+00 X52207.1	0.0E+00 BF366074.1	0.0E+00 BF365974.1	0.0E+00 BF366974.1	0.0E+00 AB030535.1	7657266	0.0E+00 AI001948.1	A1001948		4507430 NT	0.0E+00 M3719011	0.0E+00 M3719011	0.0E+00 M37190!1	Top Hit Acession
EST_HUMAN 9 NT	EST_HUMAN	EST_HUMAN	4 NT	5 NT	NT	TN	TN	NT	NT	NT	NT	NT	NT	9 NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	6 N	EST_HUMAN	EST_HUMAN	0 NT	ONT	NT	NT	NT	Top Hit Database Source
(alignment Ser and Pro with BLASTx or p)  Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA		aa86g07.s1 Stratagene fetal retine 937202 Homo septens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 6;		Homo saplens DKFZP586M0122 protein (DKFZP586M0122), mRNA	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo saplens 8q22 1 region and MTG8 (CBFAZT1) gene, partial cds	Homo sapiens 8q22,1 region and MTG8 (CBFA2T1) gene, partial cds	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Homo sepiens chromodomain protein, Y chromosome-like (CDYL) mRNA	Homo sapiens partial c-fgr gene, exons 2 and 3	Homo sapiens partial c-fgr gene, exons 2 and 3	PM2-GN0014-050900-001-f02 GN0014 Homo septens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo seplens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	Homo septens mRNA for PSP24, complete cds	Homo sepiens KIAA0929 protein Msx2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA	os88e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	Homo sepiens thyrotrophic embryonic factor (TEF), mRNA	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Top Hit Descriptor

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4657887 NT Homo sapiens keratin 18 (KRT18) mRNA
NT Homo saplens mr.NA for N.MA 14 14 plotter, permanent
7305076 NT Homo sepiens glutamate decalloxylase ( (bigit, 5) (b)
7305076 NT Homo sapiens glutamate documents (brein 67kD)
TOWE !
III II AAA
NT Homo sapiens DNA for Human P2XM: complete cds
THUMAN
8923624 NT Homo sapiens hypothetical protein in S (TUBA8 gene)
8923624 NT Homo sapiens n
Homo sapiens TRAF family member-associated NFKB act
Top Hit Accession Database

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THE STATE OF THE LINE LAZING THE LINE LAZING THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF	EST_HUMAN	0.0E+00 BE257955.1		1.02	3 27657		1429
	EST HOMAN	0.0E+00 BE267955.1		1.02	3 27656	14583	1429
EAN-MOOTESPEL NITH MICH 16 Home sapiens cDNA clone IMAGE:3350471 5'	2	0.0E+00 M14123.1			27597	14522	1368
Liumon addresso retrovirus HERV-K10	1 N	856/38/ NI	Γ		1 27584	14511	1356
Homo seniors period (Drosophila) homolog 3 (PER3), mRNA			Γ			14511	1356
Home support of (Draschila) homelog 3 (PER3), mRNA	N -		Γ		0 27582	14510	1355
Hamp separa KIAA170 cens product (KIAA0170), mRNA	2 2 -					14509	1354
Homo seriens KIAA0170 gene product (KIAA0170), mRNA	2	0.0E+00 AB011149.1	Γ		8 27680	14508	1353
Light capacity and imporpress.	N.	4508004 N	Γ		27578		1351
Homo serious the finger protein 173 (ZNE173) mRNA	S				27577		1350
Truttu septiens in a Bor general in GRNA	Z	łk,		1.7	27576	14504	1349
Doma september BERAD gene for RING finger protein	N	4508004 N I	Γ	0.83	27575		1347
nomo sapiena inga pican a (1916), maya	NT	5803146 NT		1.86			1346
Homo sapieus Arbao gaire la Luive in gar pressi.	Z	0.0E+00 Y07829.2			27573		1346
	IN	7657629 NT		1.2			1339
-11 ·	N	7657529 NT		1.2	27566		1339
Truttu saperia process in control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of the control process of	Z	0.0E+00 AF096153.1	Γ	2.16	)		1329
The representation of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of	N.	5174/48 N	Γ	3.28	27554		1328
Homo capions Wolfrem syndrome (WFS) mRNA	N	5174748 NI			27563	14485	1328
Homo conione (Volfram syndrome (WFS) mRNA	N	5174748 N I		3.28	27552	14485	1328
Dutio sapiens (Wolfrem syndrome (WFS) mRNA	2	0.0E+00 AB040940.1		1.63	27539	14472	1316
Homo septent mBNA for KIAA1507 profeb, partial cds	Z	0.0E+00 AB040940.1		1.63		14472	1316
	Z	0.0E+00 AF084479.1		2.96		14466	1310
Laws solvers Williams Bauran syndrome deleton transcript 9 (WBSCR9) mRNA, complete cds	2	4506718IN	Γ	29.88	27525	14469	1303
Lamo socione ribosomal profess S2 (RPS2) mRNA	1	Y18000.1	Γ	1.38		14451	1295
Tomo sapiens preform (1 Ott)	NT	4505740 NT	0.0€+00	0.69	27510	14442	1286
TOTIO Septens croffildin A (DEDNA) mRNA	2	4503098	0.0€+00	1.67	27504	14433	1276
Loss explains contaction of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the cont	2	0.0E+00 AF109718.1	0.0 €+00	4.86	27503	14432	1275
Homo spriens chromosome 3 subtelomento region	Z	0.0E+00 AF264750.1	0.0€+00	2.46	27478	16032	1256
Homo sapiens ALX-like protein mRNA partial cds	Z	0.0E+00 AF264750.1	0.0E+00/	3.33		14414	1266
Homo septens ALX-like protein mixix, period rule	NT	0.0E+00 AF264750:1	0.0E+00	2.89		14413	1254
HOMO Septents ALTA-line provent in a very personal and a	T	0.0E+00 AF264750.1	0.0E+00/	2.89	27475	14413	1254
		22593	0.0E+00	0.94	27471	14409	1250
Homo sapiens murt. (E. coii) nomoiog o (ML loy) illi NAO	NT .	7657336 NT	0.0E+00	1.28		14395	1236
a di la sala sa Adi La Sana			Value			S.	Ņ.
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit BLAST E	Expression Signal	ORF SEQ	Exon SEQ ID	Probe SEQ ID
			1				
	Single Exert 1000	Silling.					

				10.0	710/7	14/31	15/8
Homo sapiens titin (TTN) mRNA	4507720 NT		1		Γ	l	15/8
Homo saprens (Univ) Harris	4507720 NT		1		1	Ţ	
	N.T	0.0E+00 M98478.1		64.77	27810	7	1578
Himon transclutaningse mRNA complete cds	1817 180001		Γ	9.78	4	14724	1571
Homo saplens TNF-Inducible protein CG12-1 (CG12-1), mRNA	ייין מלייי		Ī		27804	70 14723	1570
	7882405 NT		T		l	Г	1568
1 3	4505404 NT		1	1	T	Т	200
Homo septems densinenting to proceed to Control many	4505404 NT	_	0.0E+00	2	27801	Т	
(L44L) and FTP3 (FTP3) genes, complete ods	ZT	0.0E+00 U78027.1		3.2	<u>.</u>	14720	1567
Homo sapiens Bruton's tyrosine kinase (ВТК), apha-D-galactosidase и (ЭСА), Ститика почетки ртошти			T		2//80	5 14/18	1565
Bovine mRNA for neurocalcin	NT	0 0F+00 D10884.1	T		T	Т	1004
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ESTORAGE MAGE POSSESSES MAGN Homo sergers CDNA	EST_HUMAN	0.0E+00 AW976097.1	0.0E+00	1.55		Ī	1564
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Concenting actions exclabilin A mRNA, complete cds	2	0.0E+00 AF023860.1	0.0≅+00	27.8	5 27792		1562
Compatibles is settling a cyclophilin A mRNA, complete ods	EO LOWING	0.0E+00 AA48111,2.1	0.0E+00	2.66	B 27788	14708	1656
aggasti3 r1 NCI CGAP GCB1 Homo sapiens cDNA cione IMAGE:815116 5'	4	7/06434 NI	0.0Ё+00		3 27772		1641
Home sanjers hHDC for homolog of Drosophila headcase (LOC51696), mRNA	Ž V	Weng/p	0.05+00		27743		1507
Human von Willebrand factor pseudogene corresponding to exons 23 through 34	NIT I	0.0E+00 M800/6.1	0.0€+00			14660	1507
Himan von Willebrand factor pseudogene corresponding to exons 23 through 34		7.878/DA	0.0E+00 YU/828	3.74		14654	1601
Homo sapiens RFB30 gene for RING finger protein	NT.	٠L	0.00		2//36	14653	150
Home sapiens KIAA0170 gene product (KIAA0170), mKNA	SUL		0.00	2.20	Γ	1	1500
Homo sapiens KIAA0170 gene product (KIAA0170), mKNA	SNT		0.01	Ī	T	1	1498
Homo sapiens calcineurin binding protein 1 (KIAAUSSU), ITIKINA	NT NT	6912457 NT	0 011		T	1	1490
Human mRNA for KIAA0240 gene, partial cos	NT	D87077.1	0.0E+00 D87077.1		T	1	1
Novel human gene mapping to chomosome i	NT	0.0E+00 AL137764.1	0.00+00		Ţ	Т	1
Novel human gene on chromosome 20	NT	0.0E+00 AL132999.1	0.0E+00			T	3
100	37 	0.0E+00 AF038280.1	0.05+00			Ţ	
	Z	0.0E+00 AJ238093.1	0.0€+00	29.09		٦	1483
noino sepera survertir in processor de la Tand Alu repeat elements	SNT	7705585 NT	0.0E+00	1.99			1459
HOURD SEPTEM STANDARD TO SERVICE SEPTEMBER (KIAAA11A) MRNA	SNT	7705565 NT	0.0E+00	1.99	٦	T	1459
TOTAL SEPTIME KIA A 1114 A Profess (KIAA 1114). mRNA	S N	4505646 N	0.0E+00	0.97		14610	1457
The separate provides converted subtilisin/kexin type 2 (PCSK2) mRNA	S N	4505646 N	0.0E+00	0.97		14610	1457
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	2	0.0E+00 AJ250014.1	0.01+00	1.03	27668	14593	1440
Homo sapiens mRNA for Familial Cylindrometosis cyld gene							
. Top Hit Descriptor	Top Hit Database Source	Top Hit Accession No.	Most Similar (Top) Hit BLAST E	Expression Signed	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID

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Table 4

Single Exon Probes Expressed in Placenta

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Table 4
Single Exon Probes Expressed in Placenta

	E S		<b>1</b>	Most Similar		Top Hit	
SEQ ID	SEQ ID	ID NO:	Signal	(Top) Hit BLAST E Value	No.	Database Source	Top Hit Descriptor
1579	16042		32.23	0.0圧+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1580	14732	27813	27.68	0.0⊑+00		ZT	Human laminin receptor (2H5 epitope) mRNA, 6' end
1592	14745	27828	1.43	0.0€+00	4507720	NT	Homo seplens titin (TTN) mRNA
1592	14745	27829	1.43	0.0≝+00	4507720	NT	Homo saplens titn (TTN) mRNA
1594	14747	27830	13.85	0.0€+00	4503098	TN	Homo sapiens chondroitin sulfate proteoglycan 4 (melenome-associated) (CSPG4), mRNA
1602	14755		3.25	0.0€+00	D00333[1	TIN	human c-yes-2 gene
1611	14764	27844	11.38	0.0€+00		NT	H.sapiens hH2B/e gene
1612	14765	27845	2.55	0.0€+00	5921460	TN	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1612	14785	27846	2.55	0.0E+00	5921460	TN	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1613	14766	27847	11.09	0.0≣+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOFD2 5
1613	14766	27848	11.09	0.0€+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5
1616	16043	27851	2.1	0.0€+00		NT.	Homo sapiens mRNA for KIAA1472 protein, pertial ods
1618	14770	27852	1.88	0.0 €+00		NT	Homo capions DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1620	14//2	27855	6.83	0.0E+00	7662183	ZT	Homo sepiens KIAA0569 gene product (KIAA0569), mRNA
1020	14//2	2/856	6.83	0.0E+00		Z	
ē	14//4	7/85/	56.88	0.05+00		NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
ğ	14774	27858	56.88	0.0E+00	5729876	Z	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1624	14776	27860	1.53	0.0≅+00		NT	Human sodium channel mRNA
1639	14791	27876	6.29	0.0€+00		EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo septens cDNA clone IMAGE:183848 31
1648 8	14801	27887	1.87	0.0E+00		NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14801	27888	1.87	0.0E+00		NT	Homo saplens mRNA for KIAA1609 protein, partial cds
1668	14820	27903	1.66	0.0E+00	AW444637.1	EST_HUMAN	UI-H-BI3-ejw-c-04-0-UI.st NCI_CGAP_Sub5 Homo septens cDNA clone IMAGE:2733294 3'
1698	14850	27936	212	0.0€+00	BE144364.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1698	14850	27937	212	0.0E+00		EST_HUMAN	NR0-HT0166-191199-004-b11 HT0168 Homo sapiens cDNA
1702	14854	27941	1. <sub>\(\O}</sub>	0.01		EST HUMAN	wg81b07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. :
1703	14855	27942	1.71	0.0E+00	4758513	NT	Homo septens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1704	14856	27943	2.8	0.0E+00		NT	Homo sapiens T-cell receptor gamma V1 gene region
1708	14859	27947	2.1	0.0E+00		NT	
1708	14869	27948	21	0.0E+00		NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1710	14861	27950	94.4	0.0€+00	4557887	NT	Homo saplens keratin 18 (KRT18) mRNA
1711	14862	27851	242	0.0€+00	7657065	NT.	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1714	14865	27954	1.08	0.0€+00		EST_HUMAN	hu11d05x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3166281 3' stmiler to TR:095147 095147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE;
	NO: 1579 1592 1592 1692 1692 1692 1693 1693 1693 1698 1698 1698 1698 1698 1698 1698 1698		NO: 16042 1774 1775 17774 17774 1785 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 17850 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Table 4
Single Exon Probes Expressed in Placenta

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1883	1853	1852	1850	1839	1837	1833	1830	1880	1826	1784	1762	1753	1751	1747	1747	1744	1741	1741	1737	1734	1725	1722	1722	1721	1719	1719	1/10		1714		Probe	
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28104	28103	8 28102	8 28099			28078		28073		٦	28006			27991		27988		27983	27979	27976			27963		27961	27980	2/90/	T	27955	D NO:		
		Ž							41.96						2.54						21.3	_	10.28	0.97	4.3	4.3			1.08	Signal		
24.99 0.0E+00	24.99 0.0E+00	9 0.0€+	24.06 0.0E+	1.7 0.0E+	7.66 0.0E+00	2.47 0.0E+		3.2 0.0E+00			1		8.57 0.0E+					1.95 0.0E+C	Γ	Γ				Γ			T	1		BLAST E	Most Similar	
		0.0E+00 AB00Z331.1	0.0E+00 U14967.1	0.0E+00 AA113030.1	00 4605332 N1	U63963 1	00 4557556 NT			0.0E+00 AF273841.1	00 4557538 NI	0.0E+00 S94400.1	0.0E+00 AB026542.1	0.0E+00 M75980.1	0.0E+00 M75980.1	4826973 N	M76980	0.0E+00 M75980.1	5453855			Z80780.1	0.0E+00 Z80780.1	0 A)149880.1	0.0E+00 H30132.1	0.0E+00 H30132.1		1557610 NT	0.0E+00 BE222374.1	N.c.	Ton Hit A session	Cirgio
4502264 NT	4502264 NT	12	1 2	EN HOWAIN	1	Z	56 NT	56 NT	NT	Z	NI NI	3	I S	Z	Z	32	2	2		12	221	2 2	Z	EG! HOMAN		EST_HUMAN		NT	EST_HUMAN	Dalabase Source		
Homo sepiens activating transcription factor 4 (tax-responsive enhancer element Bor) (A i r*) (iii) viv	Homo saplens activating transcription factor 4 (tax-responsive enhancer element 867) (ATF4) mRNA		Limon mRNA for KIAA0333 gene, partial cds	Liver ribosomei protain 121 mRNA, complete cds	TRANCO ST Strategene Hel a cell s3 937216 Homo sepiens cDNA clone IMAGE:563056 3'	numer College and respect to an ideal caperm protein (histone-binding) (NASP) mRNA	Homo septens E in billiang process pero (E.MS) gene, complete cds, and (SMF) gene, partial cds	PORTIO SELIZIONE E LA CITATRIA PROCESSO (FERSON) MRNA	Homo sepiens F14 hinding protein p300 (EP300) mRNA	Homo sapiels Sivio (Gwo) golly, company	Torrions SMCV (SMCV) gene complete cds	I CR zera Inuman, Genetication (Criticae), 900 m., Society (CR zera) member 2 (SLC26A2) mRNA		numan repaircy was reason gone, some respective protein, complete cds	numan repair-yis growth factor gene exan 15	- 1	Homo socioes RNA hinding maif protein. Y chromosome, family 1, member A1 (RBMY1A1) mRNA	THE HELPHONE STORY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP	Human hanafocyta growth factor gene, exon 15	Domo seniens pericentriolar material 1 (PCM1) mRNA	Homo series FOX: 17 forkhead factor (LOC65810), mRNA	Homo seriens high-mobility group (nonhistone chromosoma) protein 17 (HMG17), mRNA	H. Sapiero H. William	Li contano HURITA CIENTE	GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);  #F7360 v1 Sparse testis NHT Homo sapiens cDNA clone IMAGE:1752809 3'	GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (FLUMANY).  0.55808.rl Sogress breast 3NbHBst Homo septens cDNA clone IMAGE:182246 5' similar to qb:M84099	yo59e08.rd Soares broadt 3NbHBst Homo sapiens cDNA clone IMAGE: 182240 5 Similar to go.mo+v99	Homo sepiens gamme-aminobutyno acid (GADA) A tocologi, gamma a (GADA) a tocological to the Anno	hu11d05x1 NCI_CGAP_Lu24 Homo sepies curve come importo total  MCP-1 LIKE PROTEIN TYROSINE PHOSPHA A SEE 2 (GARRGS) TRANA	Op 111 County Pt.	Top Hit Descriptor	

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Single Exon Probes Expressed in Placenta

none saparis outyroprint, surrainty o, money - 1	5901805 NT	ğ	\$ 0.0E+00	1.84	2 28248	П	2003
Line carions with contribution such	32.1 Nr	0.0E+00 M55632.1	Γ	5.28	2	16142	2001
genes, complete cos	12	0.0E+00 AF240786.1	Γ	6.39	7	6 15137	1996
Homo saplens glutathione S-transferase theta 2 (GSTT	1000	18	0.00	2.41	5 28241	4 15135	1994
Homo sapiens death receptor 6 (DR6), mRNA	7657038 NT	t t				Т	1991
Home sapiens transforming growth factor, beta 3 (TGFB	4507464 NT	8				П	1891
Human transgutaminase minum, complete cos	8.1 NT	0.0E+00 M98478.1					1986
Human transglutaminase mkna, complete cus	8.1 NT	0.0E+00 M98478.1			28230	Т	1986
Homo sapiens DNA polymerase zeta catalytic subunit (n	476.1 NT	0.0E+00 AF157476.1	٦		Ī	15128	1985
Homo seplens mRNA for KIAA1367 protein, parvai cas	788.1 NT	0.0E+00 AB037788.1	T		1	T	100
Homo sapiene RAD1 (S. pombe) homolog (RAD1) mRN	4506384 NT	<u></u>		3.14	28219	15110	1970
Homo sapiens RAD1 (S. pombe) hamalog (RAD1) mRN	4508384 NT		0.01	1.62	Γ	Τ.	1972
Homo sapiens nuclear protein (NP220), mRNA	7657300 NT	ġ	Γ	1.62		15115	1972
Homo sarious purieer protein (NP220), mRNA	292.1 EST_HUMAN	0.0E+00 BE006292.1		1.04	28187		1943
BC3 BN0126 200300 012 NA EN0128 Home sablens of	EST	0.0E+00 BE277465.1		3.2			1924
601170184F1 NIH MGC 20 Homo saptens cDNA clone IMAGE:3547239 5		0.0E+00 BE277465.1		3.22	П	$\neg$	1924
CI-H-BIT-EIN-I-O/-O-OIS I NCI_CON _CUSS CONS CONS		0.0E+00 AW 207280.1		2.3		T	1899
OI-H-BI] - AIRT - OI-SI NOI COAR SINS Home san		0.0E+00 AW 207280.1		2.3			1899
Human retinal degeneration slow (NDS) gerie, excit		0.0E+00 U07147:1	0.0E+	7.35		Т	1896
Human retinal degeneration slow (NDS) gains, excert	'11 NT	0.0E+00 U07147.1	, 30.0	7.35			1806
Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	4826783 NT	<u>8</u> _	0.08+00	3.50	28147	15038	1895
Homo saplens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	4826783 NT	8	0.0Ё+00	3.59	28146	15038	1895
FIGURE Supports III AND TO THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE	78.1	0.0E+00 AB032978.1	0.0€+	1.84		16036	1892
Umo sociens menu for KIAA1152 protein, partial cds		0.0E+00 AB032978.1	0.0∏+	1.84		15036	1892
Homo sapiens neural deliver i Cocciniani martial cds	)5855	8	0.0€+00	7.19		15025	1881
Politic sapietie Neutra derived D	6005855 NT	8	0.0E+00	7.19	28131	15025	1881
notice september of the Application of the Control (RPF-1), mRNA	4604626 N	8	0.0E+00	3.11		15015	1870
Homo sapieris inmunoglobin superiamily member 3 (IGSF3) mRNA, and translated products	4504626 NT	8	0.0E+00	3.11		16015	1870
Homo septens activating transcription factor 4 (tex-responsive enhancer etement 867) (ATF4)	4502264 NT	8	0.0€+00	24.99	28105	14999	1853
	Top Hit Acession Database No. Source		Most Simila (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	SEO ID	Probe SEQ ID NO:
		1					

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Homo septens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA		7657468 NT	0.0E+00	3.79		16262	2126
7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo saplens cDNA clone 7B22E10	T HUMAN	0.0E+00 AA077589.1	0.0E+00	269	28381	Г	2124
7B22E10 Chromosome 7 Fetal Bráin cDNA Library Homo sapiens cDNA clone 7B22E10	h'		0.0E+00	2.59	28380	Г	2124
Homo sapiens KIAA1114 protein (KIAA1114), mRNA	3	7705565	0.0E+00	0.97	27695	Г	2122
Homo sapiens KIAA1114 protein (KIAA1114), mRNA	N	7705565	0.0E+00	0.97	27694	14612	2122
AU140831 PLACE4 Homo septens cDNA clone PLACE4000321 5'	EST_HUMAN	0.0E+00 AU140831.1	0.0E+00	67.63	28378	15258	2121
Homo explens coagulation fector IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA	NT	4503648 NT	0.0E+00	1.02	28376		2119
601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'	EST_HUMAN	BE743215.1	0.0E+00	35.36	28375	15256	2117
601573885F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'	EST_HUMAN	0.0E+00 BE743215.1	0.0E+00	35.36	28374	Г	2117
Homo sapiens TP53TG3a (TP53TG3a), mRNA		7708742 NT	0.0E+00	0.98	28370	15250	2112
Homo sapiens chromosome 21 open reading frame 7 (YG81), mRNA		8394546 NT	0.0€+00	1.63	28368	15247	2109
Homo sapiens SMCY (SMCY) gene, complete ods	NT		0,0€+00	1.85	28338	15218	2078
Homo sapiens SMCY (SMCY) gene, complete cds	NT	0.0E+00 AF273841.1	0.0E+00	1.85		П	2078
Homo saplens mRNA for KIAA1513 protein, partial cds	NT		0.0E+00	5.04	28311	15197	2056
H.sepiens genes for semenogelin i and semenogelin ii	NT		0.0€+00	1.09	28302		2048
H. sapiens genes for semenogelin I and semenogelin II	NT	247556.1	0.0E+00	1.09	28301		2049
Homo sapiens mRNA for KIAA0577 protein, complete cds	NT	0.0E+00 AB011149.1	0.0€+00	1.53		Г	2048
Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA	NT	6912457 NT	0.0E+00	9.68	28298	Г	2046
Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	NT	6912457 NT	0.0E+00	9.68	28297	15187	2046
xl69b01.x1 NCI_CGAP_Pan1 Homo saplens cDNA clcne IMAGE:2679913 3'	EST_HUMAN	0.0E+00 AW193024.1	0.0E+00	3.24	28296	Г	2045
xt69b01.x1 NCI_CGAP_Pan1 Homo saplens cDNA clcne IMAGE:2679913 3'	EST_HUMAN	0.0E+00 AW 193024.1	0.0€+00	3.24	28285	15186	2045
Human TFEB protein mRNA, partial cds	NT	0.0E+00 M33782[1	0.0€+00	1.93	28294	15184	2043
Human TFE8 protein mRNA, partial cds	NT	į	0.0E+00	1.83		Г	2043
Homo sapiens mRNA for KIAA0790 protein, partial cds	NT	.1	0.0E+00	2.11	28289	Г	2037
Homo saplens mRNA for KIAA0790 protein, partial cds	NT	0.0E+00 AB018333.1	0.0E+00	2.11	28288	15178	2037
Homo sapiens actinin, alpha 4 (ACTN4) mRNA	TN	_	0.0€+00	12.98	28275	Г	2027
Homo saplens actinin, alpha 4 (ACTN4) mRNA	NT		0.0E+00	12.98	28274	15168	2027
Homo sapiens nebulin (NEB), mRNA	NT		0.0E+00	1.41		16167	2026
Homo saplens nebulin (NEB), mRNA	TIN	8400716 NT	0.0€+00	1.41	28272	15167	2026
Homo sapiens chromosome 21 segment HS21C052	TN	AL16325	0.0€+00	1.04		15165	2024
Homo sapiens histidine ammonia-tyase (HAL) mRNA	TN	4809282 NT	0.0E+00	1.69	28256	Г	2011
	TN	4809282 NT	0.0E+00	1.69	28255	15151	2011
bb73f11.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5	EST_HUMAN	BE018056.1	0.0€+00	1.3	28250	15145	2005
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Prabe SEQ ID NO:
a mary to a second the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second to the second						1	7

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Table 4

Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Acession No.	Top Hit Database Source	Top Hit Descriptor
2128	8 15264		1.48	0.0€+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2129	9 15265	28384	29	0.0E+00 Z42399	Z42399.1	EST_HUMAN	HSC0IC021 normalized Infant brain cDNA Homo septens cDNA clone c-0ic02
2131	1 15267		238	0.0E+00	0.0E+00 AI244247.1	EST HUMAN	qv80f08.x1 NCI_CGAP_U/2 Homo septens cDNA clone IMAGE:1988871 3' similar to contains Atu repetitive element:
2136	6 15272	28393	4.37	0.0€+00	0.0E+00 BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sepiens cDNA clone IMAGE:3887747 51
2138	8 15274		2.25	0.0E+00	0.0E+00 BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 51
2138	8 16274	28396	2.25	0.0E+00	0.0E+00 BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4135320 5'
2144	4 15280	28404	-3.6		0.0E+00 BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2144	4 15280	28405	3.6		0.0E+00 BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sepiens cDNA
2152	2 15288	28414	3.43	0.0E+00 L00820.1	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, comlete cds
2152	2 15288	28415	3.43	0.0E+00 L00820.1	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, comlete cds
2153		28416	1.11	0.0E+00	0.0E+00 AJ297709.1	NT	Homo sapiens mRNA for CDC2L6 protein kinase, (CDC2L6 gene), Isoform 1
2158	8 15294	28420	1.16	0.0€+00	4758489 NT	N	Homo sepiens GTP binding protein 1 (GTPBP1) mRNA
2162	2 15298	28423	.9 <u>.</u>	0.05+00	0.0E+00 BE500995.1	EST HUMAN	7834c02.X1 NCI_CGAP_GC6 Homo sepiens cDNA done IMAGE:3220610 3' smillar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER:
2182	2 15317		3.17	0.0E+00	0.0E+00 BE767934.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2183	3 15318		1.26	0.0€+00	0.0E+00 AF018953.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds
2185	15320	28446	4.64	0.0€+00	0.0€+00 BF027552.1	EST_HUMAN	601672066F1 NIH_IMGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2186	6 15321	28447	1.5	0.0€+00	0.0E+00 BE072624.1	EST_HUMAN	PM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2188	15333	28448			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1	Homo saplens glutathlone S-transferase theta 2 (GSTT2) and glutathlone S-transferase theta 1 (GSTT1)
2190			3.41	0.0E+00	0.0E+00 AW752708.1	EST HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2192			6.48	0.0€+00,	0.0E+00 AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2192	2 15327	28453	6.48	0.0E+00	0.0E+00 AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo saplens cDNA
2225	5 15359		1.08	0.0€+00	7657252 NT	N <sub>1</sub>	Homo sepiens potassium large conductance calcium-ectivated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2249	16382		1.52	0.0E+00 L14787.1	14787.1	NT	Human CNA-binding protein mRNA, 3'end
2259	Г	28518	1.26	0.0€+00	0.0E+00 BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346588 5'
2261	1	28521	0.94	0.0E+00 D87685!1	D87685!1	NT	Human mRNA for KIAA0244 gene, pertial cds
2262	15395	28622	23.12	0.0E+00	0.0E+00 AV738288.1	EST_HUMAN	AV738288 CB Homo sepiens cDNA clone CBNBDE08 5
2262	2 15395	28523	23.12	0.0E+00	0.0E+00 AV738288.1	EST_HUMAN	AV738288 CB Homo saplens cDNA clone CBNBDE08 5
2264	I	28525	2.57	0.00+00	0.0E+00 AA931691.1	EST_HUMAN	oc32e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:15678983'
2268	Г	28529	24.38	0.0E+00	0.0E+00 BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Brn64 Hamo sapiens cDNA clone IMAGE:4150734 5'
2269	15402	28530	40.14	0.0€+00	0.0€+00 BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo septens cDNA clone IMAGE:3839012 3'

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	EST HUMAN	0.0E+00 AW 466922.1		6 4.18			2547
LALIA NO. COAD Kid13 Homo sanians cDNA clone IMAGE:2872759 3'	EST DOWN	0.0E+00 BF569144.1		8 28.11	28788	Ĩ	2539
Engylades 11 NIH MGC 42 Homo sapiens cDNA clone IMAGE:4300383 3	121	0.0E+00 U13866.1	Γ	7 1.02			2538
Human G profein-coupled receptor (GPR1) gene, complete cds	1	0.0E+00 U13666.1	Γ			8 15663	2538
Himan G protein-coupled receptor (GPR1) gens, complete cds	11/1/1/10/10				28780	0 15655	2530
Homo sapiene collagen, type XII, alpha 1 (COL12A1), mRNA	Ι,-	BF3452/	1			4 15649	2524
602018058F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4153670 5	EOT LI MAN	0.0E+00/AF106275.1	١	2.42		16646	2620
Homo septens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6	2 2	0.0E+00 D85606.1					2510
Homo santens gene for cholecystokinin type-A receptor, complete cds	2	0.0E+00 D8660617				15636	2510
Homo seniens gene for cholecystokinin type-A receptor, complete cds	OZ N -	0 6006002 N	Γ		2 28752	15632	2505
Hamp serions clutemate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA	EST HOMEN	ABOUSE		222	0	15630	2503
ARODISCO Hella cDNA (T.Noma) Homo saplens cDNA similar to adenylate kinase isozyme 2	EST HUMAN	0.0E+00 BE895635.1	Γ	1.35	9	15619	2492
En1/32PARE NIH MGC 72 Homo sapiens cDNA clone IMAGE:3918168 5'	_	0 8923620		0.94	8 28737	15616	2489
O08682 230CDA PHOSPHATIDYLINOSITOL 4-KINASE.;  Here a sections hypothetical protein FLJ20693 (FLJ20693), mRNA		0.0E+00 AI042035.1		4.63	4	15614	2487
menhoo xi Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:008662	EO L_ TON	0.0E+00 AU119682.1	Γ	1.14	28735		2485
ALI (1956) HEMBA1 Homo saplens cDNA clone HEMBA1006155 5	EST HUMAN	0.0E+00 BE814424.1	Γ	1.03	0	П	2462
MBD. BN0070-029-d12 BN0070 Homo sapiers cDNA	EST HOMAN	0.0E+00 AU118082.1	Γ	10.61	28690		2434
A11118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5	EST HOWAIN	0.0E+00 AU118082.1	Γ	10.61	28689	15562	2434
A11118082 HEMBA1 Homo sabiens cDNA clone HEMBA1002839 5	EST HOWAY	0.0E+00 AU118082.1	Γ		28688	15562	2434
A11118082 HEMBA1 Homo septens cDNA clone HEMBA1002839 5	N.	0.0E+00 AF280107.1	Γ	7.14		15560	2432
4 (CYP3A4) genes, complete cds; and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds	<u> </u>						İ
Home appliants extechrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	77.	4/0849/ NI	0.00	1.39	28686	16550	2431
Homo saniens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	NIN I		Γ			16559	2431
Homo saciens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	N N I		Γ			16558	2430
Homo saniens KIAA0244 protein (KIAA0244), mRNA	EG HOMAN	BE794025.1	Γ	9.82		15557	2429
RO15114Z N 2 N 3 CONTROL SEPTENS CONA CIONE IMAGE:3941003 5	EST HUMAN	0.0E+00 AU131142.1		3.56		٦	2428
A 14344 42 NT2PP3 Homo sapiens cDNA clone NT2PP3002064 5	87	5174678 N I		3.04			2424
Library serious signal regulatory protein, beta, 1 (SIRP-BSTA-1) mRNA	8 NT			3.83	٦	15536	2405
TOTAL Septem sporm sporms = 3 (SSFA2), mRNA	2			3.83	28663	15536	2405
Homo septems specific entiren 2 (SSFA2), mRNA	1 NT		0.0E+00	2.22		15533	2402
Toma angles of KIAA0057 probin (KIAA0057), mRNA	N.		0.0E+00	2.22	28659	15533	2402
Lines contains KIAA0952 protein (KIAA0952), mRNA	Z	0.0E+00 AB011393.1	0.0€+00	1.5	28657	15530	2399
U. and contains come for AF-A complete cds			Ame				?
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E	Expression Signal	ORF SEQ	SEQ ID	SEO D

Page 499 of 550 Table 4 Single Exon Probes Expressed in Placenta

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OF SOCIAL INIT MOC. LINIT SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCIAL SOCI	EST_HUMAN	0.0E+00 BE792472.1		2.75			npac
٩ľ	EST_HOMAN	0.0E+00 BE785445.1		1,16	28920		2682
ROLFSONTORET NIH MGC 7 Home sapiens cDNA clone IMAGE:3944304 5'	101	0.0010000000000000000000000000000000000		7.10	28919	32 15802	2682
601590108F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'	EST HIMAN	0.0E+00 ABUSTOSE.1	Τ		Γ		2681
mRNA Horno sepiens mRNA for KIAA1438 protein, partial cds	TN	5032150 NT			99 28916	79 15789	2679
Homo sapiens TATA box binding protein (TBP) associated factor, RNA polymerase II, I, 28kD (TAF2I)		OUETO ABOUT TE.	Ī	2.10	28915	16798	2678
Homo sapiens mRNA for KIAA1321 protein, partial cds	NT TOWER	0.0E+00 BF204131.1	I			Г	2676
601869073F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:4111411 5	EST LI MAN	0.0E+00 BF 204731.1				5 15795	2675
601869073F1 NIH NIGC 17 Homo sapiens cDNA clone IMAGE:4111411 5	EGT HUMAN	0.0E+00 BF613835.1				5 15786	2665
III_H.RW1-amp-f-12-0-UI s1 NCI CGAP Sub7 Homo septens cDNA clone IMAGE:3070631 3	201	0.0E+00 AB03/836.1		218	0 28902	18000	2664
Homo seniens mRNA for KIAA1415 protein, partial cds	1 2	0.0E+00 AB037836.1			0 28901	16000	2664
Homo senions mRNA for KIAA1415 protein, partial cds	2	0.0E+00 AF245535.1			1 28866	8 15751	2628
HYPOTHETICAL 93 KD PROTEIN ;	EST_HUMAN	0.0E+00 BF2230,41.1	0.0€+00	1.04	8 28864	5 15748	2625
7027h12x1 NCI_CGAP_GC6 Homo suplens cDNA clone IMAGE: 3' similar to TR:000246 000246	EOI DOMENIA	0.0E+00 BE292896.1	0.0€+00	1.25	7 28863	4 15747	2824
and 105312F1 NIH MGC 15 Homo sablens cDNA clone INAGE: 2987855 6	EO HUMAN	0.0E+00 BE282896.1	0.01+00		7 28862	16747	2624
ROTADET NIH MIGC 15 Homo septens cDNA clone IMAGE:2987855 5	EST HUMAN	0.0E+00 AU143277.1	0.0≣+00		3 28861		2623
	EST HUMAN	0.0E+00 AU143277.1	0.0≅+00	3.66			2623
00100#13071 V70AA1 Homo saniens cDNA clone Y79AA1001673 5	EST HUMAN	0.0E+00 BE536921.1	0.0E+00	1.83		П	2616
Homo sapiens autican finance, compress cDNA clone IMAGE 3451161 5	ZI	0.0E+00 AF245505.1	0.0E+00	. 1.12		П	2599
OU 148824 II I WILLING COMPLete cds	EST HUMAN	0.0E+00 BE8755;1.1	0.0€+00	13.07		П	2598
601488241F I NIT JNICC 69 Homo septens cDNA clone IMAGE:3891371 5	EST_HUMAN	0.0E+00 BE8755;1.1	0.0E+00	13.07		П	2598
2013002 11 1011 2000 20 Homo saniens cDNA clone IMAGE:3891371 5'	HOMAN	0.0E+00 BE886450.1	0.0⊞+00	1.66		П	2696
For 1502 11E4 NIH MGC 71 Homo sapiens cDNA clone IMAGE:3909866 5	Z	0.0E+00 U83239.1	0.0E+00	3.09		П	2589
		7657468 NI	0.0E+00	2.39	28831	15713	2588
Conserved in Linear in test integral membrane glycoprotein POM121 (POM121L1), mRNA	ES! HOMAN	BE910378.1	0.0Ё+00	1.07	28830		2587
PONTS SECTION MACC 70 Home sapiens cDNA clone IMAGE:3805148 5	Z	0.0E+00 5453871	0.0E+00	5.17			2585
Homo septens litraly derived growth factor receptor-like (PDGFRL) mRNA	Z	0.0E+00 Z32684.2	0.0⊑+00	2.21		П	2583
UI-H-BI4-802-0-00-0-0-131 IVC_CGN _CUCC Name or Franchist (XK gene)	EST HUMAN	0.0E+00 BF509482.1	0.0€+00	1.44		Т	2580
Homo septens death receiptor o (Chro), muser	Z	7657038	0.0E+00	1.12	1		2579
Cicio	EST_HUMAN	0.0E+00 BE795542.1	0.0E+00	7.28	28824	Т	2578
KC3-0 10187-300300-0 100-0 100 100 100 100 100 100 100 1	L	0.0E+00 AW813853.1	0.0€+00	. 202		╗	2575
UPHF-Brup-ais-out-a-out-1 will_iii-O_out-is-is-out-	L	0.0E+00 AW501010.1	0.0E+00	3.03	28798	15575	2650
TERROS - CONTROLLES NILL MICC. E1 Homo sapiens cDNA clone IMAGE:3072780 5			Value			Š	Ž
Top Hit Descriptor	Top Hit Database Source	Top Hit Accession No.	Most Similar (Top) Hit BLAST E	Expression Signal	ORF SEQ	SEQ ID	Probe SEQ ID
		(:::)					

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Table 4

Single Exon Probes Expressed in Placenta

D 3	ğ Š			Most Similar	Tan Lit Amergian	Top Hit	Tan Lii Descriptor
SEQ ID	SEQ ID	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.		Top Hit Descriptor
2700	15819	28935	252	0.0E+00	4504686 NT		Homo sapiens IMP (inosine monophosphaia) denyalogenase ( (initiation) 144-like ribosomal protein
2/00	10010						Homo sapiens Bruton's tyrosine kinase (BTK), apha-U-galaciosidase A (SCA), Entre incomina pro-
2740 <u> </u>	15828		1.16	0.01 +00	0.0E+00 U78027.1	NT	(L44L) and FTP3 (FTP3) genes, complete cds
374	15200	28942	5.67	0.0€+00	.1	NT	18
2745	Т	T	1.07	0.0E+00		NT	Homo saplens mRNA for KIAA0536 protein, perual cos
2718	П	T	0.96	0.0E+00	0.0E+00 AU133385.1	EST_HUMAN	AU133386 N I 2RP4 Homo septens cultimate NT2RP3000779 5
2724	T	T	1.16		0.0E+00 AU130403.1	EST_HUMAN	AU130403 N 12RP3 Homo septens culvix cione N 1728 P3000779 5
2721	Т		1.16		0.0E+00 AU130403.1	EST_HUMAN	AUTSUAUS NI CRTS DOING SEPTING COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS COURS
2724	П		1.66		0.0E+00 AW887015.1	L	NC 1-0 10000-22000-0 1 001 0 1000 sapiens cDNA cione IMAGE:3628923 5
2727	П		4.83	Γ	0.0E+00 BE383165.1		S01278373F1 NIH MGC 39 Homo sapiens cDNA clone IMAGE:3610287 5
2728	Т		2.8	T	0.0E+00 DE301203.1	NT L	Homo sapiens mRNA for KIAA1311 protein, pertiel cds
2763	158/8	28967		0.00			EST188414 HCC cell line (matestasis to liver in mouse) II Homo sapiens cDNA 5 end similar to ribosulting
2785	15901		11.99		0.0E+00 AA316723.1	EST_HUMAN	protein LZB
2789	7	29013	4.04		0.0E+00 U36253.;	2	Dunial Computity output (Chines) 8000 (FHL1) gene, complete ods
2791	I		3.72		0.0E+00 AF110763.1	Z	Torilo sapiers hoose many for GTD-thinding protein like 1, complete cds
2792		29016			0.0E+00 AB051828.1	2	Indianated NIH MGC 7 Homo saplens cDNA clone IMAGE:3945983 5
2797		29020			0.0E+00 BE/963/6.1	EST LINAN	RM3335485F1 NIH MGC 39 Homo sepiens cDNA done IMAGE:3689664 5
2800	16072	29024			0.0E+00 BE563433.1	COL LINAN	AV721647 HTB Homo sapiano cDNA cione HTBBYE09 5'
2801				Γ	AV/2104	EG TOWAR	Homo saplens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	7 29027		Γ		N. T.	Homo sapiens spermatogenesis associated PD1 (KIAAD757) mRNA
2803	16917	7 28028			51/4480 NI	NA PARTIES	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2804	15918	в 28029			0.0E+00 AF 250 185.1	NAME OF THE PERSON	AV651066 GLC Home saplens cDNA clone GLCCLD07 3'
2805	15919			Γ	0.0E+00 AV65 1006.1	EOT LINAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2806	15920				0.0E+00 BF37/897.1	EST HIMAN	CM1-TN0141-250900-439-508 TN0141 Homo saplens cDNA
2806	15920	0 29031		Γ	813//60	LO LONG	Humo seriens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2810				Π		N T	Homo seriens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2810	0 15924	П		Γ	0 4/5/963 N	EST HIMAN	601580803F1 NIH MIGC 9 Horno sapiens cDNA clone IMAGE:3929472 5
2813	3 15927	7 29039	21.86	Т	0.0E+00 BE/4/ ISO. I	1000	y/35h10.r1 Soares melanooyte 2NbHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
2814	16928	29040	0 1.05		0.0E+00 N44974:1	EST_HUMAN	A43773 kelch protein, long form - fruit fly ;  BCA UT0587 - 177300-012-411 HT0587 Homo sapiens cDNA
2816	6 15930	29042		Γ	0.0E+00 BE176836.1	EG HOWAIN	Homo sepiens chromosome 21 segment HS21C001
2827				Γ	O ALIBOZOLZ	EST HIMAN	UI-H-BW1-amw-e-07-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2828	15942	29052	2 3.18		0.0E+00 BF3141,10.1	E01 1 10111	

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Table 4
Single Exon Probes Expressed in Placenta

								Ī.,	Ţ.,	Ī.,										,,					,		Ŋ	_	N		Probe SEQ ID NO:
2919	2919	2918	2916	2914	2914	2911	2807	2900	2898	2897	2880	2880	2876	2876	2870	2867	2861	2861	2860	2860	2858	2857	2854	2852	2852	2848 8	2842	2841	2841	2835	
16097	16097	16096	16094	16092	16092	16089	16085	16079	16077	16076	14230	14230	13933	13933	16982	13415	15975	15975	15974	16074	15972	15971	16968	15966	15966	16982	15956	15955	16956	15949	Exon SEQ ID NO:
29109	29108			29105						29094	27288	27287	26979	26978		26444	29086	29085	29084	29083	29082	29081		29076	29075	29072	29064	29063	29062		ORF SEQ ID NO:
1.3	1.3	2.6	2.05	0.93	0.93				1.26			2.04	1.89	1.89	1.64	5.26	64.08	64.06			71.97	2.14	14.75	17.21	17.21	1.33	5.05	1.08	1.08	1.67	Expression Signal
3 0.DE+00	3 0.0E+00			Γ	Γ				Γ	Γ		4 0.0E+00	Ţ		П												0.0E+00	0.0E+00	0.0E+00	0.0€+00	Most Similer (Top) Hit BLAST E Value
7019584 NT	7018584 NT	0.0E+00 AL163268.2	0.0E+00 X73428.1	0.0E+00 BE154604.1	0.0E+00 BE154504.1	0.0E+00 M80902.1	0.0E+00 AL163201.2	0.0E+00 AB040860.1	0.0E+00 AF068624.1	0.0E+00 X8598011	4603202 NT	4503202 NT	0.0E+00 AF264750.1	0.0E+00 AF264750.1	0.0E+00 AB033281.1	0.0E+00 S76830:1	0.0E+00 BE3003,44.1	0.0E+00 BE300344.1	0.0E+00 AU131494.1	0.0E+00 AU131494.1	0.0E+00 BE872758.1	0.0E+00 BF530661.1	0.0E+00 AI879163.1	0.0E+00 AV725534.1	0.0E+00 AV725534.1	7427522	BF677694.1	7705275	7705275 NT	4503098 NT	Top Hit Acessian No.
NT	4 NT	ZT	N.T	EST_HUMAN	EST_HUMAN	21	2	2	2	2	2 NT	2NT	NT	3	Z	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	Z	NT	NT	Top Hit Database Source
Homo sapiens zinc tinger protein 221 (2NF221), mixture	Homo saplens zinc tinger protein 221 (2NF221), mixiva		H. sapiens Id3 gene for HLH type transcription racio	PMD-H10343-281299-003-e02 m10343 nomo saprens conve		HUMAN ATINAN DICIODICION MANA, O CINA	Homo sapiens chromosomic z i sogniou i razi covo	India separate ilinino di recorde present HS217001	Duno series well for KIAA4827 protein perial cds	III. Sapiens serifie hydroxylliethynansieraeo peedadydd Complete Cds	(CYP181) mRNA	(CYP181) mRNA		Homo sapiens ALK-like protein mixiva, paruai cus	Homo saplens BTRCP2 mRNA for F-box and WU-repeats protein isolorm C, complete cos	glycoprotein D=Duffy group antigen [human, blood, Genomic UNA, Superint	600944794F1 NIH_MGC_17 Homo sapiens culva cione image: 290000 o	600944784F1 NIH_MGC_17 Homo sapiens cDNA cibne IMAGE:2800000 0		AU131494 NT2RP3 Homo sapiens cDNA clone N12RP3002572 5	601450912F1 NIH_MGC_65 Homo septens cUNA clone IMAGE:3034042 3		au 55004.y1 Schneider fetet brain 00004 Homo sapiens CUNA Courte INVACE 23 10000 3 Striller to SW 1713A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;	AV725534 HTC Homo sapiens culva cione HTCCCAU3 o	AV725534 HTC Homo septens cDNA clone HTCCCA03 5	Homo sapiene protein tyrosine phosphatase, receptor type, I (FIFRI), many	602085579F1 NIH MGC 83 Homo septens curva cione invasce: 4249910 0	Homo sapiens angiopoletin-3 (ANG-3), mknA	Homo sapiens angiopoletin-3 (ANG-3), mkNA	Homo sapiens chondroitin sulfate proteoglycan 4 (metanome-associated) (Cor G4), III NIVA	Top Hit Descriptor

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Single Exon Probes Expressed in Placenta

		O.OETOO ADOTOOT		2.0	1 29169	167/1	2995
Homo sapiens mRNA for KJAA1508 protein, partial cds	27	10000044				Γ	2894
Homo sapiens mRNA for KIAA1267 protein, pertial cds	NT	O DELLON ABDRIGOR 1			Ī	Т	1,687
Homo sapiens mRNA for KIAA1267 protein, partial cds	Z,	0 0E+00 AB033093.1			20187	Т	3 5
Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mKNA, complete cos	NT	0.0E+00 AF152338.1			1	Т	2078
ZINC FINGER PROTEIN 132	SWISSPROT	P62740				П	2977
	EST_HUMAN	0.0E+00 AI561002.1	0.0€+00	1.15	29172	16151	2975
O16247 F44E7.2 PROTEIN.; In 18407 Y1 NO! CGAD Rm25 Home septens cDNA clone IMAGE:2167981 3' similar to TR:O16247	EST_HUMAN	0.0E+00 AI561002.1	0.0€+00	1.15	29171	18151	2975
In 18407 x1 NCI CGAP Bm25 Homo septiens cDNA done IMAGE:2167981 3' similar to TR:O16247	027	4303470 N	0.01+00	25,86	29170	16150	2974
Homo series surface translation elongation factor 1 alpha 1 (EEF1A1) mRNA	S N T	IN 6/2007#	0.011		Γ	1	2972
Homo saplens EphA4 (EPHA4) mRNA	2 2	Y19210.1	0.0E+00	3.89	Γ	Г	2969
repetitive element;	EST_HUMAN	0.0E+00 AA215579.1	0.0⊞+00	1.3	29158	16139	2962
z96511.s1 NCi_CGAP_GCB1 Homo septens cDNA clone IMAGE:883517 3' similar to contains Atu		,				╗	Į
Homo sapiens chromosome 21 segment HS21C006	NT	0.0E+00 AL163236.2	0.0E+00	23		T	302
Homo sepiens chromosome 21 segment HS21C006	NT	0.0E+00 AL163208.2	0.0€+00	2.3		П	2961
Homo saplens low density lipoprotein-related protein 2 (LRF2), mRNA	8NT	6806918 NT	0.0€+00	0.77		П	2958
Homo sapiens low density lipoprotein-related protein 2 (LKP2), mKNA	8 NT	TN 8169089	0.0E+00	0.77		П	2958
QV2-BT0636-130400-138-h03 B I 0636 Homo sapiens curva	EST_HUMAN	0.0E+00 BE081896.1	0.0E+00	5.16		П	2952
QV2-BT0636-130400-138-h03 BT0636 Homo sapiens curva	EST_HUMAN	0.0E+00 BE081896.1	0.0€+00	5.16	29142	7	2952
Homo sapiens chandroitin sulfate proteoglycan 4 (meianoma-associated) (CSFG4), mNNA			0.0€+00	2.44		I	2949
Homo sepiens KIAA0054 gene product; Helicase (NIAA0054), ITINIAA	3 NT	7661883 NT	0.0€+00	0.98		_ [	294
Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mKNA	3 NT	7661883	0.0Ё+00	0.98		Т	2946
DKFZp586G0621_r1 586 (synonym: hute1) Homo saptens CDNA clone DKFZp500G0021	EST_HUMAN	0.0E+00 AL047599.1	0.0E+00	1.19	1	П	2947
Homo sepiens serine/threonine kinase 9 (\$189) mixiva		4507280 NT	0.0€+00	254	٦	П	294
Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF 141) mixiva		4503470 NT	0.0€+00	74.83		П	2932
Homo septens eukaryotic translation elongation factor i appia i (CCC IAI) ITINIA		4503470 NT	0.0E+00	74.83	29122	П	2932
Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) ITININA, complete cos		0.0E+00 AF152303.1	0.0E+00	1.13			2931
	T	Y10658.1	0.0E+00 Y10658.1	6.12		1	2930
Novel human mRNA from chromosome 1, which has similarities to ball a genes	N <sub>1</sub>	0.0E+00 AL096857.1	0.0E+00	3.42	٦	П	2929
	NT	D50657.1	0.0E+00 D50657:1	30.49			2926
Homo sapiens gamma-cytopiasmic acun (ACTOP) pseudogene	N <sub>1</sub>	D50657.1	0.0E+00 D50657.1	30.49		П	2926
Human transglutaminase mitro, complete cus		M98478(1	0.0E+00 M98478	15.94	29111	16099	2921
Homo sapiens zinc finger protein 221 (ZNF221), mKINA		7019584 NT	0.0≌+00	1.3	29110	16097	2919
Top Hit Descriptor	<u> </u>	No.	.(Top) Hit BLAST E Value	Expression Signal	ID NO:	NO:	SEQ ID
	Top Hit	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Most Similar				Probe

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Single Exon Probes Expressed in Placenta

			Γ			2	21.0
Homo saplens heat shock 70kD protein 1 (HSPA1A), mRNA	NT					Т	
Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA	IN E	5579469 NT			29303	٦	2110
Homo sapiens membrane-bound aminopepitidase r (Anr Er 2) gene, complete cus	NT	AF195953.1	0.0E+00			ı	3109
Homo sepiens semenogelin i (SEWGT) mriva	ZNT	4506882 NT	0.0€+00	0.68	8 29292		3102
Human displacement protein (CCAA ) mixiva	ZT	0.0E+00 M74099.1		1.29	29285	3 16269	3093
Homo sepiene chromosome 21 segment HSZ1CV40	Z-1	0.0E+00 AL163246.2	0.0E+00	0.61	7		3091
Homo sapiens intersectin short isotorm (11 SN) minima, cumplete cos	<u>4</u>	0.0E+00 AF114438.1		1.17	3 29264		3067
ıla	3	0.0E+00 AF114438.1		1.17	3 29263	П	3067
Homo sepiens calcium charne, voltage-dependent, gamina supunit s (CACINGS), Illinina	S NT	6729765 NT	П			П	3059
Homo sapiens calcium channel, voltage-depandent, gamma subunit o (CACNICA), ITINIA	SNT	5729755 NT	0.0⊑+00	24		П	3059
PAC CLONE DJ1168D11 FROM 7P21-P22, COMPLETE SEQUENCE;	EST_HUMAN	0.0E+00 AW612526.1	0.0€+00	1.92	4 29253	16234	3058
handened NCI CCAP Kid11 Homo segiens cDNA cone IMAGE:2954055 3' similar to TR:060407 060407	SINI	1M C/7700/	0.05+00	1.85	3 29252	16233	3067
Homo copiers (1/4 40737 gene product) (K1440737) mRNA	2 2	0.0E+00 AB004884.1	0.0 €+00			Г	3047
Homo sapiens prospero-legated rolliewood i (r NOCI) iii was	8 Z T	4506118 NT	0.0€+00		29244	16222	3046
Homo sapiens neuropuin 2 (NRF2) gene, compare cus, arematively spiroco	Z,	0.0E+00 AF281074.1	0.0E+00		29243	16221	3045
	NT	0.0E+00 AF281074.1	0.0€+00	0.71	29242		3045
q143f09.x1 Soares_testis_NH1 Homo sapiens curva cione invacione invacione	EST_HUMAN	0.0E+00 A1149880.1	0.0€+00	1.44		П	3038
Homo sapiens immunoglobulin-like transcript TC variant 4 (ILI IC) geria, excit o	NT	0.0E+00 AF106275.1	0.0€+00	9.6		П	3024
Homo sapiens mRNA for KIAA1208 protein, partial cos	NT	0.0E+00 AB033034.1	0.0E+00			П	3022
Homo septens neuroxin III (NKXN3) mRNA	7 NT	4758827 NT	0.0⊑+00	1.51	29218	П	3019
Homo sapiens melanoma entigen, family 6, 4 (MAGEB4), filking	4 NT	4505084 NT	0.0E+00	3.91	29212		3011
	4 NT	4505084 NT	0.0E+00	3.91	29211		3011
Q9/LN1 CG17293 PROTEIN.:	EST_HUMAN	0.0E+00 BF110702.1	0.0E+00	1.29	29200	16178	3003
Q8VLN1 CG17283 PROTEIN.;	EST_HUMAN	0.0E+00 BF110702.1	0.0E+00	1.29	29199	16178	3003
(MLL14) TIKNA  Transport NCI CGAD 1:024 Home septens cDNA clone IMAGE:3597028 3' similar to TR:Q8VLN1	NT	5174574 NT	0.0E+00	4.93	29198	16175	2999
Homo sepiens myeloid/lymphoid or mixed-lineage leukernia (trithorex (Drosophia) homolog); translocated to, 4					Т	$\neg$	
Homo sapiens mysiciallymphoid or mixed-linesgo isuksmis (tribbinax (tribbinian) indindrey), demonstrated by the (MLLT4) mRNA	NI NI	5174574 NT	0.0E+00	4.93	29195	16175	2999
Homo sapiens KIAA0100 gene product (NIAA0100), mknA	NT	7861903 NT	0.0E+00	3.31	29194		2998
Homo saplens KIAA0100 gene product (KIAA0100), mKNA	NT	7661903 NT	0.05+00	3.31	29193	16174	2998
Homo septens mRNA for KIAA1508 protein, perual cos	NT	0.0E+00 AB040941.1	0.0E+00	6.2	29190	16171	2995
Top Hit Descriptor		Top Hit Acession No.		Expression Signal	ORF SEQ ID NO:	SEQ ID	SEQ ID
	Top Hi		<u> </u>				
	0 LY011 1000	9.6					

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Single Exon Probes Expressed in Placenta

(SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	NT	4502098 NT	0.0E+00	1.92	29485	2 16466	3292
Homo sapiens nucleotar phosproprotein ozo (NEWI) ilinxiva, compare cas	N	0.0E+00 M28693.1	0.0E+00	4.54	29482	16462	3288
Homo sapiens interieukin 1 receptor, type I (L-IX-I) mixina		4504658	0.0E+00		29464	16444	3270
Homo saplens neurezin III (NRXN3) mRNA	NT	4758827	0.0€+00	1.39	29466		3262
Homo sepiens neurexin III (NEXN3) mRNA	NT	4758827	0.0E+00	1.39			3262
1088983/ NCI_CGAP_F728 Homo sapiens cunva cione invalve: 2233370 3 stituet to SW 17730_5760 P63987 RAS-LIKE PROTEIN RASD ;	EST_HUMAN	0.0E+00 A1685950.1	0.0E+00	1.01	29444	16426	3252
H. sapiens mRNA for gamma-glutamyrransrerase	N-1	X98922.1	0.0E+00	5.36	29442	16424	3250
H.saplens mRNA for gamma-guuamyuransrerase	NT	0.0E+00 X98922.1	0.011+00	5.36			3250
wu12h10 X1 NCI_CGAP_GC8 Homo sapiens cuna done invage 2010000 3	EST_HUMAN	0.0E+00 AI968036.1	0.0E+00	1.22			3245
601878507F1 NIH_MGC_55 Hamo sapiens cDNA cione IMAGE:4107433 5	EST_HUMAN	0.0E+00 BF243336.1	0.0E+00	0.93		П	3244
ye32f03.e1 Strategene lung (#33/210) Homo sapiens culvia cione imalse: i 1 #33 3 strilleti w of 32500 et 52659 BASIC PROTEIN, 23K - ;	EST_HUMAN	0.0E+00 T94870.1	0.0€+00	25.61	29415	16403	3229
Homo sapiens mixing for Kinggord protein, partial cus	NT	0.0E+00 AB011121.1	0.0≣+00	1.05	29408	16396	3222
Homo sapiens mRNA for KIAAOOA9 protein, partial cos	NT	0.0E+00 AB011121.1	0.0E+00	1.05	29407	16396	3222
Human territin heavy chain mknva, complete cos	NT	0.0E+00 L20941:1	0.0⊞+00	20.63	29404	16393	3219
Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	NT	4826783 NT	0.0E+00	3.61	29395	16384	3210
χ92h07.x1 Sceres_NFL_T_GBC_S1 Homo septens cD/NA cione IMA/GE.Z004/33 3 stimust to SW.RNP_HYDHY P00877 RIBONUCLEASE PANCREATIC :	EST_HUMAN	0.0E+00 AW188146.1	0.0E+00	1.19	29368	16362	3187
Homo sapiens directory receptor-like protein (OLFR 42D) gene, OLFR 42D-9110 tillete, petital case	NT	0.0E+00 AF042075.1	0.0€+00	1.29	29362		3182
Homo septens KIAA0469 gene product (KIAA0469), mKNA	NT	7662139 NT	0.0€+00	3.92			3181
Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	NT	0.0E+00 AF1497/3.1	0.0⊑+00	10.17			3176
Homo sapiens SW I-SNF complex protein p270 mRNA, partial cos	NT ·	0.0E+00 AF265208.1	0.0€+00	4.71		П	3175
Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cas	NT .	0.0E+00 AF064589.1	0.0€+00	1.75	29340	П	3155
Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds	NT	0.0E+00 AF199355.1	0.0€+00	1.92	1	Ţ	3151
Human germline gene 16.1 for ig lambda L-chain C region (IgL-C15.1)	NT :	X03529.1	0.0E+00 X03529.1	3.23	29333	- 1	3145
Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA	NT (	4504684 NT	0.0E+00	3.78	29313	1	3124
complete cds; and L-type calcium channel a>	NT	0.0E+00 AF198779.1	0.0E+00	2.21		162298	3122
JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,							
Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,	·					Т	
Homo sepiens putative transcription factor CR63 (CR53) mRNA, partial cds	TIN	0.0E+00 AF017433.1	0.0E+00	1.88	29309	Т	3119
	NT	0.0E+00 AL359403.1	0.0E+00	7.27		16290	3114
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exon SEQ ID NO:	Probe SEQ ID NO:
		9.19					

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_	_		_	_		_	_	_	_			_		_		_		_	$\neg$	_			_	_	-	_	_		_	_	
3492	3483	3441	3428	3421	3419	3416	3416	3413	3413	3412	3412	3404	3401	3388	3377	3364	3363	3348	3348	3338	3335		3334	3326	3320	3308	3308	3300	3298	3298	Probe SEQ ID
Т	Т	16609	16596	16590	16588	16585	16585	16582	16582	16581	16581	16574	16571	16558	16549	16536	16535	18464	18464	16511	16508		16507	16499	16493	16482	10482	16474	16472	16472	Exen SEQ ID NO:
	29697	29627	29612	29606	29604	29802	29601	29599	29598					29573	29563		29549		29535	29527	29524			29517	29610	29504	29503	29495	29494	29493	ORF SEQ ID NO:
_	10	0.67	0.79	1.22	11.92				1.03				3.14	0.72	1.42	0.95	3.56	1.34	1.34		0.95		10.18	1.01					0.76	0.78	Expression Signal
				Γ	Γ				Γ	Γ				0.0E+00	0.0 €+00	0.0E+00		0.0E+00	П					0.0E+00					0.05+00	0.0E+00	Most Similar (Top) Hit BLAST E Value
7706239	0.0E+00 AU123664.1	0.0E+00 A1632569.1	0.0E+00 BE778039.1	0.0E+00 AB040940.1	0.0E+00 AF111163.1	4602682 NT				AF12839	0.0E+00 AF128393.1	0.0E+00 AW955400.1	0.0E+00 AI589294.1	4885312 NT	7657038 NT		0.0E+00 AF265208.1	4502014 NT		0.0E+00 AF055084.1	0.0E+00 AF019413.1		0.0E+00 M65189.1	4507720 NT	,	AF286598.1	0.0E+00 AF286598.1	0.0E+00 AA774783.1	4758055 NT	4758055 NT	Top Hil Acession No.
	EST_HUMAN	EST_HUMAN	EST_HUMAN	2	Z	2NT	2 N T	32	32	Z	NT	EST HUMAN	EST_HUMAN	2 NT	BNT	4NT	Z	NT	NT	NT	NT		3	NT	NT	N <sub>1</sub>	NT	EST_HUMAN	NT	NT	Top Hit Database Source
Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA		ZING FINGER PROTEIN.	BU1404989T I NIT JWO CO F TOTAL SERVICE STATE IMAGE 2205279 3' striller to TR 091929 091929	TOMO Septembrilliano 67 Hamper Sport Police Comp. (NACCE: Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sport Sp	Homo sapiens pyrin (METV) Berie, complete cue	9	Homo sapiens caspase o, epopularicancia cyarana processa (CASPA) mRNA	Thomo septems recorded a specific related exetains probase (CASPS) mRNA	nonino sapiens noninorany qui eguiared near trimor associated kinese (HUNK) mRNA	Homo sapiens (cionnerase reverse se uniscriptase (TEX.) gene, como e e			188108.22 NCI_CQAP_Pan1 Homo septens cunA cione IMAGE.2222333 3 stimular to 3 W. P. 17. 17. 17. 17. 188108.22 NCI_CQAP_Pan1 Homo septens cunA cione indexed 2222333 3 stimular to 3 W. P. 17. 17. 17. 17. 17. 17. 17. 17. 17. 17	Homo sapiens G protein-coupled receptor 24 (GFRC4), rinsing	Hamo sapiens death receptor to (UKO), mixivix	Hamo sapiens hypothetical protein Fulzooso (Fuzzooso), mining	Hamo septens SW -SNr complex protein p2/0 mr.in-, parual cas	Homo sapiens A kinase (PKKA) andrior protein I (ANAT I), illuvia	Homo saplens A kinase (MKKA) andnor protein 1 (MKKA) monif	Homo sapiens very large G-protein coupled receptor-1 (VLGK1) mKNA, complete cas	(Bf), and complement component C2 (C2) genes,>	Homo seplens HLA class III region containing tenescin X (tenescin-X) garia, pariai cus, o your invirier 1904 a l hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B	Human connexin 43 processed pseudogene	Homo sapiens titn (TTN) mRNA	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) MKNA	Homo capiens angiostatin binding protein 1 mkNA, complete cas	Homo sapiens angiostatin binding protein 1 mKNA, complete cas	ae87b11.s1 Stratagene schizo brain S11 Homo septens cDNA clone IMAGE:9/1133 3	Homo sapiens CREB binding probin (Rubinstain- layor syndrome) (CREDOT) IIINNA	Homo sapiens CREB binding protein (Rubinstein- I ayol syndrome) (CREBBE)	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

1	1					].	
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3493	3 16660	29672	1.26	0.0€+00	0.0E+00 AF211189.1	TN	Homo sepiens T-type celcium chennel alpha1 suburit Alpha1I-a Isoform (CACNA1I) mRNA, complete cds
3498		٦	0.94	0.0E+00	0.0E+00 AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Hamo sapiens cDNA
3511	П	29687	2.02	0.0E+00	2401	TIN	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3511	╗		2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3512	П	$\neg$	0.82	0.0⋿+00	4502398 NT	4	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
	П						Homo saplens leukocyte Immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2),
3514	4 16680	29690	2.35	0.0€+00	5803067 NT		mRNA
3523			3.08		0.0E+00 AF110763.1	NT .	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3528	$\overline{\ }$		2.46		7657038 NT	NT	Homo sapiens death receptor 6 (DR6), mRNA
3 8 3		20708	A D	י טפילטא מטיישט י	KO23BO 1	T	Bacterlophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and incC Incompatibility determinants
3535	Т	1	1.38	0.0€+00	7427522 NT	TN	ne phosphatase, receptor ty
3538	٦		1.83	0.0€+00	4557748 NT	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3544	4 16709	29719	4.17	0.0E+00	0.0E+00 Al935159.1	EST HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo saplens cDNA clone IMAGE:2484819 3" similar to TR:073634 073834 NEURAL CELL ADHESION MOLECULE.;
			i				wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634
3544	16709		4.17	0.01	0.0E+00[Al935159.1	EST HOMAN	MEDIAN CELL DUTILITATION MODELLE TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
3548	8 16713	29725	1.91	0.0E+00	0.0E+00 AJ278120.1	NT	Homo saplens mixIVA for purative anxyrin-repeat containing protein (UKFT)
3555	5 18720		5.38	0.011+00	6552332	Z	Homo sapiens vios r.b. murine osteosercome viral encogene nomelog (r.c.o.), mr.v.v.
3666	5 16720	29735	5.38	0.011+00	6552332		Homo sapiens v-los FBJ murine osteosercoma virai oncogene nomolog (FOS), minva
3560	16725	29741	1.41	0.0E+00	0.0E+00 M14123!1	NT	Human endogenous retrovirus HERV-K10
3566		29747	5.78		0.0E+00 U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3574		29765	2.67		0.0E+00 AF045452.1	NT	Homo sepiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3574	4 16739	29756	2.57	0.0€+00	0.0E+00 AF045452.1	NT	Homo sepiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3582	16747	29765	1.18		0.0E+00 AF2318:22.1	NT	Homo sapiens chromosome 21 unknown mRNA
3594			3.29		0.0E+00 BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Hamo sepiens cDNA clone IMAGE:3051373 5
3594		29774	3.29		0.0E+00 BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo septens cDNA clone IMAGE:3051373 5
3597	16761	29777	1.04	0.0≣+00	4826795 NT	NT	Homo capiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3600		29780	0.8	0.0E+00 O14867		SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAZ303)
3803	)3 16767		68'0		0.0E+00 AI384007.1	EST_HUMAN	1635g12.x1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000488 CD0498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3621	П		0.6		0.0E+00 AB032979.1	NT	Homo sepiens mRNA for KIAA1153 protein, partial cds
3621	16785	29802			0.0E+00 AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds

ြ	ü	ပ	ယ	G)	υį	ß	3	အ	ω	ω	y.	္အ	ω	ω	3	3;	3	3	ی	۱	ပ္ထ	မ္က	ی	ပ္က	ڀ	္ထ	ပ္က	ပ္ထ	မ္က	ပ္ထ	١	Probe SEQ ID NO:
П	7	3767	3767	П	3761	3759	3757	3741	3737						3707		3704	3704							П	٦	П	3631	3630		3623	
16931	16931	16928	16928	16922	16922	16920	16918	16902	16898	16881	16881	16874	16872	16868	16868	16866	16865	16865	16843	16842	16835	16830	16828	16828	16807	16806	16797	16795	16794	16787	16787	SEQ ID
29936	29935	29933	29932	29924	29923	29922	29920		29901	29887	29886	29879	29876	29872	29871		29869	29868	29850	•		29841	29838	29837	29821	29820		29812	29811	29804	29803	ORF SEQ ID NO:
	1.95	32.49	32.49	5.16	6.18	1.06	3.98	6.29	236	0.74	0.74	68.0	68.0	0.76	0.76	0.89	0.69	0.59	7.66	1.28	4.28	1.06	0.97	0.97	1.16	1.34	1.17	4.48	1.45	0.68	0.68	Expression Signal
П				Γ						0.0€+00	0.0Ё+00	0.0€+00												0.0€+00				0.0€+00			0.0€+00	Most Similar (Top) Hit BLAST E Value
0.0E+00 AL163204.2	0.0E+00 AL163204.2	0.0E+00 AA852743.1	0.0E+00 AA852743.1	0.0E+00 AF124250.1	0.0E+00 AF124250.1	0.0E+00 AB007836.2	0.0E+00 AB026542.1	7669491 NT	0.0E+00 D87327.1	4557752 NT	4567762 NT	7662319 NT	4826763 NT	0.0E+00 AW664693.1	0.0E+00 AW664693.1	4826967	0.0E+00 BF672054.1	0.0E+00 BF672054.1	0.0E+00 BF676393.1	0.0E+00 AF118846.1	0.0E+00 AW852217.1	6325463 NT	6997248 NT	6997248 NT	0.0E+00 AB040909.1	0.0E+00 AL133204.1	0.0E+00 AF078868.1	4506884	0.0E+00 AV701869.1	0.0E+00 AA456282.1	0.0E+00 AA456282.1	Top Hit Acession No.
NT	N-1	EST_HUMAN	EST_HUMAN	NT	NT	Z	NT	NT	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	3	EST_HUMAN	EST_HUMAN	EST_HUMAN	3	EST_HUMAN	l i	NT	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	Top Hit Database Source
Hamo seplens chromosome 21 segment HS21C004	Homo sapiens chromosome 21 segment HS21C004	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA cione NHTBCae15g09	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sepiens cDNA clone NHTBCae15g09	Homo captions SH2-containing protein NSp2 mXNA, complete cas	Homo sapiens SH2-containing protein Nsp2 mKNA, complete cds	Homo septens mRNA for KIAA0406 protein, partial cds	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds		Homo sapiens mRNA for G protein-coupled inward rectifier potessium channel, complete cas	Homo sapiens midline 1 (Opitz/BBB syndrome) (MIU1) mKNA	Homo sepiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo saplens KIAA0806 gene product (KIAA0806), mKNA	Homo sepiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mKNA	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3	T_GBC_S1 Homo sapiens cUN	me-binding protein 2 (RBBP2)	602182486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE: 4283643 3				QV0-CT0225-230300-169-e01 CT0225 Homo sepiens cDNA	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA	Homo saplens sal (Drosophila)-like 1 (SALL1), mRNA	Homo sapiens sel (Drosophila)-like 1 (SALL1), mRNA	Homo sapiens mRNA for KIAA1476 protein, partial cds	Novel human gene mapping to chomosome X	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds	Homo sapiens semenogelin II (SEMG2) mRNA	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5	2x89h04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5	2x89h04,r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5	Top Hit Descriptor

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3942	3940	3938	3937	3936	3935	3935	3929	3928	3928	3926	3924	3922	3869	3866	3866	3859	3855	3841	3831	3824	3823	3794	3794	3782	3782	3780	3778	3776	3774	3771	3771	Probe SEQ ID NO:
17101	17099	17097	17098	17095	17094	17094	17088	17087	17087	17084	17083	17081	17028	17025	17025	17019	17015	17000	16991	16984	16983	16955	16955	16943	16943	16941	16939	16937	16935	16932	16932	SEQ ID
30098		30095				30092	30085	30084		30079		30077	30027	30024	30023	30018	30015	30003	29993	29987	29986	28960	28969	28950	29949	29947	28945	28943	29941	29938	29937	ORF SEQ
2.14	15.6	26		1.29		1.05	1.74	236	236	2.36	0.73	1.96	8.94	1.52	1.52	18.03	5.72	0.83	3.23	1.17	1.04	5.42	5.42	1.02	1.02	0.74	1.15	2.37	2.4	0.99	0.99	Expression Signal
0.0E+00		0.0E+00	0.011+00								Г		0.0E+00			0.0€+00	0.0€+00											0.0≝+00			0.0€+00	Most Similar (Top) Hit BLAST E Value
7710148[NI	S78685.1	4758199 NT	AF16249	0.0E+00 Al377699.1	0.0E+00 AF127851.1	0.0E+00 AF127851.1	0.0E+00 AF020091.1	7857468 NT	7657468 NT	AF1797	0.0E+00 AF195658.1	0.0E+00 AF1467; 2.1	4505594 NT		7657065 NT	4508718 NT	7662183 NT	0.0E+00 AB037835.1	7657468 NT	0.0E+00 AA463659.1	0.0E+00 AB004830.1	0.0E+00 AW298134.1	0.0E+00 AW 298134.1	0.0E+00 AB020717.1	0.0E+00 AB020717.1	0.0E+00 O14867	0.0E+00 AB018389.1	5729928	AW851714.1	0.0E+00 AB0023\$1.1	0.0E+00[AB0023\$1.1	Top Hit Acession No.
N	N <sub>T</sub>	NT	Z	EST_HUMAN	NT	NT	NT	NT	NT	NT ,	NT	NT	NT	NT	NI	NT	3	NT	NT	EST_HUMAN	3	EST_HUMAN	EST_HUMAN	NT	NT	SWISSPROT	NT	NT	EST_HUMAN	NT	NT	Top Hit Database Source
nomo saprens meny opo pinang process z (wico: z), miliano	Homo seplens ATP-sensitive inwardly rectifying K-chennel subunit (KCNJ6/BiR1) gene, complete cds	Homo septens desmoplatin (UFI, UFII) (USF) IIINVA	Homo sapiens protocatarient peut 3 (FCDT-retas) III(VF, Collipted vas		Gorilla gorilla offactory receptor (GGO/1) gane, parua cos	Gorilla gorilla olfactory receptor (GGO71) gene, parties cds	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cus	Homo saptens similar to rat integral membrane glycoprotein FOW121 (FOW121C1), months	Homo sapiens similar to ret integral memorane glycoprotein POWIZI (POWIZILI), IIIVVV	Pan troglodytes directory receptor (P I KZUB) gene, partial cas		Homo sapiens soluble neuropilin-1 mkNA, complete cas	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (FAIZ) mixiva	Homo septens wets evian erythroblestosis virus E26 oncogene related (ENC), mixiva	Homo sapiens viets avian erythrobiastosis virus E26 ancogene related (ENG), mixiva	Homo sapiens ribosomal protein S2 (RFS2) mRNA	Homo sepiens KIAAU559 gane product (KIAAU506), mKINA	Homo saplens mRNA for KIAA1414 protein, partial cos	Homo sapiens similar to rat integral memorane glycoprotein r Ownizi (r Ownizi), integral	az06g01.r1 Soares_NHMPu_S1 Homo capiens cDVA ctone invisice: 12490 3 similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, HIBA 1131-1131-1131-1131-1131-1131-1131-113	Human gene for Type XIX collegen at chain, excit of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	ULH-BWO-gis-e-12-0-UI:s1 NCI_CGAP_Subo Homo saptens curva cione invade 2/1-3-3022 3	UI-H-BWO-gls-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cunA cione INA-GE-2733022	Homo sapiens mRNA for KJAA0910 protein, partial cds	Homo saplens mRNA for KIAA0910 protein, partial cds	TRANSCRIPTION REGULATOR PROTEIN BACHT (BTB AND CNC HUMULUG 1) (HAZSUS)	Homo sapiens mRNA for KIAA0786 protein, partial Cds	Homo saplens matrix metalioproteinase 24 (membrane-inserted) (MMr 24), mrvva	MR2-CT0222-281099-005-e05 C10222 Homo sepiens CUNA	Human mRNA for KIAA0333 gene, partial cds	Human mRNA for KIAA0333 gene, partial cds	Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

SEQ ID	ORF SEQ ID NO:	Expression Signed	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
I	30089	1.78	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
$\Box$		1.62	0.0€+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
7		1.62	0.0E+00	AF069631.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
П	$\neg$	1.02	0.0€+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2.complete and partial cds
П		1.02	0.0Ё+00	AB001623.1	NT	Homo sapiens gene for TMEM1 and PWP2,complete and partial cds
П		0.9	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
		6.98	0.0+∃0.0		NT	Homo saplens chromosome X open reading frame 5 (CXORF5) mRNA
П		6.96	0.0€+00		NT	Homo sapiens chromosome X open reading frame 6 (CXORF5) mRNA
		4.85	0.0€+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
0 17118		1.12	0.0E+00		NT T	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
	30124	1.23	0.0E+00	4826783	NT.	Homo capiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
		1.44	0.0€+00	AF012615.1	NT	Homo septens femillel mental retardation protein 2 (FMR2) gene, exon 11
	30128	2.87	0.0€+00	4759171	3	Homo sepiens SC35-interacting protein 1 (SRRP129), mRNA
9 17127		0.77	0.0E+00	AF099117.1	NT	Homo saplens emphiphysin gene, partial cds
		3	200	A 1864797 4	TOT LIMAN	wk01f01,x1 NCI_CGAP_Lym12 Homo septens cDNA clone IMAGE:2411065 3" similar to TR:043340 043340 R28830 2 :contains element PTR7 repetitive element :
Т	T	1.03	0.0E+00	AL163248.2	3	Homo sepiens chromosome 21 segment HS21C048
		18.17	0.0E+00	06742	TN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
		1.33	0.0E+00	AL040338.1	EST_HUMAN	DKFZp434N0413_r1 434 (synonym: htes3) Homo sepiens cDNA clone UKFZp434N0413 5
	30158	1.0	0.0€+00		3	Homo septens AP1 gemma subunit binding protein 1 (AP1GBP1), mKNA
	30169	1.9	Γ		N,	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mkNA
	30161	3.84			NT	
		2.26	0.0E+00		NT	
	30164	0.97	0.0E+00	AF149412.1	NT	Homo septens HBP17 heparin-binding and FGF-binding protein gene, complete cos
	30178	2.65	0.0⊞+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mKNA
		1.9		4585642		Homo saplens zinc finger protein (KIAA0412) mRNA
П		5.14	Г	BF365295.1	EST HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
	30193	1.37	0.0E+00	AW888221.1	EST_HUMAN	NXRAS Human matrix tissue expression library Homo sopiana culva cione incyte 1999/2e similar to MARAS. Matrix remodeling associated gene 5
		1.37	0.0⊑+00	1.122888 WA	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
		3.05		AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
П	30204	1.14	Г	U86281.1	NT	Homo sapiens offectory receptor (OR7-141) gene, partial cds
	Probe Exon SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	SEO ID ORF NO: ID ID ID ID ID ID ID ID ID ID ID ID ID	Exon ORF SEQ Express SEQ ID NO: Signal 17102 30089 17105 30102 17109 30109 17109 30109 17115 30117 17115 30118 30121 17121 30122 17118 30122 17118 30122 17118 30122 17125 30121 30122 17125 30130 30121 17139 30140 30140 30169 17145 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 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17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 30169 17168 301	Exon SEQ ID NO: Signal Signal SEQ ID NO: Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Signal Sig	Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Company   Comp	Exon   ORF SEQ   Expression   Clop Hit   Acession   Clop Hit   SEQ ID ID NO:   Signal   NO.   Signal   NO.   Signal   NO.   Signal   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   Source   NO.   NO.   Source   NO.   NO.   Source   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.   NO.

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Table 4
Single Exon Probes Expressed in Placenta

4	4	4	45	4	4	4185	4185	4178	4178	4177	4166	4167	4138	4137	4134	4127	4112	4104	4095	4093	4084	4084	4077	4077	4077	4052	<b>4061</b>	4043	4042	4038	Probe SEQ ID
4208 17357	4207 17356	4206 17355			4184 17344					77 17827	66 17316	67 17308			34 17287	27 17281	12 17268	04 17258		╗	٦				77 17233			П	42 17198	38 17194	B Exam
157 30347	156 30346	155 30345		51 30343	44 30337	35 30328				27 30318	16	08 30304		89 30284	87	1 2	66 30266	58 30258	50				33 30240			08 30218	07 30217		98 30209	94 30206	ORF SEQ
7 4.33	7.08	5 1.26		3 6.02	7 0.64			2.68		1.58	3.22		2.85		0.99	111.8	3 213	2.93	7.25			9.31	8.0			1.03	1.28	1.2	3.47	1.14	Expression Signal
Γ		26 0.0€+00			0.0E+00	3 0.0E+00	3 0.0€+00					6 0.05+0		1 0.0年+00		8 0.0 €+00			П							3 0.0⊑+00					Most Similar (Top) Hit BLAST E Value
0.0E+00 AL096857.1	0 11419297 NT	0 4758807 NT	0.0E+00 AB008625.1	0 4885306 NT	0 4503914 NT	5032026	0 5032026	0.0E+00 AJ277276.1	0.0E+00 AJ277276.1	0.0E+00 AL163203.2	0.0E+00 AJ238617.1	0.0E+00 ABQ15610.1	0.0E+00 U09366,1	0 7662183 NT	0.0E+00 Al657076.1	0 4503470 NT	0.0E+00 AL163268.2	0.0E+00 AL163284.2	0.0E+00 AL163303.2	0.0E+00 M2391011	0.0E+00 AF116195.1	0.0E+00 AF116195.1	0.0E+00 U10991.1	0.0E+00 U10991.1	0.0E+00 U10991.1	0 6360215 NT	0.0E+00 AW580740.1	0.0E+00 BE313146.1	0.0E+00 BE378602.1	0.0E+00 U88281.1	Top Hit Acession
NT	IVT	)7 NT.	Z	NT NA	A N	NT	8 NT	NT	N.T.	NT	ZŢ	NT	NT	BINT	EST_HUMAN	ONT	N.T	Z	NT	NT	NT	NT	Z	Z	NT	5 NT	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	Top Hit Database Source
Novel human mRNA from chromosome 1, which has similarities to BA12 genes	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA	Homo sepieno mRNA for KIAA0287 gene, partial cds	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA	Homo sepiens phosphoribosylglycinemide formyltrensferase, phosphoribosylglycinemide synthetase, phosphoribosylamincimidezole synthetase (GART) mRNA	Homo sepiens retinoblastoma-binding protein 4 (RBBP4) mRNA	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA		Homo sepiens mRNA for repe-2 (repa gene)	Homo sepiens chromosome 21 segment HS21C003	Homo septens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA-48 gene)	Chibrocebus aethiops mRNA for ribosomal protein S4X, complete cds		Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	KIAA0563 PROTEIN.;	Homo saplens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mkina		Homo expicno chromocome 21 segment HS21C084	Homo sapiens chromosome 21 segment HS21C103	Human MHC class II lymphocyte entigen DPw4-beta-2 pseudogene, exon 2	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds	Homo saplens cancer-testis antigen CT10 (CT10) gene, complete cds		Human G2 protein mRNA, partial cds	Human G2 protein mRNA, partial cds	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA	801153727F1 NIH_MGC_19 Homo sepiene cDNA clone IMAGE:3509743 5"	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5	Homo sapiens offactory receptor (OR7-141) gene, partial cds	Top Hit Descriptor

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Table 4

Single Exon Probes Expressed in Placenta

			0.00			Γ	1000
Human apolipoprotein B-100 mRNA, complete cds	NT	J02610.1	0.05+00 J02610.1		30512	1	4398
Homo sapiens chromosome 21 segment HS21C103	TN	0.0E+00 AL163303.2	0.0€+00	0.86		╗	4345
Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	NT	4758199 NT	0.0E+00	8.09	30462		4338
Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	NT	4758199 NT	0.0E+00	8.09	30461	17481	4338
Homo septens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	NT	0.0E+00 AF157478.1	0.0E+00	. 1.2	30443	17455	4312
zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Atu repetitive element;contains element MER35 repetitive element :	EST_HUMAN	0.0E+00 AA401438.1	0.0E+00	11.47	30439	17452	4309
zu68h07.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE;743197.3 similar to contains Alu repetitive element;contains element MER35 repetitive element;	EST_HUMAN	0.0E+00 AA401438.1	0.0E+00	11.47	30438	17452	4309
Homo sapiens mRNA for KIAA1318 protein, partial cds	NT	0.0E+00 AB037739.1	0.0E+00	1.07	30429	17443	4300
Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg Jelly, sea urchin homolog)-like (PKDREJ) mRNA	TN	5174632 NT	0.05+00	235		17432	4287
Homo saplens hypothetical protein FLJ10498 (FLJ10498), mRNA	NT	8922466 NT	0.0E+00	1.55	30412	17423	4278
Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	N <sub>1</sub>	8922468	0.0⊑+00	1.65	30411	17423	4278
UI-HF-BM0-adx-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5	EST_HUMAN	0.0E+00 AW408788.1	0.0E+00	1.12	30410	17422	4277
be51f04.x1 NIH_MGC_10 Homo septens cDNA clone IMAGE:2900095 3' stmiler to SW:THI2_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR;	EST_HUMAN	0.0E+00 AW875698.1	0.0€+00	5.76		17417	4272
Homo saplens nuclear receptor coactivator 3 (NCOA3), mRNA	NT	5729725	0.0E+00	207	30398	17410	4265
601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5	EST_HUMAN	0.0E+00 BE274217.1	0.0E+00	5.89		17404	4259
MR1-HT0707-100500-001-e02 HT0707 Homo sepiens cDNA	EST_HUMAN	0.0E+00 BE184856.1	0.0⊑+00	1	30390		4265
MR1-HT0707-100500-001-e02 HT0707 Homo sepiens cDNA	EST_HUMAN	0.0E+00 BE184856.1	0.0E+00	1			4255
wu04d04.x1 NCI_CGAP_GC6 Homo sepions oDNA clone IMAGE:2515975 3"	EST HUMAN	0.0E+00 Al982597.1	0.0€+00	5.57	30387	17398	4252
wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3*	EST HUMAN	0.0E+00 Al982597.1	0.0E+00	5.57	30386		4252
Homo saplens mRNA for KIAA0895 protein, partial cds	NT	0.0E+00 AB020702.1	0.0E+00	0.85			4244
Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	NT	8922391 NT	0.0E+00	0.91			4238
Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	NT	8922391 NT	0.0€+00	0.91	30372	17384	4238
Homo sapiens semenogelin II (SEMG2) mRNA	NT	4506884 NT	0.0€+00	0.64			4236
Homo saplens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	NT	4503854 NT	0.0E+00	1.32	30370	17381	4234
Homo saplens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	NT	4503854 NT	0.0€+00	1.32		17381	4234
	NT	4826947 NT	0.0€+00	0.7	27374	14319	4227
Homo saplens protein kinase, X-linked (PRKX) mRNA	NT	4826947 NT	0.0€+00	0.7	27373	14310	4227
Homo sapiens DGCR8 (DGCR8) mRNA, complete cds	NT	0.0E+00 AF165527.1	0.0€+00	5.32	30356	17367	4218
ze55e09.r1 Soares retina N254HR Homo sapiens cDNA clone IMAGE.362920 5' similar to contains Alu repetitive element;	EST_HUMAN	0.0E+00 AA018975.1	0.0E+00	0.98		17358	4209
Top Hit Descriptor	Database Source	Top Hit Acession No.	(Top) Hit BLAST E Value	Expression Signel	ORF SEQ ID NO:	SEQ ID	SEQ ID
			Most Similar			E	Disk
Ciligia Exolicitate Expressed in receive	0 EVOIL 1000	Ring.					

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Single Exon Probes Expressed in Placenta

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2497 Human retine CDNA randomly primed sublibrary Homo sapiens CDNA		0.0E+00 W26179.1	0.0E+00	0.69			4574
Homo sapiens ACIN2 gene for alpha-Acunin 2, exon 10		0.0E+00 AJ249765.1	0.0E+00	278			4570
Homo saptens ACTNZ gene for alpha-Actinin 2, exon 10		0.0E+00 AJ249765.1	0.0E+00	278		17708	4570
Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete ods		0.0E+00 AF195953.1	0.0≦+00	6.61		17702	4564
Homo sepiens myosin regulatory light chain interacting protein (MIK), mKNA		7019456 NT	0.0€+00	1.9	30671	17691	4553
Homo sapiens mRNA for KIAA1360 protein, pertial cds		0.0E+00 AB037781.1	0.0€+00	1.2	30648		4522
Homo sepiens chromosome 21 segment HS21C007	NT	0.0E+00 AL163207.2	0.0€+00	1.24			4819
Homo sapiens Xq pseudoautosomal region; segment 2/2	NT	0.0E+00 AJ271736.1	0.0€+00	1.16	30646		4518
Homo sapiens caudal type nomeo box transcription factor 4 (CDX4), mKNA		4885126 NT	0.0€+00	14.1	30645	17656	4517
Homo sapiens KIAA0390 gene product (KIAA0390), mRNA		7662091 NT	0.0E+00	10.05	30631	17644	4505
Homo sapiens KIAA0390 gene product (KIAA0390), mRNA		7662091 NT	0.0E+00	10.05	30630		4505
H.saplens H4/d gene for H4 histone			0.0E+00 X60483.1	1.59	30624		4500
H.saplens H4/d gene for H4 histone		X60483.1	0.0E+00 X60483.	1.59	30623	17640	4500
H.sapiens H2B/h gene	N	Z80780.1	0.0E+00 Z80780.	6.28	30617	17634	4494
H.saplens H2B/h gene		Z80780.1	0.0E+00 Z80780.	6.28	30616	17634	4494
perfiel cds	Z T	L14561.1	0.0E+00 L14561.1	3.62	30611	17630	4490
Homo septems grap jurious process contracts (2009) some formation alternative splice products.	2	0.0E+00(AF (30047.2	0.00	1.08		1/620	4480
Homo sapiens COMPLEMENT COMPONENT CHARGO FROM CONTROL OF ANY		6912281 NI	0.0E+00	10.33	30578	Г	4460
Human G2 protein mRNA, partial cds		U10991.1	0.0E+00 U10991.1	1.08	30573	17691	4451
Human G2 protein mRNA, partial cds		U10991.1	0.0E+00 U10991.1	1.08	30572	17591	4451
Homo sapiens protein kinase C, nu (PRKCN), mRNA		6563384 NT	0.0⊑+00	0.72	30566		4445
Homo saplens protein kinase C, nu (PRKCN), mRNA		6563384 NT	0.0€+00	0.72	30565		4445
(VILLT4) mRNA		5174574 NT	0.0E+00	0.96.0	30550	17568	4428
	NT	U14520.1	0.0E+00 U14520.1	4.58		17584	4424
petitive element	T_HUMAN	0.0E+00 AI189844.1	0.0E+00	2.25		17561	4420
AND SOCIAL Company Approximate Synthesis (Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Comp		N 91.80089	0.00+00	0./1	30545	17560	4419
Homo sapiens low density (poprotein-related protein 2 (LIXYZ), mixtus		6806918 NT	0.0€+00	0.71	30544	П	4419
Homo sapiens F-box protein FbM (FBL4) mRNA, partial ods		0.0E+00 AF174590.1	0.0E+00	5	30537		4410
601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5	EST_HUMAN 6	0.0E+00 BE779039.1	0.0E+00	0.65	29612		4406
PM2-DT0023-080300-004-a08 DT0023 Homo septens cDNA	EST_HUMAN F	0.0E+00 AW936689.1	0.0€+00	0.81	30529	17545	4402
Top Hit Descriptor	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	SEQ ID	Probe SEQ ID NO:
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Table 4
Single Exon Probes Expressed in Placenta

Γ—	П	_		$\Box$	$\neg$	_		ГТ	٦	٦		7	П	$\neg$		Т	7	٦	_						7			Т	<i>σ</i> ,,
4727	4724	4709	4709	4707	4702	4697	4693	4685	4674	4671	4666	4661	4652	4652	4651	4643	4642	4640	4040	4633	4631	4627	4625	4623	4613	4610	4610	4591	Probe SEQ ID NO:
17862	17859	17844	17844	17842	17837	17832	17828	17820	17809	17806	17801	18471	17788	17788	.17787	17779	17778	17776	17776	17769	17767	17763	18470	17760	17750	17747	17747	17728	Exan SEQID
30844	30841	30827	30826			30817	30814	30808	30799	30796	30788	30783	30772	30771	30770	30761	30760	30758	30757	30750		30745		30742		30727	30726		ORF SEQ
11.67	287	15.03	15.03	3.19	1.03	1.84	0.73	59.97	2.17	2.17	20.19	3.18	1.2	1.2	1.02	2.07	1.06	1.3	1.3	0.97	8.47	1.48	2.97	27.37	0.89	0.66	0.65	2.29	Expression Signal
	Г	Ī	0.0E+00			0.0€+00	0.0E+00	0.0€+00	0.0E+00			0.0E+00					0.0€+00			П	П		0.0E+00						Most Similar (Top) Hit BLAST E Value
0.0E+00 AJ245418.1	0.0E+00 AF143314.1	7662091 NT		0.0E+00 L35486.1	4502556 NT	4503098 NT	4505016 NT	4503470 NT	5464175 NT	0.0E+00 AF152337.1	0.0E+00 AF208161.1	6005973 NT	0.0E+00 AF111163.1	0.0E+00 AF111163.1	0.0E+00 S78684.1	0.0E+00 AF108830.1	4758467	0.0E+00 AJZ78120.1	0.0E+00 AJ278120.1	0.0E+00 AW381670.1	0.0E+00 AL163207:2	0.0E+00 AF016050.1	8051619 NT	0.0E+00 AW084984.1	0.0E+00 M14123 1	0.0E+00 T10233.1	0.0E+00 T10233.1	0.0E+00 AFZ00629.1	Top Hit Acession
Z	NT	NT	NT NT	NT	BNT	8 NT	6 NT	ONT	5 NT	N	NT	3NT	3	NT	3	NT	7 NT	NT	NT	EST_HUMAN	NT	NT	NT	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	NT	Top Hit Database Source
complex)		Homo septens KIAA0390 gene product (KIAA0390), mKIVA	Homo sapiens KIAA0390 gene product (KIAA0390), mKNA	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA	Homo saplens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mKNA	Homo sepiens zinc finger protein 211 (ZNF211), mRNA	Homo sepiens protocedherin gemma C3 (PCDH-gemma-C3) mRNA, complete cos	Homo sepiens syncytin precursor, mRNA, complete cds	Homo sapiens zinc finger protein 185 (ZNF 185), mRNA	Homo sepiens pyrin (MEFV) gene, complete cds	Homo sapiens pyrin (MEFV) gene, complete cds	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIK1) gene, exon	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	Homo saplens G protein-coupled receptor 50 (GPR50) mRNA	Homo sepiens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens mRNA for putative ankyrin-repeat containing protein (UK+1)	PM1-HT0305-101199-002-d03 HT0305 Homo sapiens dUNA	Homo sapiens chromosome 21 segment HS21C007	Homo sapiens vascular endomeliai cei grown iadur ioo revehormembliiin (vicor ioo) iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, voi iinviso, 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Table 4
Single Exon Probes Expressed in Placenta

CONTROCTOR AND AND CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	TOMAN	0.0E+00 BE2/8/30.1		1.18		17943	4810
ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cUNA clone IMAGE:08310 5		0.0E+00 T56945 1		2.83	28401		4806
ya83g04.r2 Stratagene fetal spieen (#937205) Homo sapiens cUNA ctone IMAGE:58510 5		0.0E+00 T56945!1		2.83	26400	13367	4806
Homo septens butyrophilin, subfamily 2, member A2 (BTN2A2), mKNA		6453812 NT		2.06			4804
Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	NT	6453812 NT		2.08			4804
		0.0E+00 M74089.1		3.06	30925		4801
Homo sapiens mRNA for KIAA1399 protein, partial cds	NT	0.0E+00 AB037820.1		2.72		17936	4800
Homo sepiens mRNA for KIAA1399 protein, partial cds	NT	0.0E+00 AB037820.1		2.72			4800
Harno sapiens chromosome 21 segment HS21C078	N <sub>1</sub>	0.0E+00 AL163278.2		1.3	30922	17934	4799
Homo septens chromosome 21 segment HS21C078	YT.	0.0E+00 AL163278.2	0.0E+00	1.3	30921	17834	4799
region	Z-T	0.0E+00 AF086641.1	0.0E+00	1.9		17929	4794
Homo capiens truncated tenescin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint							
	EST_HUMAN	0.0E+00 AA418246.1	0.05+00	1.37	30911		4788
	EST_HUMAN	0.0E+00 BE081527.1	0.0E+00	1.93	30910	17922	4787
Human endogenous retrovirus type K (HERV-K), gag, poi and env genes	3	0.0E+00 Y18890!1	0.0E+00	17.22	30902		4781
Homo sepiens mRNA for KIAA1047 protein, pertial cds	N-T	0.0E+00 AB028970.1	0.0E+00	0.86	30896		4776
Homo sapiens mRNA for KIAA1047 protein, pertial cds	3	0.0E+00 AB028970.1	0.0E+00	0.98	30895	17911	4776
Mus musculus E-cedherin binding protein E7 mRNA, complete cds		0.0E+00 AF167441.1	0.0€+00	2.62			4766
Homo sepiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds	T	0.0E+00 AF1538,19.1	0.0E+00	1.42	30882	17900	4765
Homo sepiens inwerdly-rectifying polassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds	N.T	0.0E+00 AF153819.1	0.0€+00	1.42	30881	17900	4765
Homo sapiens keratin 18 (KRT18) mRNA		4557887 NT	0.0€+00	31.32		П	4764
Homo sepiens keralin 18 (KRT18) mRNA		4557887 NT	0.0€+00	31.32			4764
Novel human gene mapping to chomosome 1	NT	0.0E+00 AL162331.1	0.0€+00	1.06			4761
Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	NT	0.0E+00 AF195658.1	0.0€+00	0.69	30870		4756
	NT	0.0E+00 AB037521.1	0.0€+00	1.95		17889	4754
Homo saplens chromosome 21 segment HS21C100		0.0E+00 AL163300.2	0.0€+00	4.83			4753
Homo sepiens cyclophilin-related protein (NKTR) gene, complete cds	3	0.0E+00 AF184110.1	0.0€+00	1.33	30868		4752
	NT	0.0E+00 AL163234.2	0.0€+00	3.31		- 1	4751
Homo septens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA		7657410 NT	0.0E+00	1.98			4749
2p18g08.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3	EST_HUMAN	0.0E+00 AA174072.1	0.0€+00	1.68		П	4746
Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	NT	0.0E+00 AJ245418.1	0.0€+00	11.67	30845	17862	4727
Top Hit Descriptor	Top Hit Datebase Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	SEQ ID	Probe SEQ ID NO:

7/7/S/10 OM

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Table 4

Single Exon Probes Expressed in Placenta

Г	7			_		_	_			Т	7	_	_		_			$\neg$		$\neg$			П	7	_	7	7	7	_	_	- 1	
}	4982	4977	4976	4974	4973	4972	4970	4967	4966	į	4925	4924	4913	4911	4907	4886	4886	4882	4872	4872	4856	4851	4846	4844	4842	4838	4838	4835	4830	4830	4814	Probe SEQ ID NO:
	18111	18106	18105	18103	18102	18101	18099	18096	18095		18055	18054	18043	18041	18037	18016	18016	18012	18005	18005	17989	17984	17979	17977	17976	17971	17971	17868	17983	17963	17947	Exon SEQ ID NO:
	31088	31082	31081	31079	31078	31077	31075	31072						31031	31025	31001	31000	30998	30988	30987	30977	30972	30968	30987	30965	30960	30959	30956	30952	30951	30932	ORF SEQ ID NO:
	3.41	1	9.88	4.54			1.09	1.95	2.87		0.64	1.33	2.01	1.18	1.29	0.82			0.74	0.74	1.29	1.15	1.73	1.05	2.07	3.07	3.07	50.79	0.95	0.95	1.13	Expression Signal
	0.0€+00	0.0100	Г	0.0€+00				0.0E+00		T							0.0E+00		0.0E+00	0.0€+00			0.05+00	0.0€+00						0.0E+00		Most Similar (Top) Hit BLAST E Value
	8923080	0.0E+00 P52740	4885048	4503768 NT	0.0E+00 AF097416.1	0.0E+00 AF084479.1	0.0€+00 X87206.1	4505394 NT	0.0E+00 AF240786.1		0.0E+00 AW335253.1	0.0E+00 M55189.1	0.0E+00 AF083242.1	0.0E+00 AF303134.1	0.0E+00 AW 444837.1	7019320 NT	7019320 NT	0.0E+00 AF026801.1	7304922 NT	7304922 NT	0.0E+00 AL098E57.1	0.0E+00 U07.583.1	7662181 NT	7682479 NT	0.0E+00 AF184110.1	0.0E+00 M69197.1	0.0E+00 M69197.1	0.0E+00 M80902.1	5729817 NT	5729817 NT	0.0E+00 BE390050.1	Top Hij Acessian No.
3	ONT	SWISSPROT		BINT	NT	NT	NT	4NT	3	и	EST HUMAN	NT	NT	NT	EST_HUMAN	TNO	ONT	ZI	2 NT	2 NT	NT	NT	NT	9 NT	TN	NT	NT	NT	7 NT	7 NT	EST_HUMAN	Top Hit Database Source
Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments: and Tcr-C-alpha gana, exons 1-4	Hamo saptens hypothetical protein FLJ20073 (FLJ20073), mRNA	ZINC FINGER PROTEIN 132	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa	Homo saplens nidogen (enactin) (NID) mRNA		Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	xz89d06x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:2871371 3'	Human connexin 43 processed pseudogene	Homo sepiens HSPC024-iso mRNA, complete cds	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds	UI-H-BI3-ajw-c-04-0-UI.st NCI_CGAP_Sub5 Homo septens cDNA done IMAGE:2733294 3"	Homo saplens proteinx0008 (AD013), mRNA	Homo septens proteinx0008 (AD013), mRNA	Homo sepiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28		Homo sepiens bromodomain adjacent to zinc finger domain, 28 (BAZZB), mRNA	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds	Homo sepiens KIAA0563 gene product (KIAA0563), mRNA	Homo sapiens KIAA1084 protein (KIAA1084), mRNA	Homo sapiens cyclophilin-related protein (NKTR) gene, complets cds	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete ods	Humen AHNAK nucleoprotein mRNA, 5' end	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA		601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'	Top Hit Descriptor

MO 01/21272 PCT/US01/00663

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37			0.00		Γ	1	0002
Homo sepiens hypothetical protein FLJ11190 (FLJ11190), mRNA	N T	TN BCCC68	0.0E+00	1 1	Ī	Т	8083
Homo sapiens KIAA0806 gane product (KIAA0806), mRNA	TN	7662319 NT	0.0E+00	0.71		٦	5073
Homo sapiens chromosome 21 segment HS21C084	NT	0.0E+00 AL163284.2	0.0⋿+00	1.28	31169	18195	5087
Homo sapiens glypican 4 (GPC4) mRNA	NT	4504082 NT	0.0€+00	1.30	31165	18177	5049
Homo sapiens glypican 4 (GPC4) mRNA	NT	4504082 NT	0.0E+00	1.39	31154	18177	5049
Homo sepiens mRNA for KIAA0287 gene, pertiel cds	NT	0.0E+00 AB006825.1	0.0⊑+00	7.67	31148		5043
Homo sapiens mRNA for KIAA0287 gene, partial cds	NT	0.0E+00 AB006625.1	0.0≣+00	7.67	31147	18171	5043
Human mRNA for transcription factor AREB6, complete cds	NT	0.0E+00 D16050.1	0.0≝+00	1.14	31146	18170	5042
Human mRNA for transcription factor AREB6, complete cds	NT	0.0E+00[D15050!1	0.0E+00	1.14	31145		5042
Horno sapiens chromosome 21 segment HS21C085	Z	0.0E+00 AL163235.2	0.0€+00	1.17			5040
dimethylallytranstransferase, geranytranstransferase) (FDPS) mRNA		4503684 NT	0.0€+00	1.56	31140	18164	5036
During september states with the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the septemb	2	0.0E+00[AF091711.1	0.01	2.77	31130	18152	5023
II in its septem successor, and it for the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of the september of t	7	I NI OOCCUCA	0.00	2.40	T	Т	200
Domo sapella wino ciasa ( legiori ) menta	2	0.0E+00 AF05006.1	0.01	11.02	3112/	Т	5020
Tomo sapiens zinc-imger Divis-oriumg protein (Town Oxi 1), illivix	2	7/05546 N	0.0E+00	86.0	Ţ	Г	5017
Homo sapiens meningioma expressed entigen 6 (colled-coll proline-rich) (MIGEA5), MIXIVA	NT	5174560 NT	0.0E+00	1.78		Г	5016
Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA		5174560 NT	0.0E+00	1.78	31120		5016
Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA		4758199 NT	0.0≣+00	4.26	31118		5014
QV0-BN0147-280400-213-g11 BN0147 Homo sapiens dDNA	EST_HUMAN	0.0E+00 BE007835.1	0.0E+00	0.94	31117	18142	5013
	EST_HUMAN	0.0E+00 BE007835.1	0.0€+00	0.94	31116		5013
	NT	5174560 NT	0.0E+00	1.02	31118	18141	5012
Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA	NT	6677648	0.0≣+00	2.74	31114		5011
Homo saplens mRNA for KIAA0633 protein, partial cds	NT	0.0E+00 AB014533.1	0.0E+00	1.39	31113		5010
Homo sapiens zinc finger protein (KIAA0412) mRNA		4585642 NT	0.0€+00	1.32	31112		5009
H. sapiens MICA gene	NT	X92841.1	0.0E+00 X92841	1.19	31110		5007
Homo sapiens I A I A box binding protein (15P)-associated tactor, KNA polymerase ti, t, 26kD (1AF2I) mRNA		5032150 NT	0.0€+00	1.08	31104	18129	5000
Homo sapiens chromosome 21 segment HS21CU80	NT	0.0E+00 AL163280.2	0.0E+00	2.55	31099	18120	4991
Human collagenase type IV (CLG4) gene, exon 2	NT	0.DE+00 M55582.1	0.0E+00	1.46	31098	18119	4990
H. Saplens MeCP-2 gene	NT	X94628.1	0.0E+00 X94828.	1.3	31095	18116	4987
H. sepiens MeCP-2 gene	NT	X94628.1	0.0E+00 X94628.	1.3	31084	18116	4987
Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-dipha) gene, J1- J61 segments; and Tcr-C-dipha gene, exons 1-4	NT	0.0E+00 M94081.1	0.0E+00	1.35	31092	18114	4985
	Source		BLAST E Value	Signal	ID NO:	S C	NO.
Top Hit Descriptor	Top Hit	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ		Probe

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Single Exon Probes Expressed in Placenta

	ę,	Į.	ģ	g	١٥	,	5197	5	6182	5170	5107	9	5148	5146	5139	5139	6135	5135	5135	5121	5121	5110	5102	5099	5097	5087	Probe SEQ ID NO:
6234 18356	П	Γ	П	5213 18334	T	Т				70 18292					39 18262	39 18262	35 18259	35 18259	35 18259		٦	П	П	П		18215	D SEQ ID
56 31324				Γ					31268	32	39	32 31247		10 26472	31230	- 32 31229	39 31227	31226	31225	31218			31201		31187	5	ORF SEQ
4.58				1.82						18.98	1.69	0.64		0.72	2.09		0.72	0.72	0.72	2.32	2.32					7.66	Expression Signal
	Γ		-	Γ		Ţ			2 0.0E+00		П		9 0.0E+00							2 0.0€+00					T		Most Similar (Top) Hit BLAST E Value
0.0E+00 M10905.1	0.0E+00 M10905.1	5902055 NT		AF24063	0.0E+00 AF240635.1	AF240635 1	0.0E+00 X72791.1	0.0€+00 X52988.1	4507720 NT	0.0E+00 D50657,1	0.0E+00 AL163209.2	0.0E+00 U5358E.1	4758225 NT	0.0E+00 AF195658.1	0.0E+00 U82671.2	0.0E+00 U82671.2	0.0E+00 AA601246.1	0.0E+00 AA601246.1	0.0E+00 AA601246.1	8923441 NT	8923441	0.0E+00 AB028868.1	4758199	0.0E+00 BE408863.1	0.0E+00 M10976.1	0.0E+00 U14967:1	Top Hit Acesslon No.
Z	3	) S	N N	2	1	N	TN	NT	NT	Z	3	T	5 NT	N N	N	T	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	1 NT	NT		EST_HUMAN	N.T	T	Top Hit . Database Source
Human cellular fibronectin mXNA	Human cellular fibronectin mRNA	Homo sapiens ring finger protein (RNF), mRNA	Homo sepiene oyelophilin (USA-CYP) mRNA	Children of	Homo saniens vascular endomelial cadherin 2 mRNA, complete cds	Homo sepiens vascular endothelial cadherin 2 mRNA, complete cds	Human endogenous retrovirus mRNA for gag protein	Bacillus amyoliquefaciens sacB gene for levansucrase (EC 2.4.1.10)	Homo sepiens titin (TTN) mRNA	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene		Homo sapiens MHC class 1 region	Homo seplens E2F transcription factor 2 (E2F2) mRNA	Homo sepiens DNA mismatch repair protein (MLH3) gene, complete cds	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma entigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	no14g09.s1 NCI_CGAP_Fhe1 Home sepiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	no14g09.s1 NCI_CGAP_Phe1 Homo septens cDNA clone IMAGE:1100704 S similar to TR:E239140 E239140 SPALT PROTEIN ;	no14g09.s1 NCI_CGAP_Phe1 Homo septens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens mRNA for KIAA1043 protein, partial cds	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 6	otrov	Human ribosomal protein L21 mRNA, complete cds	Top Hit Descriptor

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Probe SEQ ID NO:	SEQ ID	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
5630	18824	31898	. 0.73	0.0E+00 D61664.1	D61664.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
							HUM418D05B Clontech human fetal brain polyA+ mRNA (#8536) Homo sapiens cDNA clone GEN-418D05
5630	18824	31899	0.73	0.0E+00 D61564.1	D61564.1	EST_HUMAN	
5633	18827	31903	292	0.0E+00	0.0E+00 BF529931.1	EST_HUMAN	
5633	18827	31904	2.92	0.0€+00	0.0E+00 BF529831.1	EST_HUMAN	
5638		31908	262	0.0E+00	0.0E+00 BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5
5649	П	32124	4.23	0.0⊑+00	11434392 NT	NT	Homo septens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5664	18858	32141	0.59	0.0+30.0	0.0E+00 Al928131.1	EST_HUMAN	wo95b02x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similer to TR:O75054 O75054 KIAA0466 PROTEIN ;
5664		32142	0.69	0.0€+00	0.0E+00 Al928131.1	EST_HUMAN	wc95b02x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similer to TR:O75054 O75054 KIAA0466 PROTEIN ;
5682		32165	1.3	0.0⋶+00	0.0E+00 BE260?77.1	EST_HUMAN	601150252F1 NIH_MGC_19 Hamo sepiens cDNA clone IMAGE:3502909 5
5691			3.95	0.0€+00	0.0E+00 AW867316.1	EST HUMAN	
6705		32180	2.49	0.0€+00	0.0E+00 BE292889.1	EST_HUMAN	
· 5705		32191	2.49	0.0E+00	0.0E+00 BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5
5725	18918	32212	1.7	0.0E+00	11420819 NT	NT	Homo septens offectory receptor, family 2, subfamily 1, member 1 (OR211), mkNA
5725	18918	32213	1.7	0.0E+00	11420819 NT	ZT	Homo sapiens olfactory receptor, family 2, subfamily r, member 1 (UKZF1), MKNA
5733	Ι.	32221	4.16	0.0€+00	0.0E+00 AF084254.1	Z	Homo sepiens very long-chein acyl-cook syntheiase nomolog i illinuva, complete vus
5733	18926	32222	4.16	0.0E+00	0.0E+00 AF064254.1	NT	Homo sapiens very long-chain acyr-cox symmetase numacy i mruvy, complete eus
6740	18933	32232	2.64	0.0E+00	0.0E+00 AJ224639.1	NT	Homo saplens Suri-5 and Suri-6 genes
6740		32233	2.64	0.0€+00	0.0E+00 AJ224639.1	NT	
6769	18961	32282	1	0.0€+00	0.0E+00 AI198515.1	EST_HUMAN	qf84g10.xf Soeres_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1757730 3' shiller to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR;
5773		32268	7.65	0.0€+00	0.0E+00 M85719.1	EST_HUMAN	EST02238 Fetal brain, Stratagene (cat#336206) Homo saptens cDNA clone HFBCM48
5780	18972	32277	4.62		0.0E+00 AW 405472.1	EST_HUMAN	UI-HF-BL0-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5
5793			1.12		0.0E+00 Z26269.1	3	
5804	18994		1.85		0.0E+00 AW361877.1	EST_HUMAN	
5804	18994	32298	1.85	0.0€+00	0.0E+00 AW361877.1	EST_HUMAN	
5804		32299	1.85		0.0E+00 AW361877.1	EST HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5807		32302	0.59		0.0E+00 AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
5807		32303	0.59		0.0E+00 AB035266.1	27	Homo sepiens mRNA for neurexin II, complete cds
5809	18999	32306	1.67		U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5840	19030	32336	1.02	Г	0.0E+00 AB046861.1	2	nome septens minuted for nines for process, better one

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Ш	EST_HUMAN	0.0E+00 BF155670.1	0.0E+0	1.09	П	П	6082
QV4-HT0894-290900-399-a10 HT0894 Homo sapiens	EST_HUMAN	0.0E+00 BF155670.1	0.0€+0	1.09	32692	19284	6082
	EST_HUMAN	0.0E+60 AW 470846.1	0.0E+8	0.65	32581	19252	6070
Ļ	EST HUMAN	0.0E+00 BF0317.42.1	0.011+00	0.96	32566	19240	6058
	EST_HUMAN	0.0E+00 BF031742.1	0.0€+0	96.0	32565	19240	6058
l	EST_HUMAN	0.0E+00 AW276760.1	0.06+0	8.0	32555	19231	6048
	EST_HUMAN	0.0E+00 BE673986.1	0.0E+00	0.58	32551	19227	6044
	EST_HUMAN	0.0E+00 BE673986.1	0.0E+0	0.58	32550	19227	6044
L	EST_HUMAN	0.0E+00 BE958636.1	0.0€+00	1.19	32531		6028
	EST_HUMAN	0.0E+00 BE828144.1	0.0€+00	4.69	32526		6023
	NT	0.0E+00 AF217239.1	0.0E+00	2.15	32524		6021
	EST_HUMAN	0.0E+00 AA454542.1	0.0E+00	0.99	32495	Π	5989
602185852F1 NIH_MGC_45 Homo saplens cDNA clone IMAGE:4310076 5	EST HUMAN	0.0E+00 BF569905.1	0.00+00	2.09	32491	П	5984
hz83d11.x1 NCI_CGAP_Lu24 Homo sapisns cDNA cicre IMAGE:3214581 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING;	EST_HUMAN	0.0E+00 BE503096.1	0.0⊞+00	1.12	32484	19164	5979
L	EST_HUMAN	0.0E+00 BE273883.1	0.0E+00	3.07	32470		6969
Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds	NT	0,0E+00 AF142621.1	0,0E+00	0.92	32469		5968
	EST_HUMAN	0.0E+00 BF338835.1	0.0Ё+00	2.98	32466		5965
Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and Isoform beta-1B, complete cds	ΝŤ	0.0E+00 U86961.1	0.0E+00	90.E	32445	19131	5945
Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete ods	NT	0.0E+00 U86961.1	0.0E+00	3.06	32444	19131	5946
Mus musculus aczonin (Acz), mRNA	10048478 NT		0.0E+00	2.46	32443	19130	5944
Ш	EST_HUMAN	0.0E+00 BE560082.1	0.0E+00	7.24	32442		5943
Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA	9998943 NT		0.0E+00	1.1	32441		5942
601584032F1 NIH_MGC_7 Homo sapiens cDNA clone	EST_HUMAN	BE7011	0.0E+00	1.10	32430		5933
Homo sapiens protocadherin beta 2 (PCDHB2), mRNA	11416801 NT		0.0E+00	4.63	١	П	5928
HA2981 Human fetal liver cDNA library Homo sapiens cDNA	EST_HUMAN	0.0E+00 AI207615.1	0.0E+00	1.23			5906
Homo sepiens KVLQT1 gene	NT	0.0E+00 AJ006345.1	0.0E+00	1.49	32401		5899
Homo saptens KVLQT1 gene	TN	0.0E+00 AJ006345.1	0.0E+00	1.49	32400	19088	5899
	Top Hit Database Source	Top Hit Acession	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ	SEQ ID	Probe SEQ ID NO:
	_ ,						

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Prabe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6080	19271	32599	1.67	0.0E+00	0.0E+00 W33089.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo saplens cDNA clone IMAGE:321755 5'
6090	19271	32600	1.67	0.0€+00	0.0E+00 W33069.1	EST_HUMAN	zc08h06.r1 Soares_perathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6091	19272		2.3	0.0⋿+00	0.0E+00 AF012618.1	TN	Homo sepiens familial mental retardation protein 2 (FMR2) gene, exon 14
6094		32804	3.37	0.0E+00	0.0E+00 BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6100	П	32612	243	0.0€+00	0.0E+00 BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5
8102		32616	0.58	0.0E+00	0.0E+00 BE388673.1	EST_HUMAN	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6117		32633	0.65	0.0E+00	0.0E+00 AW752848.1	EST_HUMAN	L3-CT0220-111199-028-E04 CT0220 Homo sepiens cDNA
6120		32635	1.72		11433071 NT	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 28 homolog (KIAA0735), mRNA
6120		32636	1.72	0.0€+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 28 homolog (KIAA0735), mRNA
6121	19300	32637	1.15	0.0E+00	0.0E+00 BE901608.1	EST_HUMAN	601877735F1 NIH_MGC_21 Hamo septens cDNA clone IMAGE:3960200 5
6121	П	32638	1.15	0.0E+00	0.0E+00 BE901608.1	EST_HUMAN	801877735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32639	1.15	0.0E+00	0.0E+00 BE901608.1	NAMUH_TS3	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5
6137	25819	32656	10.17	0.0Ё+00	9789986 NT	Z	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6140	19318	32659	1.28	0.0E+00	0.0E+00 AA193508.1	EST_HUMAN	2740h01.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5:
6140	19318	32660	1.28	0.0E+00	0.0E+00 AA193506.1	EST_HUMAN	z/40h01.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.
6163	19339	32685	10.44	0.0E+00 U34626.1	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6163	19339	32686	10.44	0.0E+00 U34625.1	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6203	19378	32729	1.08	0.0E+00	0.0E+00 BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo septens cDNA clone IMAGE:3355565 5
6213	19388	32737	1.16	0.0€+00	0.0E+00 BE156561.1	EST_HUMAN	QV0-HT0368-090200-099-e09 HT0368 Homo saplens cDNA
6223		32747	0.66	0.0€+00	0.0E+00 M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6259	19433	32780	1.6	0.0€+00	0.0E+00 BE379007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3608490 5
6265		32786	1.35	0.0E+00	0.0E+00 AU1377721	EST_HUMAN	AU137772 PLACE1 Homo septens cDNA clone PLACE1007201 6"
6287		32812	3.33	0.0E+00	0.0E+00 U4598:21	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6316	19488	32844	4.34	0.0E+00	0.0E+00 AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648008 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN.;
6317	П	32845	3.89	0.0€+00	11545913 NT	NT	Homo sapiens χ/losyltransferase II (XT2), mRNA
6317			3.89	0.0E+00	11545913 NT	T	
6353		32880	2.23	0.0€+00	11426367 NT	1	Homo sapiens carcinoembryonic entigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6357	19527	32885	3.15	0.0E+00	0.0E+00 BE257,173.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3350622 5
6274	10540		0 08	0.05+00	0 0E+00 AIRRGAR 1	EST HIMAN	tt91f10x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839
	ı		0.00	0.01			

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		:	ļ			99		
	Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Tap Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
_	6375	19544	32902	1.32	0.0E+00 L35930!1	L35930!1	NT	Human anlon exchanger (AE1) gene, exons 1-20
	6383	19652	32908	0.96	0.0€+00	0.0E+00/BE797385.1	EST_HUMAN	
	6383	19552	32909	0.96	0.0€+00	0.0E+00 BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo septens oDNA clone IMAGE:3942329 5'
	6303	19562	32922	0.71	0.0E+00	0.0E+00 A1198025.1	EST_HUMAN	qt50b11.x1 NCI_CGAP_Bm25 Homo sepiens cDNA cbne IMAGE:1659901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT :
	6393	19562	32923	0.71	0.0E+00	0.0E+00 AI198025.1	EST HUMAN	qī50b11.x1 NCI_CGAP_Brn25 Homo sepiens cDNA cbne IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT :
	6395		32924	. 1.11	0.0 €+00	0.0E+00 BF357123.1	EST_HUMAN	MR0-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA
_	6403		32934	1.3	0.0€+00	11435630 NT	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA
	6413	19582	32943	0.59	0.0E+00 D55649.1	D55649.1	TN	Human mRNA for alpha mannosidase il isozyme, complete cds
_	6429	19597	32963	1.07	0.0E+00	0.0E+00 AW178142.1	EST_HUMAN	IL3-HT0062-010999-014-A04 HT0062 Homo saplens cDNA
	<del>045</del> 0	19017	32980	0.6	0.0E+00	0.0E+00 BE674544.1	EST_HUMAN	7e02c12x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302;3' similar to SW:Y176_HUMAN Q14681 HYPOTHETICAL PROTEIN KIAA0176 ;
_	6454	19821	32985	0.77	0.0≅+00	32039		Homo sepiens KIAA0285 gene product (KIAA0285), mRNA
	6468	19635		9.28	0.0€+00	0.0E+00 AV650020.1	EST_HUMAN	AV850020 GLC Homo sapiens cDNA clone GLCCAD09 3'
	6477	19844	33006	3.46	0.0€+00	8.1	EST_HUMAN	UI-HF-BL0-acc-g-12-0-UI.s1 NIH_MGC_37 Homo saplens cDNA clone IMAGE:3058751 3
	6480	19647	33009	4.63	0.0E+00 H01255.1		EST_HUMAN	yj27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5
	6488	19655	33018	0.71	0.0€+00	1426293	NT	Homo saplens amiloride sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
	6492	19658	33021	1.67	0.0E+00 X15377.1	X16377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
	6494	19660	33023	1.17	0.0E+00	0.0E+00 AA456375.1	EST_HUMAN	aa14e07.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5
	6495	19661	33024	1.04	0.0E+00	0.0E+00 AI612841.1	EST_HUMAN	125/408.x1 NCI_CGAP_0/35 Homo saplens cDNA clone IMAGE:2282887 3' similar to SW:NTCS_HUMAN P53786 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2;
	6501	19667	33030	4.27	0.0E+00	0.0E+00 BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
	6501	19667	33031	4.27	0.0€+00	0.0E+00 BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3638616 5'
_	6505	Г	33037	0.86	0.0€+00	0.0E+00 AW748596.1	EST_HUMAN	MR0-BT0264-221189-002-f11 BT0264 Homo saplens cDNA
	6505	П	33038	0.86	0.01100	0.0E+00 AW748598.1	EST_HUMAN	MR0-BT0264-221189-002-f11 BT0284 Homo saplens cDNA
	6507	Г	33040	52.21	0.00+00	0.0E+00 AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA cione HEMBA1005360 5
	6507	Т	33041	62.21	0.0€+00	0.0E+00 AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cuna cione HEMBA100550 5
	6512	Т	33047	0.8	0.0E+00	0.0E+00 BE780453.1	EST HUMAN	601468/12F1 NIH_WGC_5/ Home sapiens CUNA cione IMAGE.36/1689 3
	6537	Т	33048	0.84	0.05+00	0.0E+00 X9ZZ17.1	TI TI IMAN	n.septens germine immunogiopulir neavy chain, variatio region, (19-2)
	6541	19704	33076	4.08	0.01	0.0E+00 BE293:153.1	EST HUMAN	801105344F1 NIH MGC 15 Hamo saplens cDNA clone IMAGE: 2987983 5
	6541	19704	33077	4.06	0.0€+00	0.0E+00 BE293:153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sepiens cDNA clone IMAGE:2987963 5'
	6573	19735	33114	1.07	0.0€+00	0.0E+00 BE867657.1	EST_HUMAN	601443176F1 NIH_MGC_66 Hamo sapiens cDNA clone IMAGE:3847281 5'

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Table 4

Single Exon Probes Expressed in Placenta

					Çiriği	[X0] - 1020	Citigo Lacini accona
Prabe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
6009	19769	33158	1.81	0.0E+00	0.0E+00 AW 406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 51
6609	П	33159	1.81	0.0E+00	0.0E+00 AW 406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo saptens cDNA clone IMAGE:3059931 5'
6640	19799	33188	0.94	0.0€+00	0.0E+00 AV719414.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clane GLCEHC06 5'
6849		33195	0.74	0.0E+00	0.0E+00 BE898340.1	EST_HUMAN	601661150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6649		33196	0.74	0.0E+00	0.0E+00 BE8983.10.1	EST_HUMAN	601681150F1 NIH_MGC_9 Hamo saplens cDNA clone IMAGE:3951301 5'
							Homo sepiens low voltage-activated T-type calcium channel alpha 1G splice veriant CavT.1a (CACNA1G)
6652	19811	33199	2.13	0.0E+00	0.0E+00 AF180830.1	NT	mRNA, complete cds
6855	19814	33202	0.64	0.0E+00	L48546.1	NT	Homo sepiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6667	19816	33203	0.89	0.0€+00	11420658 NT	NT	Homo sapiens transformation/transcription domain-essociated protein (TRRAP), mRNA
6664	19823	33210	ය ග	0.01100	0.0E+00 AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 6' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206;
6664	19823	33211	3.5	0.0€+00	0.0E+00 AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O16390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
6668	19827	33214	1.08	0.0E+00	0.0E+00 W37163.1	EST_HUMAN	±20e06.rl Soeres_fetel_lung_NbHL18W Homo septens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6668	19827	33215	1.06	0.0+30.0	0.0E+00 W37165.1	EST_HUMAN	252006.r1 Soares_fetal_lung_NbHL18W Homo saptens cDNA clone IMAGE:302826 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6684	П	33232	1.21	0.0€+00	0.0E+00 BE794853.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3943504 5'
6691	10849	33239	5.1	0.0€+00	0.0E+00 BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6692	19850	33240	1.38	0.0€+00	0.0E+00 BE767955.1	EST HUMAN	QV1-GN0065-140800-318-h02 GN0065 Horno eapiens cDNA
6692	Г	33241	1.38		0.0E+00 BE767955.1	EST_HUMAN	QV1-GN0005-140800-318-h02 GN0065 Homo sapiens cDNA
6608	19854		6.83		0.0E+00 BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5
9696	19854	33245	6.83		0.0E+00 BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3913311 5
6705	19863	33253	4.51	0.0E+00 L24493.1	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6710	19868	33257	2.62		0.0E+00 AL163204.2	N,T	Homo saplens chromosome 21 segment HS21C004
6710	19868	33268	2.62		0.0E+00 AL163204.2	NT	Homo sepiens chromosome 21 segment HS21C004
6716	19874	33265	3.68	0.0€+00	6005983 NT	NT	Homo sapiens zana pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6720	19877	33268	4.12	0.0E+00	0.0E+00 Al638412.1	EST_HUMAN	tt31f11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similer to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR.;
6722	19879	33270	1.46	0.0€+00	0.0E+00 L32832!1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6735	19891	33283	0.82	0.0€+00	0.0E+00 AW505430.1	EST_HUMAN	UI-HF-BN0-ama-c-01-0-UI.r/ NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6737	19893	33284	4.11	0.0€+00	0.0E+00 AA434584.1	EST_HUMAN	zw52c03.r1 Scares_total_fetus_Nb2HF8_9w Homo saptens cDNA clone IMAGE:773668 5
6751			1.13	0.0€+00	0.0E+00 BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4103693 5'
<i>6756</i>	19912	33307	1.63		0.0E+00 BE925876.1	EST_HUMAN	CV3-BN0047-300800-278-cus BN0047 Homo sapiens cUNA

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Ŧ		П						П	٦		П	٦			П	П		٦	П	٦	٦	٦	٦	٦			- SE -
7036	7004	7004	6998	6998	6991	6972	6867	6964	6963	6951	6940	6940	6930	6926	6915	6878	6876	6854	28 28	6832	6810	810	6808	6790	6789	6789	Prabe SEQ ID
20100	20140	20140	18517	18517	18510	20200	20195	20192	20191	20264	20253	20253	20245	20241	20230	20030	20028	20007	20007	19985	19964	19964	19962	19945	19944	19944	Exon SEQ ID
33588 33594		33558	31510		31502	33626	33621	33618			33690	33689	33678	33676	33663	33440	33438	33417	33416	33393	33569	33368	33366	33345	33343	33342	ORF SEQ ID NO:
1.4		1.74	13.63	13.63	1.28		0.92	11.05					0.76	0.83	3.33		7.79	2.43					1.64	69.0	0.76	0.78	Expression Signal
			Г							0.0€+00		•		Γ											0.0€+00	0.0E+00	Most Similar (Top) Hit BLAST E Value
0.0E+00 AA195106.1	0.0E+00 BE550162.1	0.0E+00 BE560162.1	0.0E+00 BE867889.1	0.0E+00 BE867889.1	0.0E+00 BE566381.1	0.0E+00 BE734087.1	0.0E+00 AI168270.1	0.0E+00 X56163;1	0.0E+00 AL042443.1	11435626	0.0E+00 AI940621.1	0.0E+00 AI940621.1	0.0E+00 BE671587.1	0.0E+00 U39573.1	0.0E+00 AA190755.1	0.0E+00 BF085637.1	0.0E+00 BE169131.1	0.0E+00 BE006012.1	0.0E+00 BE006012.1	0.0E+00 BE142383.1	0.0E+00 BE701434.1	0.0E+00 BE701434.1	0.0E+00 AU125928.1	0.0E+00 AW611864.1	11426758 NT	11426758 NT	Top Hit Acession No.
EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	26 NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	T	EST HUMAN	EST_HUMAN	EST_HUMAN	SB NT	38 NT	Top Hit Oatebase Source							
2/34g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665332.5'	O8879 GOLGIN-95, THE TORITE SEPTEMENT HOME SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED S	0	601443667F1 NIH_MGC_65 Homo septens culvia cione IMAGE:3847697 9					H. septens immunoglobulin heavy chain gene, variable region	DKFZp434D2021_r1 434 (synonym: htes3) Homo septens cDNA clone UKFZp434U2021 6	Homo eaplens CD6 antigen (CD6), mRNA	IL3-ST0024-230799-001-E01 ST0024 Homo septens cDNA	IL3-ST0024-230799-001-B01 ST0024 Homo septens cDNA	TEKTIN.;	Human salivary peroxidase mRNA, complete cds	zp88e03.r1 Stratagene HeLe cell s3 937216 Homo saprens cDNA cione IMAGE:627292 5	IL5-GN0032-180900-145-dC7 GN0032 Homo sapiens cDNA	PN3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA	RCO-BN0121-280300-032-e04 BN0121 Homo sepiens cDNA	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA	CMC-HT0143-270999-062-c08 HT0143 Homo saplens cDNA	PW2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA	PW2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA	AU125928 NT2RM4 Homo sapiens cDNA cione NT2RM4002430 5	hg82e04x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952126 3	Homo sepiens solute carrier family 1 (high affinity espartate) grutamate transporter), member o (SLC140), mRNA	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA	Top Hit Descriptor

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Prabe SEQ ID NO:	SEQ ID	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7044	20097		11.81	0.0E+00	11034810 NT	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-rotated arm-repeat protein) (CTNND2), mRNA
7048	20099	33515	1.11	0.0E+00	11431474 NT	NT	Homo sepiens sodium ohannei, nonvoltago-gated 1, beta (Liddie syndrome) (SCNN1B), mRNA
7061	20114	33529	2.69	0.0€+00	0.0E+00 BF569905.1	EST_HUMAN	602165652F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7068		33535	0.66	0.0E+00	4557364 NT	NT	Homo saptens Bloom syndrome (BLM) mRNA
7076	$\neg$		206	0.05+00 J03069.1	J03069.1	TN	Human MYCL2 gene, complete cds
7083		33599	2.66	0.0E+00	0.0E+00 AF217239.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7083	20177	33600	258	0.0E+00	0.0E+00 AF217239.1	NT	Homo septens cadherin 20 (CDH20) mRNA, complete cds
7084	20178	33601	1.07	0.0E+00 M38113.1	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x6
7095	18522	31515	3.59	0.0€+00	11420775 NT	NT	Homo sepiens melanoma entigen, family B, 2 (MAGEB2), mRNA
7099	18526	31518	0.7	0.0E+00	0.0E+00 BE256708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5
							wf21c09.x1 Soares_Disckgraefs_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEOBOX PROTEIN HOX-A4 (HUMAN);contains PTR5.b1 MER22 MER22 repetitive
7111	18537	31,483	0.62	0.0E+00	0.0E+00 Al660911.1	EST_HUMAN	element;
							wf21c09.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEOBOX PROTEIN HOX-A4 (HUMAN),contains PTR5.b1 MER22 MER22 repetitive
7111	18537	31494	0.62	0.0E+00	0.0E+00 AI66091,1.1	EST_HUMAN	element;
7120	18546	31457	1.21	0.0E+00	0.0E+00 AU118478.1	EST_HUMAN	
7123	18549	31461	7.52	0.0E+00	0.0E+00 BE262941.1	EST_HUMAN	601148954F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:3501829 5'
7124	18550	31462	272	0.0E+00 Z37978.1	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7124	18550	31463	272	0.0E+00 Z37976.1	Z37976.1	NT	H.suplens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7125		31464	3.01	0.0E+00	0.0E+00 AF257737.1	TN	Homo saplens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7125	18551	31465	3.01	0.0E+00	0.0E+00 AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7132	18558	31472	1.26	0.0E+00	0.0E+00 AF310105.1	NT.	Homo septens NALP1 mRNA, complete cds
7137	20272	33711	0.61	0.0E+00	0.0E+00 BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo saplens cDNA
7142	20277	33717	2.58	0.0E+00	0.0E+00 BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sepiens cDNA clone IMAGE:4310076 5
7144	20279	33719	0:78	0.0€+00	0.0E+00 AJ404438.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7144	Г	33720	0.78	0.0E+00	0.0E+00 AJ404468.1	NT	Homo saptens mRNA for dynein heavy chain (DNAH9 gene)
7148	20283	33725	3.26	0.0E+00 L01978.1	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7153	20287	33728	0.72	0.0E+00	0.0E+00 AW502362.1	EST_HUMAN	UI-HF-BR0p-eke-d-10-0-UI:r1 NIH_MGC_62 Homo expienc cDNA clone IMAGE:3076290 5
7153	20287	33730	0.72	0.0€+00	0.0E+00 AW502362.1	EST_HUMAN	UI-HF-BR0p-eka-d-10-0-UI.r1 NIH_MGC_52 Homo sepiens cDNA clone IMAGE:3076290 5
7162	20295	33738	0.87	0.0E+00	0.0E+00 AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5
7162	20295	33739	0.87	0.0E+00	0.0E+00 AL039581.1	EST_HUMAN	
7171	20304	33747	5.81	0.0E+00	0.0E+00 BF306996.1	EST_HUMAN	601868822F1 NIH_MGC_17 Homo sapiens CUNA clone IMAGE:4123846 3

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repetitive element;	EST HUMAN	0.0E+00 AI128344.1	0.0⊑+00	36.37	33953	20484	7406
qc67a07.x1 Soares_placenta_8tx9weeks_2NbHP8tx9W Homo sapiens cDNA cione IMAGE:1714644 3' similar to SW.ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR							
	EST_HUMAN	0.0E+00 AI128344.1	0.0€+00	36.37	33952	20484	7406
qc07a07.x1 Soares_placenta_8tx9wecks_2NbHP8tx9W Homo septens cDNA clone IMAGE:1714844 3"  smilar to SW-ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR							
	3	0.0E+00 AF2277:H.1	0.0E+00	0.63	33927	20463	7385
Homo sepiens voltage-dependent calcium channel alpha 1G subunit Isoform ae (CACNA1G) mRNA,						1	
Homo sapiens vitamin D (1,25- dlhydroxyvitamin D3) receptor (VDR), mRNA	NT	11436699 NT	0.0E+00	4.07		7	7371
Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA	TI	11436699 NJ	0.0€+00	4.07	Ì	٦	7371
601580948F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3929722 5	EST_HUMAN	0.0E+00 BE747231.1	0.05+00	0.67	33902		7361
601580948F1 NIH_MGC_9 Homo septens cDNA clone IMAGE:3929722 5	EST_HUMAN	0.0E+00 BE747231.1	0.0E+00	0.67	33901		7361
	NT	0.0E+00 AF137288.1	0.0€+00	2.43	31437	18569	7350
Homo sapiens keratin 12 (KRT12) gene, comptete cds	NT.	0.0E+00 AF137238.1	0.0E+00	2.43	31436	18569	7350
601431819F1 NIH_MGC_72 Homo seplens cDNA clone IMAGE:3917164 5	EST_HUMAN	0.0E+00 BE891286.1	0.0E+00	1.25	33873	20411	7329
	EST_HUMAN	0.0E+00 BE891286.1	0.0E+00	1.25	33872	20411	7329
Homo sepiens netrin 1 (NTN1), mRNA	NT	4758839 NT	0.0E+00	0.71	33864	20402	7320
AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'	EST_HUMAN	0.0E+00 AU143706.1	0.0E+00	2.82			7319
	NT	11428081 NT	0.0E+00	1.06	33857	20385	7313
AU133213 NT2RP4 Homo septens cDNA clone NT2RP4001556 5	EST_HUMAN	0.0E+00 AU133213.1	0.0€+00	1.47	33837	20379	7297
	T	0.0E+00 AB007835.1	0.0E+00	1.03		20373	7291
Homo sepiens mRNA for KIAA0466 protein, partial cdo	NT	0.0E+00 AB007835.1	0.0€+00	1.03			7291
Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14	NT	L01973.1	0.0E+00 L01973.1	1			7283
	EST_HUMAN	0.0E+00 BE254103.1	0.0€+00	0.72		╗	7269
EST366876 MAGE resequences, MAGC Homo sapiens cDNA	EST_HUMAN	0.0E+00 AW954806.1	0.0€+00	1.16		П	7268
AU137738 PLACE1 Homo sepiens cDNA done PLACE1007120 5'	EST_HUMAN	0.0E+00 AU137738.1	0.0E+00	0.84		╗	7262
AU137738 PLACE1 Homo sepiens cDNA clone PLACE1007120 5	EST_HUMAN		0.0€+00	0.84		20345	7262
Homo sapiens mRNA for vascular cadherin-2, complete cds	NT	0.0E+00 AB026893.1	0.0€+00	0.62		20340	7257
Homo sapiens mRNA for vascular cadherin-2, complete cds	TN	0.0E+00 AB026893.1	0.0E+00	0.62		20340	7257
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	EST_HUMAN	0.0E+00 AW513069.1	0.0€+00	0.64	33506	20089	7225
Novel human gene mapping to chomosome 13	NT	0.0E+00 AL049784.1	0.0E+00	1.15			7219
Human chromosome 18 creatine transporter (SLC8A8) and (CDM) paralogous genes, complete cds	NT	U41302.1	0.0E+00 U41302.1	213	33752	20309	7177
i op Hil Descriptor	Database Source	No.	BLAST E Value	Signal	ID NO:	SEQ ID	SEQ ID
	Top Hit	Top Hit Acession	Most Similar	Evaression	ORFSEO	Exon	Probe

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Single Exon Probes Expressed in Placenta

					_		_			_		_		_	_			$\overline{}$	_		_						_	_		_	
7622 7629		7602	7600	7581	7580	7553	7552	7531	7531	7631	7504	7502	7489	7480	7487	7479	7467	7467	7466	7463	7461	7431	7420	7420	7415	7413	7410	7410	7408	7408	Probe SEQ ID NO:
20692 20698		20672	20670	20653	20652	20825	20624	20604	20604	20604	20579	20577	20564	20564	20562	20554	20542	20542	20541	20538	20536	20508	20497	20497	20493	20491	20488	20488	20486	20486	NO:
34168 34174		34146		34129		34101		34080	34079	34078	34051	34049	34034	34033	34031	34026	34016	34015		34012	34011	33980	33968	33967	. 33961		33959	33958	33956	33955	ORF SEQ ID NO:
0.63		3.8	1.5	1.81	1.09	0.8	0.58	1.03	1.03	1.03	2.31	0.89	5.81	5.81	6.47	0.83	1.71	1.71	1.33	0.91	1.13	0.69	0.77	0.77	3.49	13.11	5.41	5.41	0.74	0.74	Expression Signal
		8 0.0€+00																								Γ	Г	0.0E+00			Most Similar (Top) Hit BLAST E Value
0.0E+00 AA211663.1 0.0E+00 BF229235.1	1	11427135	0.0E+00 AU117553.1	0.0E+00 AW23E326.1	0.0E+00 R87430.1	0.0E+00 BE408293.1	0.0E+00 M90354.1	0.0E+00 AF001543.1	0.0E+00 AF001543.1	0.0E+00 AF001543.1	0.0E+00 AW950516.1	0.0E+00 AW956503.1	0.0E+00 U4544E.1	0.0E+00 U4544E.1	0.0E+00 X70172.1	0.0E+00 AF245505.1	0.0E+00 AF005213.1	0.0E+00 AF005213.1	0.0E+00 AU118607.1	0.0E+00 11427985	BE295499.1	0.0E+00 AJ270936.1	0.0E+00 AL079497.1	0.0E+00 AL078497.1	0.0E+00 AA128453.1	0.0E+00 BF337375.1	11426392 NT	11426392	0.0E+00 AF227135.1	0.0E+00 AF227135.1	Top Hit Acessian No.
EST_HUMAN	TOT LI MAN	5 NT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	NT	NT	NT	NT	NT	EST_HUMAN	5 NT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	} `	2 NT	NT	NT	Top Hit Database Source
MRO-ANDOS3-270900-004-107 ANDOS3 Homo sapiens cDNA	zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:552203 5' similar to gb:X03740	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA	AU117553 HEMBA1 Homo sapians cDNA clone HEMBA1001661 5'	x638a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050 HNF3/FH TRANSCRIPTION FACTOR GENESIS ;		601302879F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3637434 5	Human BTF3 protein homologue gene, complete cds	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200 :	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sepiens cDNA clone kappa_200	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200	EST362586 MAGE resequences, MAGA Homo saplens cDNA	EST369573 MAGE resequences, MAGD Homo sapiens cDNA	Human P2x1 receptor mRNA, complete cds	Human P2x1 receptor mRNA, complete cds	H. sapiens DNA for ZNGP2 pseudogene, exon 4	Homo sepiens adlican mRNA, complete cds	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	AU118807 HEMBA1 Homo sapiens oDNA clone HEMBA1003869 5	Homo sapiens hypothetical protein (FLJ20261), mRNA	601174576F1 NIH_MGC_17 Horno sapiens cDNA clone IMAGE:3529784 5	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0228 5'	DKFZp434B0226_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434B0226 5	zn60108,r1 Strategene musicie 93 / 209 Homo septens cuina cione invalse::562501 o similiar to incissosoz. G806562 NEBULIN.;	602035089F1 NCL_CGAP_Brn64 Homo sapiens cUNA clone IMAGE:4182839 5		Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA	Homo sapiens candidate taste receptor T2R9 gene, complete cds	Homo sapiens candidate taste receptor T2R9 gene, complete cds	r Top Hit Descriptor

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Table 4
Single Exon Probes Expressed in Placenta

						_																				
7925	7924	7924	7922	7915	7811	7811	7891	7886	7881	7877	7871	7863	7863	7835	7821	7813	7813	7798	7733	7733	7675	7667	7667	7641	7634	Probe SEQ ID NO:
20975		20974		П	╗	7	╗			20929	20925	20917	20917	20890	20876	20868	20868	20852		20794	20740		20733	l	20703	Exan SEQ ID NO:
34482	34481	34480	34479	34472		34469	34449	34444		34435	34432	34423	34422	34382	34375	34364	34363	34344		34281	34220	34210	34209	34189	34182	ORF SEQ
0.78	5.78	5.78	0.92	6.67	0.95	56.0		0.62	6.1	0.88	1.84	0.7	0.7		1.34	1.79	1.79	0.6	4.41	4.41	1.08	0.9	0.9	0.8	0.67	Expression Signal
6 0.0E+00											4 0.0€+00			1 0.0E+00	Γ											Most Similar (Top) Hit BLAST E Value
0 6912461 NT	0.0E+00 BE739870.1	0.0E+00 BE739870.1	0.0E+00 AV758487.1	0 4501848 NT	0.0E+00 AW069274.1	0.0E+00 AW069274.1	0.0E+00 AU129622.1	0.0E+00 BF569862.1	0.0E+00 BF217905.1	0.0E+00 N76126.1	0 6912735 NT	0.0E+00 AI825504.1	0.0E+00 AIB25504.1	0 11417342 NT	0.0E+00 U74315.1	0.0E+00 AF064205.1	0.0E+00 AF064205.1	0.0E+00 AL046347.2	0.0E+00 AI752561.1	0.0E+00 AI752561.1	0.0E+00 AU118767.1	0.0E+00 BF306998.1	0.0E+00 BF306998.1	0.0E+00 L32832.1	0.0E+00 AW 405627.1	Top Hit Acession No.
61 NT	EST_HUMAN	EST HUMAN	EST_HUMAN	48 NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	S NT	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	N	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	Top Hit Database Source
Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA	601593158F1 NIH_MGC_9 Homo saprens CUNA clone IMAGE:3947300 0			Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mKNA	cr42e09.x1 Jia bone merrow stroma Homo sapiens cUNA clone HBMSC_cr42e09.3	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09.3	AU128622 NT2RP2 Homo sapiens cDNA clone N12RP2W08913 5	802185808F1 NIH_MGC_45 Homo sapiens cUNA cione IMAGE:4310200 0	601885465F1 NIH_MGC_57 Homo sapiens cDNA cione IMAGE:4103729 3	za86e05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cunA cione IMAGE:239430 3	Homo saplens transient receptor potential channel 5 (THPC5), mRNA	WEIT 1905 XT NCI_CGAP_GC5 Homo septens culviv can be introduced a simulation in the Crosses of some	AIBC1:	Homo saplens sema domain, seven unonicosporauli repeata (ypo i anu ypo i nazy, sanianicinaria) en el (TM) and short cytoplasmic domain, (semaphorin) 84 (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEMA5A), mRNA (SEM	HSU74315 Human chromosome 14 Homo sepiens cunk cione 1-4	nomo capient dynacun i (UC IIVI) gene, auemauvay spinoso producio, comina i umody i ve one composo ode	nomo sepens dynacin I (UC IN I) gene, auemauvay spirod producis, owner 7 through 12 and complete cds	UK-LP434JUS/_r1 434 (synonym: ness) name sapiens colors done on the same 32 and complete	cn17d05x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clore NHTBC_cn17d05 random	cn17d05x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random	AU118767 HEMBA1 Homo sapiens curva cione riemba juvas 14 o	601889823F1 NIH_MGC_17 Homo sapiens CUNA cione IMA-GC:4123949 9			UFHF-BL0-abs-d-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 5	Top Hit Descriptor

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					O. G.		o Baylor occording to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hii Acessian No	Top Hit Delabase Source	Top Hit Descriptor
7925	20976	34483	0.76	0.0€+00	6912461 NT	NT	Homo seplens strophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7926	_ [		1.05	0.0€+00	0.0E+00 AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5
7926	20976	34485	1.05	0.0E+00	0.0E+00 AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo septens cDNA clone HEMBB1000655 6
7948	20998	34508	12.57	0.0⊞+00	0.0E+00 BF590267.1	EST_HUMAN	nab2zc04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo explans cDNA clone IMAGE:3263214 3 similar to contains element TAR1 repetitive element;
7959			1.86	0.0€+00	0.0E+00 BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5
7959		34520	1.86	0.0€+00	0.0E+00 BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Hamo sepiens cDNA clone IMAGE:3884258 5
7998		34561	0.63	0.0€+00	0.0E+00 Y16785.1	NT	Homo saplens psihHaA pseudogene
7999	21049	34562	3.86	0.0E+00	0.0E+00 AI346148.1	EST_HUMAN	gp43f05.x1 NCI_CGAP_Co8 Hamo septens cDNA clone IMAGE:1925/93 3 stimiler to SW:EVX1_HUMAN P49640 HOMEOBOX EVEN-SKIPPED HOMOLOG PROTEIN 1;
803	ヿ	34564	0.68	0.0€+00	0.0E+00 W52673.1	EST_HUMAN	zc90f10.r1 Pancreatic Islet Homo saplens cDNA clone IWAGE:338443 5
8002			0.58	0.0€+00	11425128	NT	Homo sepiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8003	21053	34566	0.59	0.0€+00	0.0E+00 AU117333.1	EST HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5
8004	21054		0.57	0.0E+00	0.0E+00 BE613963.1	EST_HUMAN	801504084F1 NIH_MGC_71 Home sapiens cDNA clane IMAGE: 3905/33 5
8018 18	21069	34580	0.73	0.0∏+00	6995995 NT	Y.	Homo sepiens cystic fibrosis transmembrane conductance regulator, A i r-binding cassette (sub-ternity c, member 7) (CFTR), mRNA
8018		34581	0.73	0.0⊑+00	6995995	NT	Homo sepiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8037	21120	34640	0.49	0.0€+00	0.0E+00 AU133187.1	EST HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5
8083	21165		0.69	0.0E+00	0.0E+00 BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo saptens cDNA clone IMAGE:4103683 5
8098			0.61	Γ	0.0E+00 BE313013.1	EST_HUMAN	
8108	21180		1.36		0.0E+00 AA148791.1	EST_HUMAN	2001c06.r1 Stratagene colon (#937204) Homo sapiens cuiva cione invalue: 500910 5
8121	21203	34724	0.72	Γ	0.0E+00 BF026628.1	EST HUMAN	601672310F1 NIH_MGC_20 Homo saprens CUNA Crone IMAGE:3855131 5
8135	21217		0.55		0.0E+00 AA017021.1	EST_HUMAN	ze33h08.r1 Soares retina N2b4HR Homo sapiens cDNA cione IMAGE:35053 5
8153	21235		2.08		0.0E+00 BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens culva cione IMAGE:3059903 o
8170		34772	3.19	Γ	0.0E+00 M34872.1	ZT	Human amyloid-beta protein (APP) gene, exen 11
8170	21252	34773	3.19	Τ	0.0E+00 M34872.1	Z	Human amyood-beta protein (AFF) gene, exun 11  Shaadoo ya NiH MGC 10 Homo saniens cDNA clone IMAGE 2885123 5' similar to TR 064652 064652
8200	21282	34804	0.56		0.0E+00 AW674581.1	EST_HUMAN	
8200	21282	34805	95.0		0.0E+00 AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo capiene cDNA clone IMAGE:2985123 5" similar to 1R:084652 064652 F17K2.28 PROTEIN.;
8207			2.07		0.0E+00 AA387551.1	EST_HUMAN	Z81604./1 Strategene schizo brain S11 Homo seplens cDNA clone IMAGE:728719 5 similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
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	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hii Descriptor
	8209	21291	34812	0.85	0.0≅+00	0.0E+00 AW387131.1	NAMUH_TS3	MR0-ST0031-061099-003-e11 ST0031 Homo sapiens cDNA
	82 <u>1</u> 2	1	١	0.64	0.0E+00		IN	Homo saplens mRNA for KIAA0884 protein, partial cds
	8213		34814	6.15	0.0€+00	0.0E+00 AU142402.1	NAMUH_TSE	AU142402 Y78AA1 Homo sapiens cDNA clone Y78AA1000277 5'
_	8216			0.86	0.05+00	0.0E+00 BE388421.1	NAMUH_TSH	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
	8216	П		0.86	0.0E+00	0.0E+00 BE388421.1	NAWOH_TSE	601285550F1 NIH_MGC_44 Homo saptens cDNA clone IMAGE:3607237 5
					0.011	765776		Homo saptens killer cell Immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1),
_	8233	21316	34835	0.84		0.0E+00 W95278.1	EST HUMAN	ze05d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
	8233			0.84		0.0E+00 W95278.1	EST_HUMAN	ze05d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5
	8235			4.11	0.0E+00	0.0E+00 BF673098.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo septens cDNA clone IMAGE:4294128 5'
	8239	21321		0.83	0.0€+00	0.0E+00 AU134114.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001286 5
	8253	21335	34853	0.95	0.0E+00	0.0E+00 BF626534.1	EST_HUMAN	602069632F1 NCI_CGAP_Bm64 Homo sepiens cDNA clone IMAGE: 4212727 5
	8253	П	34854	0.95	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Bm64 Home capient cDNA clone IMAGE:4212727 5
	8285		34886	1.35	0.0E+00	0.0E+00 AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym; hamy2) Homo sapiens cDNA clone DKFZp761P092 6
_	8285	21367	34887	1.36	0.0E+00	0.0E+00 AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hemy2) Homo sepiens cDNA clone DKFZp761P092 5
_	8328	21410		1.16		0.0E+00 BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Hamo sapiens cDNA clone IMAGE:3887773 5
_	8351	21432	34956	1.27	0.0E+00	0.0E+00 AW500549.1	EST_HUMAN	UI-HF-BND-akj-f-01-0-UI.r1 NIH_MGC_50 Homo sepiens cDNA clone IMAGE:3077496 5
	8359	21440	34962	14.12	0.0E+00	0.0E+00 AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo septens cDNA clone IMAGE:2783789 3' similar to TR:060463 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
		П	٦					xaD7d12.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2567639 3' similar to contains
	8376	21467	34981	0.68	0.0E+00	0.0E+00 AW072395.1	EST_HUMAN	element OFR repetitive element;
	8394	21475	35002	1,11	0.0E+00	11421722	N T	Homo sapiens centrosomal protein 2 (CEP2), mRNA
	8397	21478	35005	0.57		0.0E+00 W01818.1	EST_HUMAN	za36d05.r1 Soares fetal liver spieen 1NFLS Homo septens cDNA clone IMAGE:294633 5
	8399	21480	35007	1.3		0.0E+00 BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Home septens cDNA clone IMAGE:3926998 5
	8399	21480	35008	1.3		0.0E+00 BE745597.1	EST_HUMAN	12
	8411	21492	35022	1.13		0.0E+00 AJ271735.1	N T	Homo saplens Xq pseudoautosomal region; segment 1/2
	8431			0.46		0.0E+00 D45032-1	NT	Human DNA for ceruloplasmin, exon 5
	8450	21591		0.53	0.0⊑+00	0.0E+00 AI367350.1	EST_HUMAN	qv85c12.x1 NCI_CGAP_U2 Homo sepiens cDNA clone IMAGE:1989334 3' similer to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
	8462			2.23	0.0€+00	0.0E+00 BE674'157.1	EST_HUMAN	7d76s04x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:32788623' similar to TR:095783 095783
	8484			1.96		0.0E+00 AI885671.1	EST_HUMAN	w60b10.x1 NCL_CGAP_Brn25 Homo sapiens cDNA dane IMAGE:2428275 3' similar to SW:COGT_HUMAN P60281 MATRIX METALLOPROTEINASE-14 PRECURSOR;
_	8477	П	П	1.47	П	0.0E+00 BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5*

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Table 4
Single Exon Probes Expressed in Placenta

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8709	8709	8709	8704	8697	8635	8635	8631	8631	· 8630	8630	8604	8601	8593	8588	8581	·	8572	8672	8557	8557	8538	8638	8637	8528	8487	8487	8485	8485	8477	Probe NO:
21789	21789	21789	21784	21777	21715	21715	21711	21711	21710	21710	21685	21682	21874	21869	21662	١	21653	21653	21638	21638	21619	21619	21618	21609	21568	21568	21566	21568	21668	SEQ ID
35325	35324	36323	35317		35253	35252	35249	35248	35247	35246		35220		35208	35202			35194			35157	35156	35155		35106	35105	35103	35102	36092	ORF SEQ ID NO:
2.81	2.81	2.81	0.7	0.48	0.61	0.61		2.13	0.61	0.61	2.08	0.52	0.66	0.71	0.93		1.16	1.16	1.24	1.24	1.34	1.34	5.0	3.61	0.84	0.84	1.72	1.72	1.47	Expression Signel
Γ								Γ	Γ	П			0.0E+00			٦					,						0.0E+00	0.0E+00		Most Similar (Top) Hit BLAST E Value
0.0E+00 X989221	0.0E+00 X98922.1	0.0E+00 X989221	0.0E+00 AJ251760.1	0.0E+00 U84744.1	0.0E+00 U88084.1	0.0E+00 U88084.1	4758685 NT	4758695 NT	AW2467	0.0E+00 AW245765.1	0.0E+00 BE890797.1	0.0E+00 AI580780.1	11416799	0.0E+00 AA502294.1	0.0E+00 AI884477.1		0.0E+00 AL163209.2	0.0E+00 AL163209.2	0.0E+00 BE612586.1	0.0E+00 BE612586.1	0.0E+00 AW384874.1	0.0E+00 AW364374.1	0.0E+00 BE837593.1	0.0E+00 AA398511.1	0.0E+00 AA403192.1	0.0E+00 AA403192.1	11427235 NT	11427235 NT	0.0E+00 BE563650.1	Top Hit Acession
NT	NT	N,	Z	N	NT	NT	35 NT	5NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN		NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	SNT	EST_HUMAN	Top Hit Database Source
H. sepiens mRNA for germme-glutamytransferase	H. sepiens mRNA for gemma-glutamy/transferase	H. sepiens mRNA for gernme-glutemy/transferase	Homo saplens NESP55, GNAS1 antisense (partial) and XLaiphas (partial) genes	.12		Human zinc finger protein (ZNF165), gene, exons 2 and 3	Homo septens mitogen-ectivated protein kinase kinase kinase 13 (MAP3K13), mRNA	Homo sepiens mitogen-activated protein kinase kinase kinase 13 (MAPSK13), mkina	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5		601431238F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3916569 5		Homo septens protocadherin beta 3 (PCDHB3), mRNA	G1136434 KIAA0187 PROTEIN.;		wm33a11.x1 NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2437724 3' similar to TR:075457 075457	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	601452412F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3856179 5			QV3-DT0045-221299-046-c07 DT0045 Homo saplens cDNA	RC2-FN0094-120600-013-h07 FN0094 Homo saplens cDNA	zt/3a08.s1 Scares_testis_NHT Homo sepiens cDNA done IMAGE:/72/958 3' similer to gb:S85655 PROHIBITIN (HUMAN);	x66102.rt Scares_total_fetus_Nb2H+8_9w Homo sepiens cUNA cione IMAGE:/cestite o similiar to TR:G1304132 G1304132 TPRD.;	TR.G1304132 G1304132 TPRD.;	Homo septens Chediak-Higeshi syndrome 1 (CHS1), mKINA	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	601334790F1 NIH_MGC_39 Homo septens cDNA clone IMAGE:3688655 5"	

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Table 4
Single Exon Probes Expressed in Placenta

35339 0.76 35386 0.81 35388 0.67 35406 0.64 35406 0.64 35409 1.62 35446 2.15 35446 2.15 35446 1.35 35461 1.41 36461 1.41 36461 1.41 36461 2.16 35483 2.16 35483 2.16 35483 2.16 35483 2.16 35484 2.91 35485 0.84 35487 2.91 35549 3.69 35541 0.84 35541 0.84 35547 3.69	35339 0.76 35336 0.81 35336 0.87 35338 0.87 35406 0.64 35409 1.35 35449 1.62 35449 2.16 35449 2.16 35460 1.41 35460 1.41 35460 2.16 35460 2.91 35460 2.91 35460 2.91 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84 35460 0.84	35339 36386 35386 35388 35406 35409 36442 35446 35461 35483 35483 35489 35581 3556 3556 3556 3556 35583	35339 35386 35386 35388 35406 35409 35446 35446 35446 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461 35461	35339 35386 35386 35388 35406 35409 35442 35446 35446 35461 35483 35487 35487 35587 35587 35587 35583 35583 35583	35339 35386 35386 35388 35406 35406 35446 35447 35483 35483 35483 35481 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586	35339 35386 35386 35388 35406 35406 35446 35447 35461 35488 35489 35489 35489 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586 35586	35339 35386 35386 35388 35406 35406 35446 35447 35483 35489 35489 35587 35583 35583 35583 35685 35685 35685
	1.03 0.54 1.02 4.15 2.16 1.35 1.35 1.35 1.41 1.41 2.16 2.16 2.16 2.16 2.16 2.16 3.69 3.69	1.62 1.62 4.15 2.16 1.35 1.35 1.41 1.41 2.16 2.29 2.29 2.29 2.29 3.69 3.41	1.62 4.15 2.16 1.35 1.35 1.41 1.41 1.41 2.91 2.91 2.91 2.91 2.91 2.91 3.69 3.41 1.65 1.65	1.63 0.55 1.63 2.14 1.44 1.44 1.44 1.44 1.44 1.44 1.44	1.62 1.62 4.15 4.15 2.16 1.35 1.41 1.41 1.41 2.16 2.91 2.91 2.91 2.91 3.69 3.41 3.41 3.41 3.41 3.41 3.41 3.41 3.41	1.62 1.62 4.15 2.16 1.35 1.35 1.41 2.91 2.91 2.91 2.91 2.91 3.69 3.69 3.41 3.41 3.41 3.41 3.41 3.41 3.41 3.41	1.8: 0.55 1.3: 0.5 1.4: 1.4: 1.4: 2.4: 2.4: 2.4: 2.4: 2.4: 2.4: 2.4: 2
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0.0E+00 11424387 NT 0.0E+00 AW139873.1 ES 0.0E+00 AW139873.1 ES 0.0E+00 BE280272.1 ES 0.0E+00 BF700165.1 ES 0.0E+00 BF700165.1 ES 0.0E+00 BF700765.1 ES 0.0E+00 AA480770.1 ES 0.0E+00 AA882927.1 ES 0.0E+00 AA882927.1 ES	1142438 AW139873.1 AW139673.1 BE280272.1 BF700765.1 BF700765.1 BF700765.1 AL449770.1 AL449770.1 AA862327.1 1094703	1142438 AW139873.1 BE260272.1 BE700165.1 BF700165.1 BF700165.1 AR1449770.1 AA862827.1 1094703 Y11107.3	1142438 AW139873.1 BE260272.1 BE700165.1 BF700165.1 BF700165.1 AR1449770.1 AA862427.1 1094703 Y11107.3 BE278917.1	1142438 AW139873.1 BE260272.1 BF700165.1 BF700165.1 BF700165.1 AR1449770.1 AL1449770.1 AL149770.1 AL149770.1 AN902827.1 1094703 Y11107.3 BE278917.1 AV718377.1	1142438 AW139873.1 BE260272.1 BF700765.1 BF700765.1 BF700765.1 AR1449770.1 AA962927.1 AA962927.1 AA962977.1 AA962977.1 AA962977.1 AA962977.1	1142438 AW139873.1 BE250272.1 BF700765.1 BF700765.1 BF700765.1 AL449770.1 AA962327.1 AA962327.1 AA962377.1 AW1107.3 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703 1094703	1142438 AW139873.1 BE280272.1 BF700765.1 BF700765.1 BF700765.1 AL449770.1 AL449770.1 1094703 1094703 YY1107.3 BE278917.1 AW718377.1 AW718377.1 AW337277.1 AW337277.1 AU124051.1
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T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone Homo sapiens leukocyje immunoglobulin-like receptor, su (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mRNA   (LILR83), mR	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone Homo sapiens leukocyje immunoglobulin-like receptor, su (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mR	T_HUMAN   601900571F1 NIH_MGC_18 Homo capiens cDNA clone
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Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo saplens cDNA clone   T_HUMAN	Homo saplens leukocyte immunoglobulin-like receptor, su   (LILRB3), mRNA   UI-H-Bi1-adr-a-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapi   HUMAN   UI-H-Bi1-adr-a-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapi   T_HUMAN   601150051F1 NIH_MGC_19 Homo sapiens cDNA clone   T_HUMAN   602127664F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127664F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_56 Homo sapiens cDNA clone   T_HUMAN   602127694F1 NIH_MGC_21 Homo sapiens cDNA clone   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LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRB3   LILRb3   LILRB3   LILRb3   LILRb3   LILRb3   LILRb3   LILRb3   LILRb3   LILRb3	Homo saplans leukocyte inmunoglobulin-like receptor, su   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   UI-HBI1-adr-o-12-0-UI.st NCI_CGAP_Sub3 Homo sepi   HUMAN   UI-HBI1-adr-o-12-0-UI.st NCI_CGAP_Sub3 Homo sepi   HUMAN   602127664F1 NIH_MGC_18 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   AL449770 Homo sepiens fetal brain (Stavrides GS) Hom   Or80g02.st NCI_CGAP_Lu5 Homo sepiens cDNA clone   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NHOMO sepiens sepiens ankyrin 1, erythrocytic (ANK1), transcript NHOMO sepiens sepiens sepiens sepiens sepiens sepiens cDNA clone   HUMAN   Homo sepiens ITGB4 gene for Integrin beta 4 subunit as the sepiens sepiens sepiens sepiens cDNA clone   HUMAN   HOMO sepiens CDNA clone   HUMAN     HOMO sepiens ITGB4 gene for Integrin beta 4 subunit as the sepiens sepiens cDNA clone     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA clone     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA CLONE     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA CLONE     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA CLONE     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA CLONE     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA CLONE     HUMAN   HOMO SEPIENS HOMO SEPIENS CDNA CLONE     HUMAN   HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO SEPIENS HOMO	(LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB3), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (LILRB), mRNA  (	Homo sapians leukocyts immunoglobulin-like receptor, su   (LILRB3), mRNA   (LILRB3), mRNA   (LILRB3), mRNA   UI-HBI1-adr-a-12-0-UI.st NCI_CGAP_Sub3 Homo sepi   HUMAN   UI-HBI1-adr-a-12-0-UI.st NCI_CGAP_Sub3 Homo sepi   THUMAN   602127664F1 NIH_MGC_18 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   602127664F1 NIH_MGC_56 Homo sepiens cDNA clone   HUMAN   AL449770 Homo sepiens fetal brain (Stavrides GS) Hom   ox80g02.st NCI_CGAP_Lu5 Homo sepiens cDNA clone   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythrocytic (ANK1), transcript   HUMAN   HOMO sepiens ankyrin 1, erythroc
T_HUMAN UI-H-BI1-edr-e-12-0-UI.st NCI_CGAP_Sub3 Horno sepi I_HUMAN UI-H-BI1-edr-e-12-0-UI.st NCI_CGAP_Sub3 Horno sepi I_HUMAN	T_HUMAN UI-H-BI1-edr-e-12-0-UI.st NCI_CGAP_Sub3 Horno sepi T_HUMAN UI-H-BI1-edr-e-12-0-UI.st NCI_CGAP_Sub3 Horno sepi T_HUMAN 601160051F1 NIH_MGC_18 Horno sepiens cDNA clone T_HUMAN 602127664F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Horno sepiens cDNA clone	T_HUMAN UI-H-Bi1-edr-e-12-0-Ui.st NCI_CGAP_Sub3 Homo sepi T_HUMAN UI-H-Bi1-edr-e-12-0-Ui.st NCI_CGAP_Sub3 Homo sepi T_HUMAN 601150051F1 NIH_MGC_18 Homo sepiens cDNA clone T_HUMAN 602127664F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127664F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN RBOSOMAL PROTEIN L7A (HUMAN); Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \ Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \	T_HUMAN UI-H-BI1-edr-o-12-0-UI.st NCI_CGAP_Sub3 Homo sepi T_HUMAN UI-H-BI1-edr-o-12-0-UI.st NCI_CGAP_Sub3 Homo sepi T_HUMAN 601150051F1 NIH_MGC_18 Homo sepiens cDNA clone T_HUMAN 602127664F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127664F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN 602127604F1 NIH_MGC_56 Homo sepiens cDNA clone T_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); 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 NT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \  NT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \  NT	EST_HUMAN  UI-H-BI1-adr-\$-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepi EST_HUMAN  601150051F1 NIH_MGC_19 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  AL449770 Homo sepiens feial bein (Stavrides GS) Hom EST_HUMAN  AL409770 Homo sepiens feial bein (Stavrides GS) Hom EST_HUMAN  RIBOSOMAL PROTEIN L7A (HUMAN);  NT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \  NT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \  NT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript \  NT  Homo sepiens iTGB4 gene for integrin beta 4 subunit as	EST_HUMAN  UI-H-BI1-adr-\$-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepi EST_HUMAN  601150051F1 NIH_MGC_19 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone EST_HUMAN  AL449770 Homo sepiens ferial brein (Stavrides GS) Hom EST_HUMAN  AL409770 Homo sepiens cDNA clone EST_HUMAN  RIBOSOMAL PROTEIN L7A (HUMAN); 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 NT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ITGB4 gene for integrin beta 4 subunit, ex EST_HUMAN  601156330F1 NIH_MGC_21 Homo sepiens cDNA clone EST_HUMAN  601156330F1 NIH_MGC_21 Homo sepiens cDNA clone EST_HUMAN  601156330F1 NIH_MGC_51 Homo sepiens cDNA clone EST_HUMAN  601156330F1 NIH_MGC_51 Homo sepiens cDNA clone	EST_HUMAN  UI-H-BI1-adr-o-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepies  EST_HUMAN  601150051F1 NIH_MGC_19 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  For Sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens cDNA clone  EST_HUMAN  601156330F1 NIH_MGC_21 Homo sepiens cDNA clone  EST_HUMAN  INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)  INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)	EST_HUMAN  UI-H-BI1-adr-o-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepies  EST_HUMAN  601150051F1 NIH_MGC_19 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  RIBOSOMAL PROTEIN L7A (HUMAN), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens cDNA clone  EST_HUMAN  601156330F1 NIH_MGC_21 Homo sepiens cDNA clone  EST_HUMAN  INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)  INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)	EST_HUMAN  UI-H-BI1-adr-o-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepies  EST_HUMAN  601150051F1 NIH_MGC_19 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  602127664F1 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  AL449770 Homo sepiens fizial brain (Stavrides GS) Hom  603163072 NIH_MGC_56 Homo sepiens cDNA clone  EST_HUMAN  AL449770 Homo sepiens fizial brain (Stavrides GS) Hom  603163030F1 NIH_MGC_51 Homo sepiens cDNA clone  EST_HUMAN  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIH  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens ankyrin 1, erythrocytic (ANK1), transcript NIT  Homo sepiens cDNA clone  EST_HUMAN  601153330F1 NIH_MGC_21 Homo sepiens cDNA clone  EST_HUMAN  INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)  EST_HUMAN  AU124051 NT2RM2 Homo sepiens cDNA clone PLACE-1  EST_HUMAN  AU140704 PLACE-4 Homo sepiens cDNA clone PLACE-1
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7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1, NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1, NT Homo sapiens 1TGB4 gene for integrin beta 4 subunit, ex EST_HUMAN 601166330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN 801166330F1 NIH_MGC_21 Homo sapiens CDNA clone EST_HUMAN 801166330F1 NIH_MGC_21 Homo sapiens CDNA clone	EST_HUMAN 601150051F1 NIH_MGC_19 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 7030702.91 NC] CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN 7030902.91 NC] CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN 7030902.91 NC] CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN 7030903911 NC] CGAP_CON CANK1), transcript NC] NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NC] NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NC] EST_HUMAN 801156330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN 801156330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN NC] EST_HUMAN NC] NCTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN) NTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)	EST_HUMAN 601150051F1 NIH_MGC_19 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 7080g02.91 NCI_CCAP_Lu5 Homo sapiens cDNA clone EST_HUMAN 7080g02.91 NCI_CCAP_Lu5 Homo sapiens cDNA clone EST_HUMAN 7080g02.91 NCI_CCAP_Fent Homo sapiens cDNA clone EST_HUMAN 7080g02.91 NCI_CCAP_Pent Homo sapiens cDNA clone EST_HUMAN 801168330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN 801168330F1 NIH_MGC_97 Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone EST_HUMAN 80718377 FHTB Homo sapiens cDNA clone	EST_HUMAN 601150051F1 NIH_MGC_19 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_57 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_57 Homo sapiens cDNA clone EST_HUMAN 602127677.x1 NCI_CCAP_Pent Homo sapiens cDNA clone EST_HUMAN 602127671 NTZRM2 Homo sapiens cDNA clone EST_HUMAN 602127671 NTZRM2 Homo sapiens cDNA clone EST_HUMAN 602127671 NTZRM2 Homo sapiens cDNA clone EST_HUMAN 602127671 NTZRM2 Homo sapiens cDNA clone EST_HUMAN 602127671 NTZRM2 Homo sapiens cDNA clone FLACE27
EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127604F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN AL449770 Homo capiens fetal brain (Stavrides GS) Homo capiens cDNA clone EST_HUMAN AL449770 Homo capiens fetal brain (Stavrides GS) Homo capiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); transcript variations analysin 1, erg/throcytic (ANK1), transcript variations.	EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN AL449770 Homo capiens feial brain (Stavrides GS) Homo capiens cDNA clone EST_HUMAN AL449770 Homo capiens feial brain (Stavrides GS) Homo capiens cDNA clone EST_HUMAN RBOSOMAL PROTEIN L7A (HUMAN); 47037 NT Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127694F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 7080602.51 NCI_CGAP_L15 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1 Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1 Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1 Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127694F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 70480502.51 NCI_CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, ery	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 702002.51 NCI_CSAP_Lu5 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT Homo sapiens ITGB4 gene for integrin beta 4 subunit, experiments ankyrin 1, erythrocytic (ANK1), transcript NIT Homo sapiens ITGB4 gene for integrin beta 4 subunit, experiments ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ITGB4 gene for integrin beta 4 subunit, experiments ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript NIT A7037 NT Homo	EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN LTA (HUMAN); Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo capiens iTGB4 gene for integrin beta 4 subunit, ex EST_HUMAN 601156330F1 NIH_MGC_21 Homo capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN Homo capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN TOBA gene for integrin beta 4 subunit, ex 47037 NT Homo capiens iTGB4 gene for integrin beta 4 subunit, ex 47037 NT HOMO capiens iTGB4 gene for integrin beta 4 subunit, ex 47037 NT HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone EST_HUMAN RIBOSOMAL FROTEIN HOMO capiens cDNA clone	EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN AL449770 Homo capiens feld brain (Stawfdes GS) Homo EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN): Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo capiens iTGB4 gene for integrin beta 4 subunit, ex EST_HUMAN 601166330F1 NIH_MGC_21 Homo capiens cDNA clone EST_HUMAN AV718377 FHTB Homo capiens cDNA clone EST_HUMAN INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN) INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)	EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo capiens cDNA clone EST_HUMAN AL449770 Homo capiens feld brain (Stavides GS) Homo EST_HUMAN RIBOSOMAL PROTEIN LTA Homo capiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN LTA Homo capiens cDNA clone EST_HUMAN Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v Homo capiens ankyrin 1, erythrocytic (ANK1), transcript v Homo capiens TGB4 gene for Integrin beta 4 subunit, ex EST_HUMAN 601166330F1 NIH_MGC_21 Homo capiens cDNA clone EST_HUMAN AV718377 FHTB Homo capiens cDNA clone EST_HUMAN INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN) EST_HUMAN AU124051 NT2RM2 Homo capiens cDNA clone NT2RM EST_HUMAN AU140704 PLACE4 Homo capiens cDNA clone PLACE4
EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127604F1 NIH_MGC_58 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens feial brain (Stavrides GS) Hom or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); transcript v	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127604F1 NIH_MGC_58 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens feial brain (Staurides GS) Hom or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127604F1 NIH_MGC_58 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens feial brain (Staurides GS) Hom or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens feid brain (stavrides GS) Hom EST_HUMAN RDG02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN); Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1 Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1 Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1 Homo sapiens ITGB4 gene for integrin beta 4 subunit, ex	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens feid brain (Stavrides GS) Hom EST_HUMAN REDSOMAL PROTEIN L7A (HUMAN); Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic (ANK1), transcript 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, erythrocytic 1, eryt	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 802127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens feial brain (Stavirides GS) Homo EST_HUMAN RIBOSOMAL PROTEIN LTA (HUMAN); Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v Homo sapiens iTGB4 gene for integrin beta 4 subunit, ex EST_HUMAN 801156330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMAL PROTEIN LTA (HUMAN)  Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v Homo sapiens iTGB4 gene for integrin beta 4 subunit, ex EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN RIBOSOMF1 NIH_MGC_21 Homo sapiens cDNA clone	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 802127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN AL449770 Homo sapiens felal brain (Stavirides GS) Homo EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN): Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v Homo sapiens iTGB4 gene for integrin beta 4 subunit, ex EST_HUMAN 801166330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN AV718377 FHTB Homo sapiens cDNA clone EST_HUMAN INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN) INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN) EST_HUMAN AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM	EST_HUMAN 602127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN 802127664F1 NIH_MGC_56 Homo sapiens cDNA clone EST_HUMAN AL.449770 Homo sapiens feld brain (Stavirides GS) Homo EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN): Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript v 47037 NT Homo sapiens iTGB4 gene for integrin beta 4 subunit, ex EST_HUMAN 801166330F1 NIH_MGC_21 Homo sapiens cDNA clone EST_HUMAN AV718377 FHTB Homo sapiens cDNA clone EST_HUMAN INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN) EST_HUMAN AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM EST_HUMAN AU124051 NT2RM2 Homo sapiens cDNA clone PLACE4
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	10947037 NT Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript	10947037 NT Y11107:3 NT	0947037 NT NT R1 EST_HUMAN	0947037 NT NT 7.1 EST_HUMAN 7.1 EST_HUMAN	9947037 NT  NT  NT  7.1 EST_HUMAN  7.1 EST_HUMAN  7.1 EST_HUMAN	9947037 NT  NT  NT  7.1 EST_HUMAN  7.1 EST_HUMAN  7.1 EST_HUMAN  1.1 EST_HUMAN	9947037 NT  NT  NT  NT  1.1 EST_HUMAN  1.1 EST_HUMAN  1.1 EST_HUMAN  4.1 EST_HUMAN

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Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9345	5 22421		0.76	0.0€+00	0.0E+00 BE410768.1	EST_HUMAN	801301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9359	9 22434	35983	1.32	0.0€+00	0.0E+00 BF002024.1	EST_HUMAN	7g97h12x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:08UH62 Q8UH62 HYPOTHETICAL 42.5 KD PROTEIN. ;
9373	П		1.62	0.0E+00	_	NT	Homo sapiens mRNA for KIAA0578 protein, partial cds
9374	П	36010	3.42	0.0E+00	·	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE 3943463 5'
9378	8 22453	36015	0.47	0.0€+00	0.0E+00 BE810292.1	EST_HUMAN	RC3-PT0151-280600-011-c05 PT0151 Homo sepiens cDNA
9378	8 22453	36016	0.47	0.0€+00	0.0E+00 BE810292.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sepiens cDNA
9381			0.97	0.0E+00	0.0E+00 AU136229.1	EST_HUMAN	AU136229 PLACE1 Homo seplens cDNA clone PLACE1003804 5'
9386	6 22461	36024	1.19	0.0E+00	0.0E+00 BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3911986 5
9386		36025	1.19	0.0€+00	0.0E+00 BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3911986 5'
9403	3 22477	36040	0.57	0.0E+00	0.0E+00 AB011165.1	NT	Homo saplens mRNA for KIAA0594 protein, partial cds
9407	7 22481	36044	1.43	0.0€+00	0.0E+00 AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo saplens cDNA 5" end
9407		35045	1.43	0.0≝+00	0.0E+00 AA344001.1	EST_HÜMAN	EST50505 Call bladder I Homo capieno cDNA 5' end
9464	22521	36083	0.96	0.0€+00	AW673469.1	EST_HUMAN	be54d08.y3 NIH_MGC_10 Homo septens cDNA clone IMAGE:2900367 5 similar to TR:060275 O60275 KIAA0522 PROTEIN ;
9464	4 22521	36084	0.96	0.0=+00	0.0E+00 AW673469.1	EST_HUMAN	ba54d08,y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:060275 O60275 KIAA0522 PROTEIN ;
9498	8 22554		0.99	0.0€+00	0.0E+00 BE207063.1	EST_HUMAN	ba06f05.y1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2823873 5' similar to gb.L35049 Mus musculus Bct-xL mRNA, complete cds (MOUSE);
							be09f05;/1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2823873 5' stmilar to gb:L35049 Mus musculus
9509	22775	36346	1 95	0.05+00	0.0E+00 RF348013.1	EST HUMAN	602023150F1 NCI CGAP Brif67 Homo sablens cDNA clone IMAGE:4158300 5
9545	П	٦	3.1	0.0⊞+00	0.0E+00 BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA
9577			0.49	0.0€+00	0.0E+00 BF034377.1	NAWUH_TSE	601455116F1 NIH_MGC_68 Hamo sapiens cDNA clane IMAGE:3859035 5'
9577	7 22719	36288	0.49	0.0E+00	0.0E+00 BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo septens cDNA clone IMAGE:3859035 5'
9583	13 22725	36295	0.58	0.0E+00	0.0E+00 AI906351.1	EST_HUMAN	
9586	)6 2 <i>2</i> 728	36297	0.77	0.0€+00	5803069 NT	NT	Homo sepiens leukocyte immunoglobulin-like receptor, subfamilly B (with TM and ITIM domains), member 6 (LILRB5), mRNA
9586	15 2 <i>21</i> 728	36298	ó.77	0.0€+00	5803069 NT	NT	Homo sepions leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9596		36223	0.85	0.0€+00	0.0E+00 AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: https3) Hamo sepiens cDNA done DKFZp434L0120 51
9831	22686	36257	1.3	0.0∐+00	0.0E+00 Al088043.1	EST_HUMAN	ow60h01.x1 Soeres_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IWAGE:1651249 3' striller to TR-Q14677 Q14677 KIAA0171 PROTEIN.;
9638	П	П	0.67	П	0.0E+00 BF308962_1	EST_HUMAN	601892245F1 NIH_MGC_17 Homo papiens cDNA clone IMAGE:4138066 5'

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9850	9850	9841	9841	9821	9788	9788	9776	9759	9739	9739	9739	9729	9727	9727	9709	9697	9688		9696	9886	9683	9673	9673	9670	9643	9642	9642	9640	9640	Probe SEQ ID NO:
22890	22890	22881	22881	22861		22828	22816						П	22792	22758	22746	22737	Т	٦	П	П	22635	22635	22632		21085	21085	27083	21083	Exon SEQ ID NO:
38471	36470	36465	38484	36442	36406	36405	36394	36265	36380	36379	36378	36368	36365	36364	36329	36315	36307		36306	36305		36206	36205	36201	34601	34600	34599	34598	34595	ORF SEQ
1.87	1.87	1.72	1.72	1.13	2.55	255	1.5		203			3.38		4.49			5.46				5.87	69.0		3.95	216	6,62	6.52	232	232	Expression Signal
0.0E+00	0.0E+00	Γ				П							0.0€+00	0.0€+00					-		0.0€+00	0.0€+00	0.0⊑+00	0.0E+00	0.0圧+00	0.0€+00	0.0€+00	0.0E+00	0.0€+00	Most Similar (Top) Hit BLAST E Value
0.0E+00 AF02930B.1	0.0E+00 AF029308.1	0.0E+00 AW500293.1	0.0E+00 AW500283.1	0.0E+00 BE082977.1	0.0E+00 AF019084.1	0.0E+00 AF019084.1	0.0E+00 AV701829.1	0.0E+00 BE900549.1	11437282 NT		11437282 NT	0.0E+00 BE746215.1	0.0E+00 C06158.1	0.0E+00 C06158.1	0.0E+00 BE263191.1	0.0E+00 D87675.1	0.0E+00 AW163779.1		0.0E+00 BE781332.1	0.0E+00 BE781382.1	0.0E+00 BE255829.1	0.0E+00 BE885128.1	0.0E+00 BE885128.1	0.0E+00 AF153456.1	0.0E+00 AW953838.1	0.0E+00 A1290909.1	0.0E+00 Al290909.1	11560151 NT	11560151 NT	Top Hit Acession No.
ZT	NT.	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	TN	EST_HUMAN	EST_HUMAN	2 NT	2 NT	2NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	ì	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT NT	Top Hit Database Source
Homo saplens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	Homo saplens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5	UI-HF-BN0-ekg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5	RC2-BT0642-130300-017-g01 BT0642 Homo sepiens cDNA	Homo sepiens keretin 2e (KRT2E) gene, complete cds	Homo septens keretin 2e (KRT2E) gene, complete cds	AV701829 ADB Homo septens cDNA clone ADBBYH01 5'		Homo septens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	601578683F1 NIH_MGC_9 Hamo septens cDNA clone IMAGE:3927548 5'		C06158 Human pancreatic islet Homo sapiens cDNA done hbc5605	601145054F2 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3160477 5	Homo septens DNA for emyloid precursor protein, complete cds	60S RIBOSOMAL PROTEIN L7A (HUMAN);		801466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5	601466828F1 NIH_MGC_67 Homo septens cDNA clone IMAGE:3870007 5	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 51.	601510882F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3912165 5'	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8	EST366026 MAGE resequences, MAGC Homo sepiens cDNA	qm09a06.x1 NCL_CGAP_Lu5 Homo sapiens cDNA cione IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;	qm09e06X1 NCI_CGAP_Lu6 Home septens cUNA cione IMAGE:1881286 3 similar to 5W:RL28_HUWAN P28316 60S RIBOSOMAL PROTEIN L23A.;	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo seplens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Тор Нit Descriptor

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9852	2 22892	36472	0.62	0.0€+00	0.0E+00 BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo saptens cDNA clone IMAGE:3874037 5'
9852	2 22892	36473	0.62	0.0€+00	0.0E+00 BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9861	1 22801	36485	0.63	0.0€+00	0.0E+00 W 58629.1	EST HUMAN	zd16e11.r1 Scares_fetal_heart_NbHH19W Homo sapiens cDNA cione IMAGE:340844 5'
9861		36486	0.63	0.0 <b>E+</b> 00	0.0E+00 W56629.1	EST_HUMAN	zd16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA cione IMAGE:340844 5
9874	22914	36499	0.46	0.0€+00	0.0E+00 AF208054.1	NT	Homo sapiens non-inhibitory killer-cell Ig-like receptor KIR (KIR2DS5) mRNA, complete cds
9876		36500	1.04	0.0E+00	0.0E+00 AB035356.1	NT	Homo sapiens mRNA for neurexin Leipha protein, complete cds
9879	22919		0.64	0.0€+00	0.0E+00 AI124760.1	EST_HUMAN	am56a11.x1 Johnston frontal cortex Homo sepiens cDNA clone IMAGE:1539548 3'
9881	22921	36505	3	0.0€+00	0.0E+00 AW500526.1	EST_HUMAN	U⊨HF-BN0-akj-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5
9925	5 22965	36554	265	0.0€+00	0.0E+00 AF009638.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9953	3 22992	36585	2.69	0.0E+00 S78468,1	S78468,1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 6 of 6]
9953	22992	36586	269	0.0E+00	0.05+00 878468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9956	22895	36591	2.72	0.0E+00	0.0E+00 BE563320.1	EST HUMAN	601334603F1 NIH_MGC_39 Hamo sapiens cDNA clone IMAGE:3688680 5
9976	3 23015	36608	1.26	0.0E+00	0.0E+00 AW363135.1	EST_HUMAN	CN2-CT0311-301199-043-h11 CT0311 Homo sepiens cDNA
9997	7 23035	36627	0.66	0.0E+00	11436432 NT	NT	
8686	3 23036	36828	0.62	0.0E+00	11424387 NT	Z .	Homo septens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (ULRB3), mRNA
10007	П	36638	0.91	0.05+00	0.0E+00 BE206710.1	EST_HUMAN	bb26c01.x1 NIH_MGC_5 Homo sapians cDNA clone IMAGE:2984000 3*
10024	23062	36658	4.49	0.0Ε+00	0.0E+00 AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo septens cDNA clone NT2RP3004260 5
10024	23062	36659	4.49	0.0E+00	0.0E+00 AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo septens cDNA clone NT2RP3004260 5
10033		36871	0.95		0.0E+00 AW500938.1	EST_HUMAN	UI-HF-BP0p-air-f-05-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5
10039	9 23077	36677	13.26		0.0E+00 BE740490.1	EST_HUMAN	60159558F1 NIH_MGC_9 Homo septens cDNA clone IMAGE:3949383 5
10039	9 23077	36678	13.26		0.0E+00 BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo septems cDNA clone IMAGE:3949383 5
10052		36692	1.56	0.0E+08	82087		Homo sepiens KIAA0345 gene product (KIAA0345), mKNA
10069	23107		1.52	0.0≌+00	0.0E+00 AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: https://enhosapiens.cuna.cone.ukrzp434L0120 5
10074	Г		0.57	0.0€+00	0.0E+00 AL041084.2	EST HUMAN	DKFZp434B2416_r1 434 (synonym: htes3) Homo sapiens cDNA clone UKrZp434B2416 5
10084	1		2.32		0.0E+00 AU132349.1	EST_HUMAN	AU 132348 N 1 2RT3 Floring Segrens CUNA Cione N 1 2RT3004200 3
10085	П	Γ	2.16	Γ	0.0E+00 AF162308.1	NT NT	Homo sepiens protocednenn alpha 12 (PCUH-alpha12) mRNA, complete cus
10112	Г		2.84	Γ	0.0E+00[AF009220.1	Z	Homo sapiens ieucocyke immunogłobulin-like receptor-i rinkiwy, complete cas
10112	Т	Γ	2.84	Γ	0.0E+00 AF009ZZ0.1	2	Thoras septens recevely a minute graphical forms septens spiles spiles continues one
82101	Т		1.13	Τ	O.UE+UU BFU8Z898.1	EST TOWAR	WINT-INDIES VIII MOO 14 Lamp continue appeira contro
10160			2.75	Ī	0.0E+00 BE280733.1	EST HUMAN	CO1200227 T NIT MICC 41 Home seniors CONA close IMAGE 3643045 5
80101	9 23200	88/00	0.97	Γ	0.001001000000.1	E-O-I TOWN	AN IMPAGE 1. THE THINK AND AND AND AND AND AND AND AND AND AND

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Single Exon Probes Expressed in Placenta

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. 13	1	Tellocit.	0.05+00	0.77	Ī	Г	10475
Upon positions hypothesis of COHO the figures profess El (OOSOA (El 19950A) mRNA	EULHOMAN	0.0E+00 BE891113.1	0.01	0.64	Γ	Г	10473
12010 September 20 Homo services cONA clone IMAGE 3017508 5	ų.	1N /789C/4	0.05.00	0.65	Γ	Г	10461
EDITIOS SETTING III (NIEVNIS EDINA O EIN	EST_HUMAN	0.0E+00 AA311624.1	0.0E+00	0.91		Г	10460
601432317F1 NIH_MGC_72 Homo capiens CUNA clone IMAGE:3917453 5	EST HUMAN	0.0E+00 BE897487.1	0.011+00	0.48	Γ	Г	10450
	EST_HUMAN	0.0E+00 BE958611.1	0.0E+00	0.89	37074	23467	10432
601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3830177 5	EST_HUMAN	0.0E+00 BE958511.1	0.0€+00	0.89			10432
AU127403 NT2RP2 Homo sepiens cDNA clone NT2RP2001212 5	EST_HUMAN	0.0E+00 AU127-03.1	0.0E+00	0.8			10422
601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5	EST_HUMAN	BE7307,72.1	0.0€+00	6.34			10417
601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'	EST_HUMAN	0.0E+00 BE7307/72.1	0.0€+00	5.34			10417
801491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5	EST_HUMAN	0.0E+00 BE880658.1	0.0E+00	0.99	37046		10404
	NT	0.0E+00 AF179308.1	0.0E+00	1.61			10359
zl31f01.r1 Soares_pregnant_utarus_NbHPU Homo saplens cDNA clone IMAGE:503545 5	EST_HUMAN	0.0E+00 AA131248.1	0.0€+00	0.76			10317
z/31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5	EST_HUMAN	0.0E+00 AA131248.1	0.0€+00	0.76			10317
zp97h11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5	EST_HUMAN	0.0E+00 AA196387.1	0.0E+00	2.42			10290
Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4	NT	0.0E+00 AF072408.1	0.0E+00	0.72			10288
AV895712 GKC Homo sapiens cDNA clone GKCDXA07 5'	EST_HUMAN	0.0E+00 AV695712.1	0.0E+00	0.73			10282
AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'	EST_HUMAN	0.0E+00 AV695712.1	0.0€+00	0.73			10282
Homo saplens partial RANBP7 gene for RenBP7/importh7 and partial ZNF143 gene	NT	0.0E+00 AJ2958,14.1	0.0E+00	2	36910	23312	10277
Homo sapiens partial RANBP7 gene for RanBP7/Importin7 and partial ZNF143 gene	NT	0.0E+00 AJ2958;14.1	0.0€+00	.2		23312	10277
AU136637 PLACE1 Homo capieno cDNA clane PLACE1004737 5	EST HUMAN	0.0E+00 AU136637.1	0.0E+00	3.07			10261
AU136637 PLACE1 Homo saplens cDNA clone PLACE1004737 5	EST_HUMAN	0.0E+00 AU136637.1	0.0E+00	3.07			10261
	NT	11421001	0.0E+00	2.75	36852		10228
Homo sapiens HEF like Protein (HEFL), mRNA	NT	11421001 NT	0.0E+00	2.75	38851	П	10228
Homo sapiens killer cell inhibitory receptor KIRCl gene, exons 2, 3, and 4	N.T	0.0E+00 AF072438.1	0.0E+00	3.31			10225
AU143873 Y78AA1 Homo sapiens cDNA clone Y79AA1002307 5	EST_HUMAN	0.0E+00 AU143673.1	0.0€+00	6.99	36846		10222
AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 6	EST_HUMAN	0.0E+00 AU143673.1	0.0€+00	5.99		П	10222
EST376186 MAGE resequences, MAGH Homo sepiens cDNA	EST HUMAN	0.0E+00 AW984113.1	0.0€+00	0.94	36834		10208
Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	NT	11427235	0.0€+00	0.69	36819	23225	10188
EST46740 Fetal kidney II Homo sapiens cDNA 5' end	EST_HUMAN	0.0E+00 AA341305.1	0.0€+00	0.84	36807	23216	10179
xx72501.x1 NCI_CGAP_CML1 Homo sepiens cDNA clone IMAGE:2898977 3' similar to gb:X02182_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);	EST_HUMAN	0.0E+00 AW236269.1	0.0E+00	0.87	30896	23215	10178
601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'	EST_HUMAN	0.0E+00 BE388700.1	0.0E+00	6.67	36800	23206	10169
Top Hit Descriptor	Top Hit Datebase Source	Top HIt Acession	Most Similar (Top) Hit BLAST E Value	Expression Signel	ORF SEQ.	Exon SEQ ID NO:	Probe SEQ ID NO:
		9.0					

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	SEO ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10487	23522	37131	0.5	0.0+30.0	0.0E+00 BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo septens cDNA clone IMAGE:2887918 5
10487	$\neg$		0.5	0.0€+00	0.0E+00 BE304E22.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10494	П		5.8	0.0Ё+00	0.0E+00 AB008590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10494			5.8	0.0E+00	0.0E+00 AB006590.1	NT	Homo sepiens mRNA for estrogen receptor beta, complete cds
10502	23537	37147	0.77	0.0+⊒0.0	0.0E+00 AA704457.1	EST HUMAN	319b06.s1 Scares_fetal_liver_spleen_fNFLS_S1 Homo saplens cDNA clone IMAGE:450707 3' similar to qb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10604	Т	$\exists$	1.08	0.0E+00	0.0E+00 M22921.1	T	Human beta 1,4-galactosy-transferase mRNA, complete cds
10506			4.81	0.0€+00	0.0E+00 BF340331.1	EST_HUMAN	602037045F1 NCL_CGAP_Brn84 Homo sapiens cDNA clone IMAGE;4184939 5
10506	23541	37152	4.81	0.0€+00	0.0E+00 BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5
10530	23565	37172	0.69	0.0E+00	0.0E+00 BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Hamo sepiens cDNA clone IMAGE:3924578 6'
10530			0.59	0.0€+00	0.0E+00 BE897149.1	EST_HUMAN	801439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10595	23630	37237	1.07	0.0€+00	0.0E+00 Al6318;8.1	EST_HUMAN	wa36903.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10595	23630	37238	1.07	0.0E+00	0.0E+00 Al6318;8.1	EST HUMAN	ws36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE::2300189 3' similer to TR:Q61204 Q61204 NOTCH2-LIKE ;
10610		37252	1.64	0.0E+00 T03078;1	T03078!1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3'end
10638		37282	0.67	0.0E+00	0.0E+00 AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sepiens cDNA clone MAMMA1002368 5'
10644		37288	0.48	0.0E+00	6005921 NT	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10668	23702	37312	2.22	0.0⋶+00	0.0E+00 BF436218.1	EST_HUMAN	nab45e12x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:3265271 3
10669	23703		1.71	0.0E+00	0.0E+00 AV654765.1	EST_HUMAN	AV654765 GLC Homo sepiens cDNA clone GLCDZC07 3'
10689	23722	37328	3.08	0.0€+00	0.0E+00 AW517960.1	EST_HUMAN	x174501 x1 NCI_CGAP_KIC8 Homo sepiens cDNA done IMAGE:2807401 3' strilter to gb:M69066 MOESIN (HUMAN);
10693		37332	2.88	0.0E+00	0.0E+00 BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5
10709		37348	0.82	0.0€+00	11436005	NT	Homo sepiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10735	23768	37378	0.52	0.0E+00 X89893.1	X89893,1	NT	H. sepiens mRNA for NK receptor (183 Acti)
10736	23769	37379	3.36	0.0€+00	0.0E+00 BE7817,42.1	EST_HUMAN	601487419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10758	П	37409	2.32		0.0E+00 BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sepiens cDNA
10758	23781	37410	2.32		0.0E+00 BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-003 BT0642 Homo sepiens cDNA
10764		37417	0.67		Y080321	NT T	Human endogenous retrovirus-K, LTR U5 and gag gene
10772	23805	37428	0.77		0.0E+00 AI656890.1	EST_HUMAN	#54e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244612.3
10779			9.15		0.0E+00 BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5
10779	23812	37436	9.15		0.0E+00 BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3835198 5'
10784	23817	37439	0.63	0.0E+00	0.0E+00 BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Hamo sapiens cDNA clone IMAGE:3845956 3
10784	23817	37440	. 0.63	0.0E+00	0.0E+00 BE617655.1	EST_HUMAN	60144172311 NIH_MGC_55 Home sapiens cDNA clone IMAGE:3845956 3

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	1	0020000 141	0.01.00	1.00	37003	24004	20801
Homo sapiens myosin, heavy polypoptide 2, skeletal muscle, adult (MYH2), mRNA		202203	0.05±00		T	Т	
Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	IN	6666268	0.0E+00	1,65	٦	٦	10952
601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918636 5	EST_HUMAN	0.0E+00 BE891630.1	0.0E+00	6.12	37687	24032	10950
601505204F2 NIH_MGC_71 Homo sapiens cUNA clone IMAGE:3806865 5	EST_HUMAN	0.0E+00 BE882109.1	0.0⋶+00	3.22	37665		10946
wu32b06x1 Scares_Dieckgraefe_colon_NHCU Homo sapiens cuna cione invage: 2021710 3	EST HUMAN	0.0E+00 Al991827.1	0.0E+00	2.68	37659	24024	10942
Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1tt (HIK1tt) mikiva	3	4504536 NT	0.0€+00	8.39	37658	24023	10941
Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTRTE) mRNA	N	4504536 NT	0.0E+00	8.39	37657	24023	10941
Homo saplens hypothetical protein FLJ20079 (FLJ20079), mRNA	NT	11424829	0.0E+00	2.85	37656	24022	10840
UI-HF-BL0-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5	EST_HUMAN	0.0E+00 AW404795.1 EST	0.0E+00	1.52	37651	24018	10936
Homo sapiens NOD2 protein (NOD2), mRNA	ZT	11545911 NT	0.0€+00	3.59	37638	24003	10920
Homo sapiens NOD2 protein (NOD2), mRNA	<b>3</b> 1	11545911 NT	0.0€+00	3.59	37637	24003	10920
601451502F1 NIH_MGC_55 Homo sapiens cUNA cione IMAGE:3855289 5	EST_HUMAN	0.0E+00 BE872908.1	0.0€+00	1.74	37630	23996	10913
601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3856289 5	EST_HUMAN	0.0E+00 BE872908.1	0.0€+00	1.74	37629	23996	10913
801888704F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122649 5	EST_HUMAN	0.0E+00 BF306642.1	0.0€+00	1.48	37628	23995	10912
WSR1 MSR1 repetitive element;	EST HUMAN	0.0E+00 Al652239.1	0.0E+00	2.72	37623	23990	10907
ANDI COAD COS Home emisers cONA close IMAGE: 2306074 3' similar to contains element	10,000	0.0000000000000000000000000000000000000	0.00	2.16	22010	DRACT	/Oaci
wb28a12x1 NC _CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305974 3' similar to contains element   NSR1 MSR1 repetitive element :	EST HUMAN	A 185222 1	00+30	2 72			1000
TCAAP3D0917 Pediatric ecute myelogenous leukemia cell (FAB M1) Baylor-HIGGC project= I CAA Fiormo sapiens cDNA clone TCAAP0917	EST_HUMAN	0.0E+00 BE243270.1	0.0E+00	8.59	37621	23989	10906
TR:Q60566 Q60566 VDX;	EST_HUMAN	0.0E+00 AW057821.1	0.0€+00	1.7	37614	23982	10898
w61f09.x1 Spares NSF F8 9W OT PA P S1 Hamo capiano cDNA clone IMAGE:2553065 3' similar to					Ī	Т	1000
Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	NT	11431124 NT	0.05+00	2.52	I	T	10895
Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	NT	11431124 NT	0.05+00	2.62	Ī	Т	10995
EST375636 MAGE resequences, MAGH Homo septens cDNA	EST HUMAN	0.0E+00 AW963563.1	0.00+00	5.5	37595	Т	10882
RC3-ST0197-120200-015-a03 ST0197 Homo saplens dDNA	EST_HUMAN	0.0E+00 AW813783.1	0.0H+00	2.55	٦	Т	10874
AV711075 Cu Homo sapians cDNA cione CuAAKG05 5	EST_HUMAN	0.0E+00 AV711075.1	0.0€+00	1.84		٦	10872
AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5	EST_HUMAN	0.0E+00 AV711075.1	0.0E+00	1.84		$\neg$	10872
AU125996 NT2RM4 Homo sapiens cDNA clone NT2RM4002536 5	EST_HUMAN	0.0E+00 AU125696.1	0.0분+00	0.62		٦	10863
601308167F1 NIH_MGC_44 Homo saptens cDNA clone IMAGE:3626128 5	EST_HUMAN	0.0E+00 BE392276.1	0.0€+00	0.69	$\neg$	П	10846
Homo saptens DNA for amybid precursor protein, complete cds	NT	0.0E+00 D87675,1	0.0E+00	0.54	37491	7	10835
yp01a10.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:186138 5"	EST_HUMAN	0.0E+00 H39805.1	0.0E+00	0.51		П	10809
Horno septens mRNA for estrogen receptor beta, complete cds	NT	0.0E+00 AB006590.1	0.0E+00	0.46	37443	23819	· 10786
Homo sapiens mRNA for estrogen receptor beta, complete cds	NT .	0.0E+00 AB006590.1	0.0E+00	0.46	37442	23819	10786
Top Hit Descriptor	Database Source	Top Hit Acession No.	(Top)Hit BLASTE Value	Expression . Signal	ORF SEQ ID NO:	NO:	SEQ ID
	Top Li		Most Similar				7
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Table 4

Single Exon Probes Expressed in Placenta

		ı				Singi	e Exon Plobe	Single Exon Process Expressed in Placenta
	Probe SEQ ID NO:	Exon NO:	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Тор Нії Descriptor
_	10965	24046	37680	22 14	0.0E+00	0.0E+00 BE903304.1	EST_HUMAN	601674332F1 NIH MGC 21 Homo septens cDNA clone IMAGE:3957343 5'
	10968	19087	32389	1.85	0.0=+00	0.0E+00 AA195905.1	EST HUMAN	zp95b11.r1 Stretagene muscle 937209 Homo sepiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
	10990	24069	37703	4.49	0.0€+00	0.0E+00 BE793498.1	EST_HUMAN	601588829F1 NIH MGC_7 Hamo septens cDNA clone IMAGE:3943015 6'
	10998	24077	37710	2.4	0.0€+00	0.0E+00 BE729706.1	EST_HUMAN	601562854F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3832575 5'
	10998	24077	37711	2.4	0.0€+00	0.0E+00 BE729708.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
	10999	24078	37712	11.66	0.0E+00	0.0E+00 AV727362.1	EST_HUMAN	AV727362 HTC Homo sepiens cDNA clone HTCAQH06 5
_	10999	24078	37713	11.66	0.0⊞+00	0.0E+00 AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5
_	11003	24082	37718	1.6	0.0E+00	0.0E+00 R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1NIB Homo sepiens cDNA clone IMAGE:31674 5
	11003	24082	37719	1.6	0.0E+00	0.0E+00 R171321	EST_HUMAN	yg09e09,r1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31874 5
	11009	24088		262	0.0€+00	0.0E+00 AW139414.1	EST_HUMAN	OFFI-BIT-BIT-BIT-BIT-BIT-BIT-BIT-BIT-BIT-BI
	11014	24083	37732	11.61	0.015+00	0.0E+00 AW516058.1	EST_HUMAN	RIBOSOMAL PROTEIN \$16 (HUMAN);
	11020	24099	37737	4.44	0.0E+00	0.0E+00 AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sepiens cDNA clame PLACE1002794 5
<u>.                                    </u>	11026	24105	37741	2.56	0.011+00	0.0E+00 AW593533.1	EST HUMAN	hg13d02x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element ;
								hg13d02x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2945476 3' similar to contains
	11026	24105	37742	256	0.0E+00	0.0E+00 AW693833.1	EST_HUMAN	element WORT repeative element;
	1	34105	37743	٠ ١	0.05+00	0 0E+00 AW#03533 1	NAMIN TOTAL	hg13d02x1 Socres_NFL_I_GBC_S1 Homo septens cUNA cione IMAGE:2840473 3 stirtular lo contatins element MSR1 repetitive element :
	11028		37744	1.67	0.0E+00	0.0E+00 Z34897.1	NT	H.saplens mRNA for H1 histamine receptor
_	11029	24108	. 37745	276	0.0E+00	0.0E+00 F13069.1	EST_HUMAN	HSC3IC031 normalized Infant brain cDNA Homo sapiens cDNA clone c-3ic03
	11037	24116	37750	236	0.0E+00	0.0E+00 D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
	11054	24131	37767	1.71	0.0E+00	0.0E+00 AW338094.1	EST_HUMAN	xw66f01.x1 NCI_CGAP_Pan1 Homo sepiens cDNA cione IMAGE:2832985 3' similar to gb:X17115 IG MUCHAIN C REGION (HUMAN);
	11055	24132	37768	3.75		0.0E+00 AW451230.1	EST_HUMAN	UI-H-Bi3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo septens cDNA clone IMAGE:2736649 3
	11055	24132	37769	3.75		0.0E+00 AW451230.1	EST_HUMAN	UI-H-BI3-elh-e-01-0-UI.s1 NCI_CGAP_Sub5 Homo sepiens cDNA clone IMAGE:2736649 3
	11058	13443		9.52	Γ	4506632 NT	ZT	Homo sapiens ribosome protein L31 (KPL31) mKNA
_	11060	24136	37771	1.79		0.0E+00 AB014567.1	Z	Homo septens mRNA for KIAA0667 protein, partial cds
	11073	24148	37787	1.92		0.0E+00 BE298440.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cUNA clone IMAGE: 3029219 5
	11087	24161	37797	1.47		0.0E+00 AB011117.1	N.T	Homo septens mRNA for KIAA0546 protein, partial cds
	11092	24166	37803	1.39	Γ	0.0E+00 AA377505.1	EST_HUMAN	EST90347 Synovial sarcoma Homo septens cUNA 5 end similar to similar to LEKK-2, piacenta
	11106		37813	3.3	Π	0.0E+00 BE792155.1	EST_HUMAN	601582046FT NIH_MGC_/ Home septens CDNA clone IMAGE:390039 5
	70111	241/8		70.8	Г	O.VETOOIDF COTOO!	EG! TIOMSIN	

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Table 4
Single Exon Probes Expressed in Placenta

]	$\Big]$						
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Acesslon No.	Top Hit Database Source	Top Hit Descriptor
11108	24180	37814	1.45	0.0E+00	0.0E+00 BE269238.1	EST_HUMAN	601186342F1 NIH_MGC_8 Homo sepiens cDNA clone IMAGE:3544259 5'
11110	24182	37816	7.93	0.0E+00	0.0E+00 AU118396.1	EST_HUMAN	AU118386 HEMBA1 Homo capiens cDNA clone HEMBA1003486 5
1111	24183		1.81	0.0E+00	0.0E+00 AW236269.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sepiens cDNA clone IMAGE:2699977 3" similar to gb:X02162_cds1 L- LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11118		37820	6.71	0.0€+00	0.0E+00 AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testts_NHT Homo sapiens cDNA clone IMAGE:1752772.3
11116		37821	5.71	0.0€+00	0.0E+00 AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3
11117		37822	2.53	0.0E+00	0.0E+00 AW391937.1	EST_HUMAN	QV4-ST0234-121199-032-b08 ST0234 Homo sepiens cDNA
11127			11.83	0.0€+00	0.0E+00 AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11130		37827	9.67	0.0€+00	11424726		Ното sapiens insulin receptor (INSR), mRNA
11132	24204	37828	214	0.0€+00	0.0E+00 AI367350.1	EST_HUMAN	qv95c12.x1 NCI_CGAP_Ut2 Homo sepiens cDNA clone IMAGE:1988334 3' similer to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
11132	24204	37829	. 214	0.0€+00	0.0E+00 Al367350.1	EST_HUMAN	qv95c12.x1 NCI_CGAP_U2 Homo sepiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN.;
11137	24209	37835	1.63	0.0E+00	0.0E+00 BF340308.1	EST HUMAN	602037014F1 NCI_CGAP_Bin64 Hamo capiens cDNA clone IMAGE:4184979 5
11139	24211	37837	13.91	0.0E+00	0.0E+00 BE261209.1	EST_HUMAN	601146357F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3163310 5
11144	24216	37843	2.19	0.0E+00	0.0E+00 AB029040.1	NT	Homo saplens mRNA for KIAA1117 protein, partial cds
11147	24219	37846	1.61	0.0E+00	0.0E+00 AB007932.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
11151	24222	37850	3.89	0.0E+00	0.0E+00 U50326.1		Human protein kinase C substrate 80K-H (PRKCSH) gene, exxn 15-17
11155	П	37855	243	0.0E+00	0.0E+00 BE773036.1	EST HUMAN	RC1-FT0134-170700-012-107 FT0134 Homo septens cUNA
11155	24226	37856	2.43	0.05+00	0.0E+00 BE773036.1	EST_HUMAN	RC1-F10134-170700-012-107 F10134 Homo septens cONA
11177	24246	37879	51.22	0.0€+00	0.0E+00 AA740782.1	EST_HUMAN	MSR1 repetitive element;
11186	24255	37890	2.81	0.0E+00	0.0E+00 AF252303.1	NT	
11199	24268	37903	1.71	0.0E+00	0.0E+00 BE266478.1	EST_HUMAN	
11189	24268	37904	1.71	0.0분+00	0.0E+00 BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo septens cDNA clone IMAGE:3536867 5
11201	24270	37906	4.9	0.0E+00 C05089.1	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4817
11208		37914	21	0.0€+00	0.0E+00 AA746375.1	EST_HUMAN	ca56h01.r1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1309009 6
11208	24277	37915	21	0.0E+00	0.0E+00 AA746375:1	EST_HUMAN	ca56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5
11218	24287	37926	2.69	0.0€+00	0.0E+00 M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (catt/936206) Homo septens cDNA clone HFBCC28
11218	24287	37927	2.69	0.0€+00	0.0E+00 M78448.1	EST HUMAN	EST00596 Fetal brain, Stratagene (oat#936205) Homo sapiens cDNA clone HFBCC26
11221	24290	37930	1.76	0.0E+00	0.0E+00 BF353625.1	EST_HUMAN	QV2-HT0698-020800-295-d07 HT0698 Homo sepiens cDNA
11222	24291	37931	6.6	0.0E+00	0.0E+00 AL157608.1	EST_HUMAN	DKFZp781J2116_r1 761 (synonym: hamy2) Homo saptens cDNA clone DKFZp761J2116 5
11234	П	37940	1.86	0.0E+00	0.0E+00 BE562822.1	EST HUMAN	601336530F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3690390 5
11236	24305	37942	6.05	0.0E+00	0.0E+00 AU116988.1	ESI_HUMAN	AUTTORGO HEMBAT Homo sapiens CONA Cigne HEMBAT 1000424 3

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11411 11416	114	1141		11405	11404	11390	11390	11390	11369	11355	11355	11353	11345	11346	11314	11311	11311	11305	11290	11288	11288	11260	11250	Probe SEQ ID
11416 24477	Т		7		24465	24451	0 24451	24451	9 24430			П	٦	ヿ	4 24378	1 24375						24329	0 24319	SEQ E
38142	I				38130	38114	. 38113	38112	38087	38074			1	_	38023	38020		38011		37995		37969	37959	ORF SEQ
3.93		3.93	11.86	24.41	8.8	1.37	1.37	1.37	1.89	2.24	2.24	3.23	1.45	1.46	2.49	1.83	1.83	3.02	1.51	24	24	2.97	1.75	Expression Signal
	1				0.0€+00								T	٦				٦						Most Similar (Top) Hit BLAST E Value
0.0E+00 AB018260.1	AD CASO A	0.0E+00 AB018260.1	0.0E+00 AW2077,34.1	0.0E+00 BF206561.1	4758827	0.0E+00 AI073917.1	0.0E+00 AI073917.1	0.0E+00 AI073917.1	0.0E+00 AL042278.1	0.0E+00 AI458545.1	0.0E+00 AI459545.1	0.0E+00 BE897853.1	0.0E+00 AW387766.1	0.0E+00 AW387766.1	0.0E+00 BE018293.1	0.0E+00 AW500307.1	0.0E+00 AW 500307.1	0.0E+00 BE896423.1	0.0E+00 AV701152.1	0.0E+00 BE182350.1	0.0E+00 BE182360.1	0.0E+00 BF366553.1	0.0E+00 AV693656.1	Top Hit Acession No.
곡	1	Z	EST_HUMAN	EST_HUMAN	7 NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Top Hit Database Source
Homo sapiens mRNA for KIAA0717 protein, partial eds	Home serious mBNA for KIAAAA77 protein postial cide	Homo capiens mRNA for KIAA0717 protein, partial cds	UI-H-BI2-age-h-01-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'	801870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5	Homo seplens neurexin III (NRXN3) mRNA	ou81d04 x1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;	ou81d04 x1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:1832285 3' similer to SW:LRP1_HUMAN G07854 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;	ou61d04x1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'	ao86g11x1 Schiller meningloma Homo saplens cDNA cione IMAGE:19528043'	ao86g11.x1 Schiller meninglama Homo sapiens cDNA clone IMAGE:1952804 3'	601440446F1 NIH_MGC_72 Hamo septens cDNA clone IMAGE:3925403 5'	MR4-ST0118-041099-010-A12 ST0118 Homo capiens cDNA	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA	bb78c04.y1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);	UI-HF-BNO-ekg-d-02-0-UI.r1 NIH_MGC_50 Homo septens cDNA clone IMAGE:3077019 5'	UI-HF-BN0-akg-d-02-0-UI-r/ NIH_MGC_50 Homo sepiens cDNA clone IMAGE:3077019 5	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5"	AV701152 ADA Homo saplens cDNA clone ADAAAD00 5	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA	PMC-HT0645-060500-002-E05 HT0645 Homo sapions cDNA	IL3-NT0104-200500-143-A07 NT0104 Homo saplens cDNA	AV693656 GKC Homo sapiens cDNA clone GKCCNC03 5	Top Hit Descriptor

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	11571	11567	11662	11560	11553	11636	11535	11531	11531	11516	11511	11503	11603	11501	11501	11486	11490	11490	11476	11475	11462	11452	11448	11448	11445	11438	11429	11418	Probe SEQ ID S
200	24626	24622	24617	24615	24608	24691	24591	24687	24687	24573	24569	24561	24661	24559	24559	24554	24549	24649	24534	24534	24512	24512	20710	24609	24506	24499	24490	24479	Exan SEQ ID NO:
38307	38305		38297	38294	38287	38267	38266	38263	38262		38246	38239	38238	38235	38234	38229	38224	38223	38205	38204	38179	38178	34189	38176	38172	38166	38165	38145	ORF SEQ ID NO:
3.37	1.75	42.5	9.53	2.06	6.13	3.09	3,09	1.81	1.81	3.87	1.61	4.06	4.08	2.07	2.07	4.65	4.84	4.84	1.66	1.66	4.61	4.61	1,94	1,98	1.73	1.68	2.37	2.63	Expression Signel
0.00+00	0.0E+00	. 0.0E+00	0.0E+00	0.0€+00	0.0E+00	0.0€+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0€+00	0.0E+00	0.0E+00	0.0€+00	0.0€+00	0.0E+00	0.0€+00	0.0€+00	0.0≝+00	0.0E+00	0.0€+00	0.0E+00	0.0E+00 L32832.1	0.0E+00	0.0€+00	0.0€+00	0.0€+00	0.0E+00	Moet Similar (Top) Hit BLAST E Value
0.0E+00 BF306998.1	0.0E+00 A1660968.1	0.0E+00 M55083.1	0.0E+00 AW328173.1	0.0E+00 BF576267.1	4503544 NT	11430868 NT	11430868 NT	0.0E+00 AB037737.1	0.0E+00 AB037737.1	0.0E+00 BF240536.1	0.0E+00 D87682.1	0.0E+00 BE876401.1	0.0E+00 BE876401.1	0.0E+00 BF576138.1	0.0E+00 BF576138.1	0.0E+00 AU135170.1	0.0E+00 BF507876.1	0.0E+00 BF507876.1	0.0E+00 AW673469.1	0.0E+00 AW673469.1	0.0E+00 BE148076.1	0.0E+00 BE148076.1	L32832.1	0.0E+00 BF093687.1	11024711 NT	0.0E+00 A1075915.1	11526409	0.0E+00 BE206346.1	Top Hit Accession
EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	NT	8 NT	NT	NT	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	TNI	EST_HUMAN		EST_HUMAN	Top Hit Database Source
601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5		Human gamma actin-like pseudogene, complete cds	dr04g05.x1 NIH_MGC_3 Horro septiens cDNA clone IMAGE:2847177 5'	602134132F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4289502 5'	Homo sapiens eukaryotic translation initiation factor 6A (EIF5A) mRNA	Homo sapiens retinoblastome-like 2 (p130) (RBL2), mRNA	Homo sapiens retinoblestoma-like 2 (p130) (RBL2), mRNA	Homo sapiens mRNA for KIAA1316 protein, partial cds	Homo sapiens mRNA for KIAA1316 protein, partial cds	601875630F1 NIH_MGC_55 Homo sepiens cDNA clone IMAGE:4099710 5	Human mRNA for KIAA0241 gene, partial cds	601486828F1 NIH_MGC_69 Homo capiene cDNA clone IMAGE:3889207 6'	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5	602132459F1 NIH_MGC_81 Homo sepiens cDNA done IMAGE:4271630 5'	602132459F1 NIH_MGC_81 Homo seplens cDNA done IMAGE:4271630 5'	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5	Ui-H-Bi4-aok-b-10-0-Ui.s1 NCI_CGAP_Sub8 Homo sepiens cDNA clone IMAGE:3085028 3'	UI-H-BI4-ack-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sepiens cDNA clone IMAGE:3085026 3*	be54d08.y3 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2900367 5' similar to TR:060275 O60275 KIAA0522 PROTEIN ;	be54d08.y3 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2900367 5' similar to TR:060275 060275 KIAA0522 PROTEIN :	RC3-HT0230-040500-110-h04 HT0230 Homo sepiens cDNA	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds	QV0-UN0091-120900-385-b12 UM0091 Homo saplens cDNA	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	ov46g07.x1 Soares_testis_NHT Homo sepiens cDNA clore IMAGE:1640412 3' similar to TR:Q14507 Q14507 EPIDIDYMIS-SPECIFIC GENE PRODUCT, ALPHA.;	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA	be04d07.y1 NIH_MGC_7 Homo septens cDNA clone IMAGE::2823373 5' similer to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN :	Top Hit Descriptor

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601501090F1 NIH_MGC_70 Homo sepiens cDNA clone IMAGE:3902826 5	EST_HUMAN	0.0E+00 BE910546.1	0.0E+00				11713
nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA Q13686 ALKB HOMOLOG PROTEIN.;	EST HUMAN	0.0E+00 AA7609:13.1	0.0€+00	4.47		24748	11708
nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3: similar to IN:013886 Q13686 ALKB HOMOLOG PROTEIN.;	EST_HUMAN	0.0E+00 AA760913.1	0.0E+00	4.47	38440	24748	11708
wn83g03.x1 NCI_CGAP_Uff Home septens cDNA clone IMAGE::2452488 S' similar to go::S3/431 LAMININ RECEPTOR (HUMAN);	EST_HUMAN	0.0E+00 Al923118.1	0.0E+00	10.19	38395	24703	11706
DKFZp434G178_r1 434 (synonym: htes3) Homo septens cDNA cione UKFZp434G176 5	EST_HUMAN	0.0E+00 AL046540.1	0.0E+00	7.19	38385	24693	11696
DKFZp434G178_r1 434 (synonym: htes3) Homo sepiens cDNA clone DKFZp434G178 5	EST HUMAN	0.0E+00 AL046540.1	0.0E+00	7.19	38384	24693	11686
UI-H-BW1-amv-a-05-0-UI.s1 NCI_CGAP_Sub7 Homo	EST_HUMAN	0.0E+00 BF513960.1	0.0 €+00	1.39		П	11682
IL5-HT0731-020500-077-f05 HT0731 Homo sapiens of	EST_HUMAN	0.0E+00 BE185656.1	0.0€+00	. 3.81	38371	╗	11681
601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3	EST_HUMAN	0.0E+00 BE965509.2	0.0€+00	1.79		П	11680
601659038R1 NIH_MGC_70 Homo septens cDNA clone IMAGE:3895916 3	EST_HUMAN	0.0E+00 BE985909.2	0.0€+00	1.78		7	11680
601113903F1 NIH_MGC_16 Hamo sepiens cDNA clone IMAGE:3354600 5	EST_HUMAN	0.0E+00 BE254058.1	0.0E+00	1.35		7	11677
Homo saplens neurexin III (NRXN3) mRNA	7 NT	4758827 NT	0.0€+00	1.93		$\neg$	11671
UI-H-BWO-aij-d-07-0-UI.s1 NCI_CGAP_Sub6 Homo saplens cDNA clone IMAGE:2729509 3	EST_HUMAN	0.0E+00 AW 2927,76.1	0.0E+00	1.78		П	11664
dro2b08x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5	EST_HUMAN	0.0E+00 AW327895.1	0.0€+00	7.51		٦	11845
wp06g08.x1 NCL_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2464094 3	EST_HUMAN	0.0E+00 A1834954.1	0.0E+00	256	31562	Т	126
n/42c08.91 NCI_CGAP_Pr4 Homo sapiens cDNA cicres IMAGE::1043342 similar to gb::M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);	EST_HUMAN	0.0E+00 AA558707.1	0.0€+00	3.01		24723	11843
QV0-CT0225-101299-071-f06 CT0225 Homo septens	EST_HUMAN	0.0E+00 AW753028.1	0.0€+00	3.69	38410		11638
ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5 cimilar to IR:0/6022 0/6022 E18-55KDA-ASSOCIATED PROTEIN.;	EST_HUMAN	0.0E+00 BE206846.1	0.0E+00	4.53	38408	24716	11636
55KDA-ASSOCIATED PROTEIN.:	EST_HUMAN	0.0E+00 BE206846.1	0.0E+00	4.53	38407	24716	11636
601861947F1 NIH_MGC_53 Homo sepiens cDNA clone IMAGE:4081715 5	EST_HUMAN	0.0E+00 BF207682.1	0.0E+00	2.07		╗	11823
Homo sapiens golgin-like protein (GLP), mRNA	8 NT	8923698 NT	0.0E+00	234	38361	7	11621
Homo saplens fyn-related kinase (FRK) mRNA	8 NT	4503786 NT	0.0E+00	237		П	11607
601439605F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3924577 5	EST_HUMAN	0.0E+00 BE897051.1	0.0€+00	4.33		П	11606
(Human beta-prime-adaptin (BAM22) gene, exon 16	NT	0.0E+00 U36264.1	0.0Ё+00	232	38339	24654	11601
Human beta-prime-adaptin (BAM22) gene, exon 16	TN	U36264.1	0.0E+00 U36264.1	232	38338	╗	11601
QV2-NN0054-230800-333-e04 NN0054 Homo sapiens	EST_HUMAN	0.0E+00 BF362452.1	0.0≅+00	47.2	38315	24636	11681
601889823F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:4123948 5	EST_HUMAN	0.0E+00 BF306986.1	0.0E+00	3.37	38308	24629	11574
	Top Hit Database Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal	ORF SEQ ID NO:	Exan SEQ ID NO:	Probe SEQ ID NO:
	1						

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			-			
Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hil Acession No.	Top Hit Database Source	Top Hit Descriptor
24898	38601	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5
24903	38606	4.87	0.0E+00	AW 500056.1	EST_HUMAN	
24918	38621	2.05	0.0€+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5
	38622	65.18	0.0€+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5
•	38623	1.6	0.0€+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
	38629	1.38	0.0€+00	4758827	T	Homo sapiens neurexin III (NRXN3) mRNA
	38630	1.38	0.0€+00	4758827	NT	Homo saplens neuredn III (NRXN3) mRNA
24932	38635	1.68	0.0€+00	AF053543.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
	38642	7.29	0.0E+00	BE409993.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628544.5
24940	38643	2.22	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-102 HT0241 Home sapiens cDNA
	38644	2.89	0.01100	AF223391.1	NT	spiloed
						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
Г	38645	2.89	0.0E+00	AF223391.1	NI	
18785	31831	1.48	0.0€+00	D26535.1	NT .	Human gene for dinydrolipoamide succinylitansferase, complete cgs (exon 1-10)
18785	31832	1.48	0.0€+00	D26535.1	NT	Human gene for dihydrolipoamide succinylitransferase, complete cas (exon 1-10)
24943	38647	11.38	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cLNA clone IMAGE:4296725 5
24943	38648	11.38	0.0€+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cUNA clone IMAGE:4296725 5
24949	38655	1.79	0.05+00	AU132940.1	EST_HUMAN	AU132940 NT 2RP4 Homo sepiens cDNA clone N I 2RP4000929 5
	38657	4.99	0.0≅+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo saplens CUNA Clone IMAGE:3958955 5
	38671	1.58	0.0≅+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MIGC_19 Homo sapiens cUNA clone IMAGE:4127055
24968	38672	1.58	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo saplens cUNA cicre IMAGE:4127059 5
24971	38675	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
	38676	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulh constant region complex (germline)
24883		1.98	0.0€+00	BE908402.1	EST HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA cicre IMAGE:3900398 5
24997	38700	1.46	0.0€+00	9635487		Human endogenous retrovirus, complete genome
		8.57	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5
	38713	2.37	0.0E+00	BE698861.1	EST HUMAN	RC4-NN0026-120600-016-b07 NN0025 Homo sapiens cUNA
25012	38714	2.37	0.0E+00	BE698861.1	EST HUMAN	RC4-NN0026-120600-016-607 NN0026 Homo sepiems cDNA
2 25015	38717	60.96	0.0E+00	BE297,175.1	EST_HUMAN	
3 25027	38733	1.42	0.0E+00	BE744311.1	EST_HUMAN	-
3 25027	38734	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cUNA clone IMAGE:383/2225
25035	38741	2.02	0.0€+00	BE257612.1		601113009F1 NIH MGC 16 Homo sapiens cUNA clone IMAGE:3353378 5
Г	Γ		0.0⊞+00	BE257612.1		6011130U9F1 NIH_MGC_16 Homo sapiens CUNA Gone IMAGE:3535376 C
Probe SEQ ID NO: NO: NO: 11911 11937 11937 11937 11937 11937 11937 11937 11937 11937 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 11938 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NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO: Sign ID NO:	Exon SEQ ID NO: Signal P. 24898 38601 26.74 24903 38606 4.87 24927 38623 1.6 24927 38623 1.8 24944 38644 2.89 38644 2.89 38644 2.89 38644 2.89 38644 2.89 38645 1.38 38644 2.89 38645 1.38 38644 2.89 38645 1.48 38645 1.38 38646 1.38 38646 1.38 38646 1.38 38646 1.38 38647 1.38 38646 1.38 38647 11.38 38646 11.38 38647 11.38 38646 11.38 38647 11.38 38647 11.38 38647 11.38 38647 11.38 38647 38647 11.38 38648 38647 11.38 38648 38647 11.38 38648 38647 38648 38647 38648 38648 38647 38648 38648 38647 38648 38648 38677 38677 38677 38677 38677 38677 38677 38677 38677 38677 38677 38677 38774 2.37 38774 2.37 38774 2.37 38774 2.37 38774 2.37 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 38774 2.30 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ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF SEQ ID   ORF

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Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ	Expiression ·Signal	Most Similar (Top) Hit BLAST E Value	Top Hil Acession No.	Top Hit Database Source	Top Hii Descriptor
12084	25064	38770	2.85	0.0E+00	0.0E+00 BE545535.1	EST_HUMAN	601070391F1 NIH_MGC_12 Homo sapiens cDNA cicne IMAGE:3456407 5
12087	25087	38773	1.34	0.0€+00	0.0E+00 AA398001.1	EST HUMAN	293e01.rl Scares_testis_NHT Homo sepiens cDNA clone IMAGE:729912 5' similar to SW PMT1_SCHPO P40999 DNA METHYLTRANSFERASE PMT1 ;
12088	25068	38774	1.55	0.0E+00	0.0E+00 AU117974.1	EST_HUMAN	AU 117874 HEMBA1 Homo sepiens cDNA clone HEMBA1002612 5'
12088	П	38775	1.55	0.0E+00	0.0E+00 AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5
12091		38778	1.72	0.0E+00	0.0E+00 BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5
12108		38792	2.15	0.0+30.0	0.0E+00 AW 269390.1	EST_HUMAN	xx46h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816213 3' similar fo
12118	П	38803	1.99	0.0E+00	0.0E+00 AU132584.1	EST_HUMAN	AU132394 NT2RP3 Homo sapiens cDNA clone NT2RP3004339 5'
12131		38815	1.35	0.0€+00	0.0E+00 BE292840.1	EST_HUMAN	601105652F1 NIH_MGC_15 Homo saplens cDNA clone IMAGE:2988325 5
12147		31540	9.34	0.0€+00	0.0E+00 BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo saplens cDNA clcne IMAGE:3503020 5
12160			3.02	0.0E+00	0.0E+00 AL163246.2	NT	Homo septens chromosome 21 segment HS21C046
12162	26013		5.49	0.0E+00	0.0E+00 A1190903.1	EST_HUMAN	qe17b12.x1 Scares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231.3
12172	25134		3.73	0.0E+00	0.0E+00 AB011999.1	ZT	Homo capiens gene for AF-6, complete cds
12192	25149		6.87	0.0E+00	0.0E+00 AL163246.2	NT	Homo saplens chromosome 21 segment HS21C046
12194	25161		1.35	0.0E+00	0.0E+00 AB016195.1	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
12201	25156		3.2	0.0€+00	11417862 NT	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12220	25170		4.05	0.0€+00	5802973 NT	NT	Home capiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochandrial protein, mRNA
205	25072	292.00	• 47	00120	0.05100 05240788 1	Z	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) comes, complete cds
12267	Т		3.47	0.0€+00	0.0E+00 ALD41931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434K0819 5'
12295	П		3.39	0.0€+00	11418318 NT	ı	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12304	25222		4.77	0.0€+00	0.0E+00 AL046544.1	EST_HUMAN	DKFZp434G218_r1 434 (syncnym: https3) Homo sapiens cDNA clone DKFZp434G218 5
12317			2.92	0.0€+00	0.0E+00 AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sepiens cDNA
12356	26172		1.88	0.0E+00	0.0E+00 N54484.1	EST_HUMAN	yv40e08.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN;
12371			4.08		0.0E+00 AF108656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12374		27106	5.36	0.0€+00	4507500 NT	NT	
12374	П	27107	5.36	0.0E+00	4607600 NT	N	Homo saplens T-ceil lymphoma invasion and metastasis 1 (TIAM1) mKNA
12383			3.07	0.0E+00	10092587 NT	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12415			4 89		0.0E+00 AF003528 1	NT	Homo sapiens X-linked anhidrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO: 12450 12510 12542 12573 12618	<u>ω</u> _	ORF SEQ ID NO: 31837 31765	Expression Signal 1.85	Most Similar (Top) Hit BLAST E Value 0.0E+00 0.0E+00 0.0E+00 0.0E+00	t Similar op) Hit Top Hit Accession AST E No. Value 0.0E+00	Top Hit Database Source NT NT NT NT HUMAN EST_HUMAN	Top Hit Descriptor  Homo sapiens low density ipoprotein-related protein 2 (LRP2), mRNA hg31e06x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element;contains element MER22 repetitive element; Human gamma-glutamyl transpeptidese mRNA, complete ods Homo septens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cids Human endogenous retrovirus, complete genome AV720678 GLC Homo sapiens cDNA clone GLCEPG09 5'
12618			4.61 1.19	0.0E+00	0.0E+00 AV720878.1	NT EST_HUMAN	Human endogenous retro 1V720678 GLC Homo s
12680	П		3.51	0.0E+00	0.0E+00 AI204914.1	EST_HUMAN	an05h04x1 Stratagene schizo brain S11 Homo saplens
12694 12702	25462 2 25008		1.33 2.29	0.0E+00	0.0E+00 Al904646.1 0.0E+00 BE439792.1	EST_HUMAN	QV-B1065-020399-103 B1065 Homo septens cDNA HTM1-654F HTM1 Homo septens cDNA
12714	П		1.39	0.0€+00	12457	NT	Homo sepiens calcineurin binding protein 1 (KIAA0330)
12714	9 25490	32027	1.39	0.0E+00	0.0E+00 AF036365.1	ZI Z	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12751			3.26	0.0E+00	0.0E+00 H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo septens cDNA clone IMAGE:182248 5' similar to gb:M84089 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12761	14869	27961	3.26	0.0E+00	0.0E+00 H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sepiens cDNA clone IMAGE: 182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12765	П		1.6		0.0E+00 AB011299.1	NT	Homo septens gene for AF-8, complete cds
12766 12771	1 25509	31997	33.13 5.44	T	0.0E+00 D50669.1 NE	Z	Human gamma-sycpiasmic acun (AC i Gr e) pseudogei Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G
12771		31998	5.44	0.0E+00	11418189 NT	Z	Home septems thyroid autoantigen 70kD (Ku antigen) (322P1), mRNA Home septems DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,
12798	38 15294	28420	1.7	П	0.0E+00 4758489	NT	Homo saplens GTP binding protein 1 (GTPBP1) mRNA
12837	П		2.11	Π	0.0E+00 AW664999.1	EST HUMAN	hB6e06.x1 Soares_NFL_T
12847	2 25563 2 14409	31988	1.74	0.0E+00	8922593 NT	NT	Homo saplens hypothetical protein FLJ10697 (FLJ10697), mRNA
12927	П	П	3.11	П	4885312 NT	IN	Homo sapiens G protein-coupled receptor 24 (GPR24),
12935 12938	35 18494 38 25617	31532	2.3 1.88	П	0.0E+00 AB029900.1 NT	N	Homo capiens tow density lipoprotein-retated protein 2 (LNF2), move Homo capiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12981	П	31983	1.82	Τ	9558724 NT	13	Homo sepiens chromosome 21 segment HS21C046
13017	17 13828	26851	2.46		0.0E+00 6806918 NT	3	Homo sepiens low density lipoprotein-related protein 2 (I
13113	13 25728	31943	1.17	0.05+00	7747/86ZINI	N	Tallo sapielis carciledili Jumii g proteiri (Nicosoco)

Page 550 of 550
Table 4
Single Exon Probes Expressed in Placenta

13215	13208	13209	13190	13151	13140		13119	13116	Probe SEQ ID NO:	
14345	16135	16135	25774	28207	25740		25731	25728	Exon SEQ ID NO:	
27402	29152	29151							ORF SEQ ID NO:	
1.29	1.37	1.37	1.61	1.16	5.96		3.11	1.4	Expression Signal	
0.0€+00	0.0E+00	0.0E+00	0.0€+00				0.0E+00		Most Similar (Top) Hit BLAST E Value	
9966844 NT	6806918 NT	6806918 NT	0.0E+00 X57147:1	0.0E+00 AW505,176.1	0.0E+00 AB026898.1		7657020 NT	0.0E+00 AB002059.1	Top Hit Acession	1
NT	NT	ZT	NT	EST_HUMAN	NT		NT	ZT	Top Hit Database Source	
Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saptens low density lipoprotein-related protein 2 (LRP2), mRNA	Human endogenous retrovirus pHE.1 (ERV9)	UI-HF-BNO-aly-g-08-0-UI./1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081399 5	complete cds)	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	Homo sepiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens DNA for Human P2XM, complete cds	Top Hit Descriptor	

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CLAIMS

complementary sequence, or a portion of such a sequence. nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a nucleic probes, said probes comprising any one of the from human placenta comprising a plurality single exon probes for measuring gene expression in a sample derived 1. A spatially-addressable set of single exon nucleic acid

of probes is separately and addressably amplifiable. probes as claimed in claim I wherein each of said plurality 2. A spatially-addressable set of single exon nucleic acid

of probes is separately and addressably isolatable from probes as claimed in claim 1 wherein each of said plurality 3. A spatially-addressable set of single exon nucleic acid

probes comprise any one of the nucleotide sequences set out probes as claimed in any of claims 1 to 3 wherein said 4. A spatially-addressable set of single exon nucleic acid

in SEQ 1D NOS.: 13,233 - 26,232.

said plurality.

5. A spatially-addressable set of single exon nucleic acid

common primer. said plurality of probes is amplifiable using at least one probes as claimed in any of claims 1 to 4, wherein each of

. aedoxq comprises between 50 - 20,000 single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set 6. A spatially-addressable set of single exon nucleic acid

35 probes as claimed in any of claims 1 to 6, wherein the 7. A spatially-addressable set of single exon nucleic acid

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average length of the single exon nucleic acid probes is between 200 and 500 bp.

- 8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least probes asid single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
- 9. A spatially-addresable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 10. A spatially-addressable set of single exon nucleic acid frobes as claimed in any of claims 1 9 characterised in that said set of probes is addressably disposed upon a substrate.
- 11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims
- 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta

  10 comprising a nucleotide sequence as set out in any of SEQ fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the stringency to a nucleic acid molecule expressed in the

32

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ID NOs.: 13,233 - 26,232 or a complementary sequence or a comprising a nucleotide sequence as set out in any of SEQ 14. A single exon nucleic acid probe as claimed in claim 13

fragment thereof.

- of SEQ ID Nos.: 26,233 38,837, or a complementary a peptide comprising a peptide sequence as set out in any which is a nucleic acid molecule having a sequence encoding gene expression in a sample derived from human placenta 15. A single exon nucleic acid probe for measuring human
- in the human placenta. hybridizes at high stringency to a nucleic acid expressed sequence or a fragment thereof wherein said probe
- said SEQ ID NO. probe comprises between 15 and 25 contiguous nucleotides of of claims 13 to 15 wherein said single exon nucleic acid 16. A single exon nucleic acid probe as claimed in any one
- in length. of claims 13 to 15, wherein said probe is between 3 - 25 kb 17. A single exon nucleic acid probe as claimed in any one
- of claims 13 17, wherein said probe is DNA, RNA or PNA. 18. A single exon nucleic acid probe as claimed in any one
- labeled. of claims 13 - 18, wherein said probe is detectably 19. A single exon nucleic acid probe as claimed in any one

30

- pacteriophage vector sequence. of claims 13 - 19, wherein said probe lacks prokaryotic and 20. A single exon nucleic acid probe as claimed in any one
- 21. A single exon nucleic acid probe as claimed in any one

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of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

derived from human placenta, comprising: 22. A method of measuring gene expression in a sample

from mRNA of human placents; and then said first collection of nucleic acids derived collection of detectably labeled nucleic acids, contacting the microarray of claim 12, with a first

measuring the label detectably bound to each probe of

said microarray.

23. A method of identifying exons in a eukaryotic genome,

comprising:

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detecting specific hybridization of detectably labeled genomic sequence of said eukaryote; and then algorithmically predicting at least one exon from

nucleic acids to a single exon probe,

is a single exon probe having a fragment identical in from mRNA from the placenta of said eukaryote, said probe wherein said detectably labeled nucleic acids are derived

according to claim 12, and said fragment is selectively predicted exon, said probe is included within a microarray sedneuce to, or complementary in sequence to, said

hybridizable at high stringency.

24. A method of assigning exons to a single gene,

identifying a plurality of exons from genomic comprising:

sequence according to the method of claim 23; and

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hybridization to single exon microarrays having a plurality of tissues and/or cell types using measuring the expression of each of said exons in a

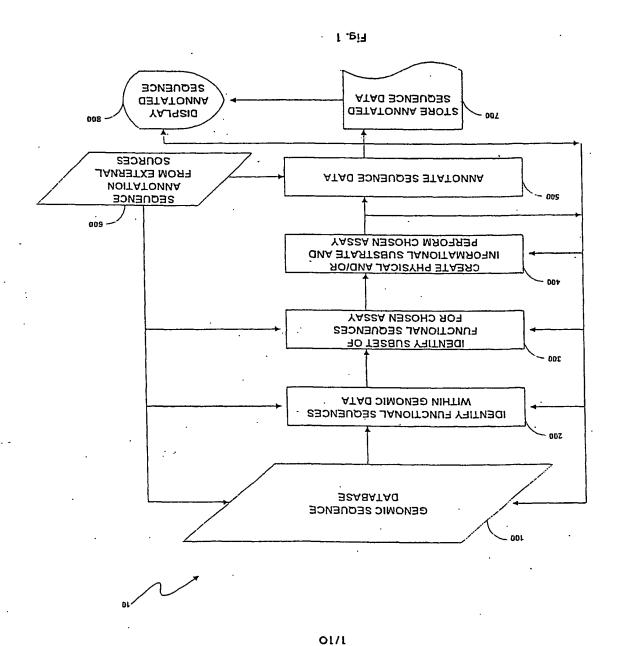
probe with said exon,

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wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that

- NOs: 1 26,232 which encodes a peptide.
- SEQ ID Nos: 1 26,232.
- SEQ ID Nos: 26,233 38,837.

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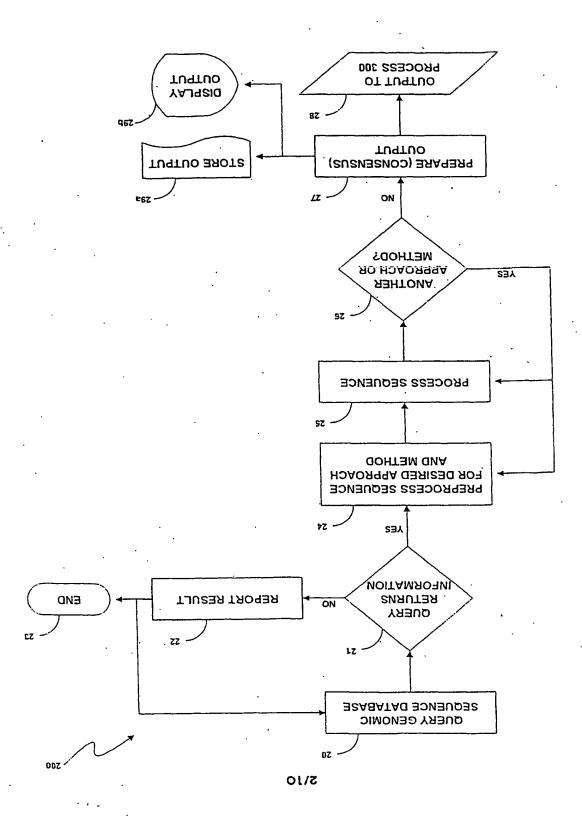
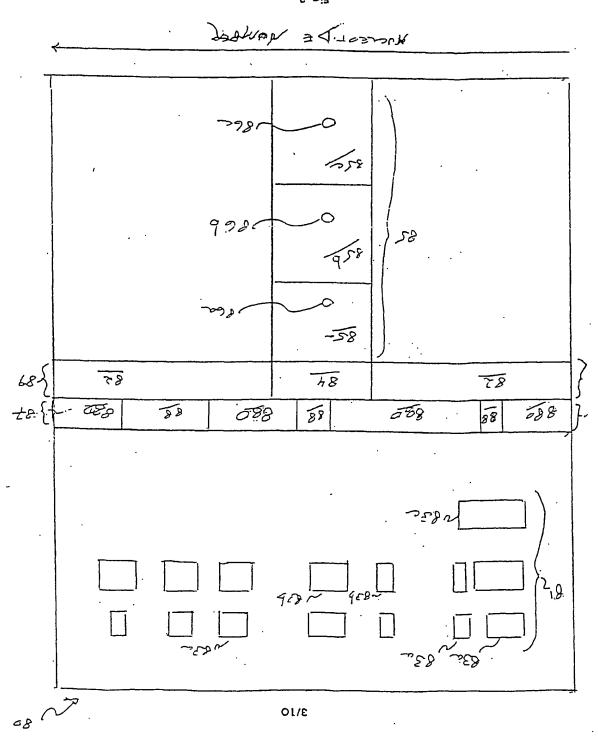
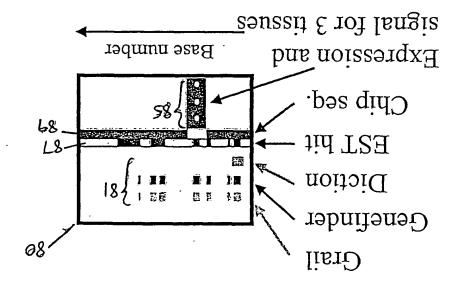


Fig. 2



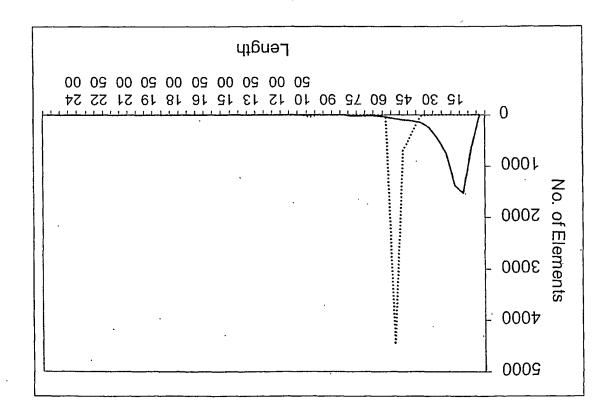
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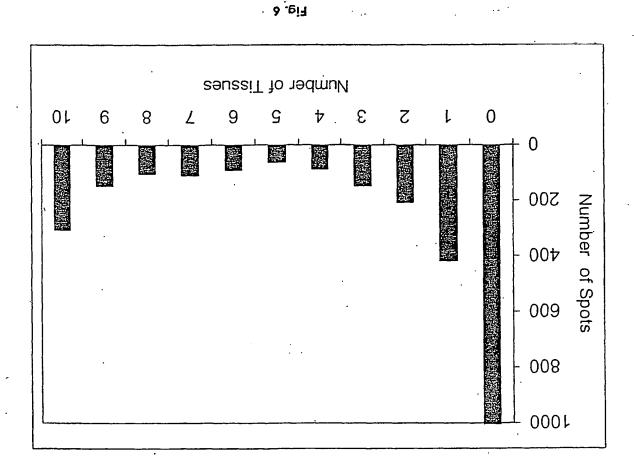
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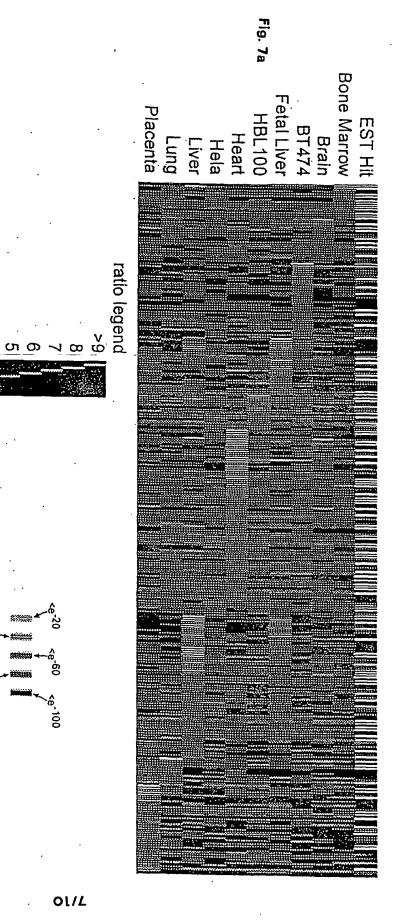
Fig. 5



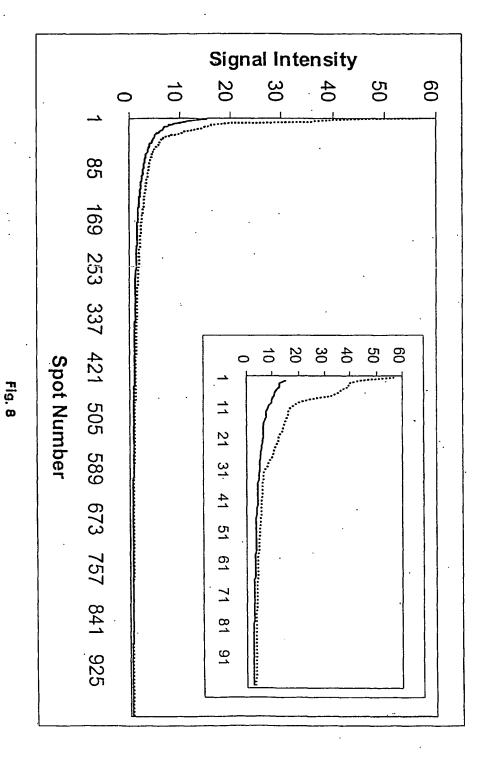
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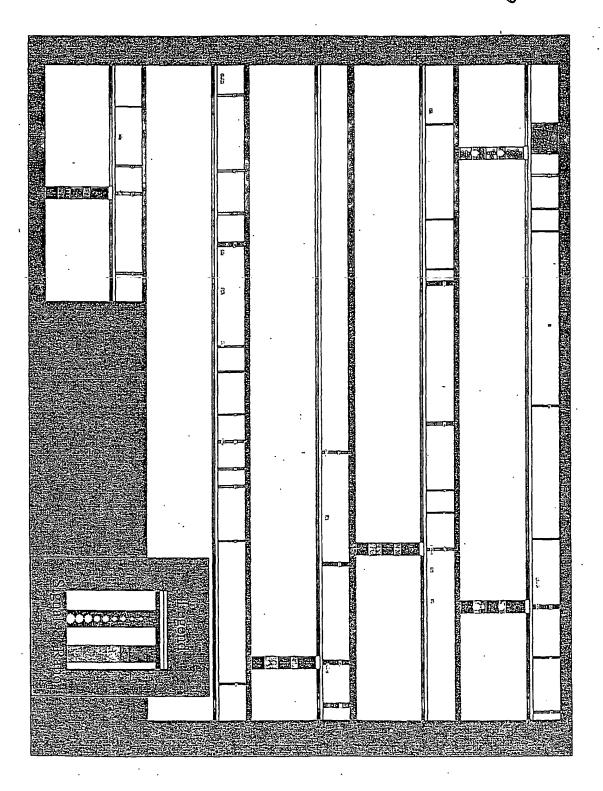




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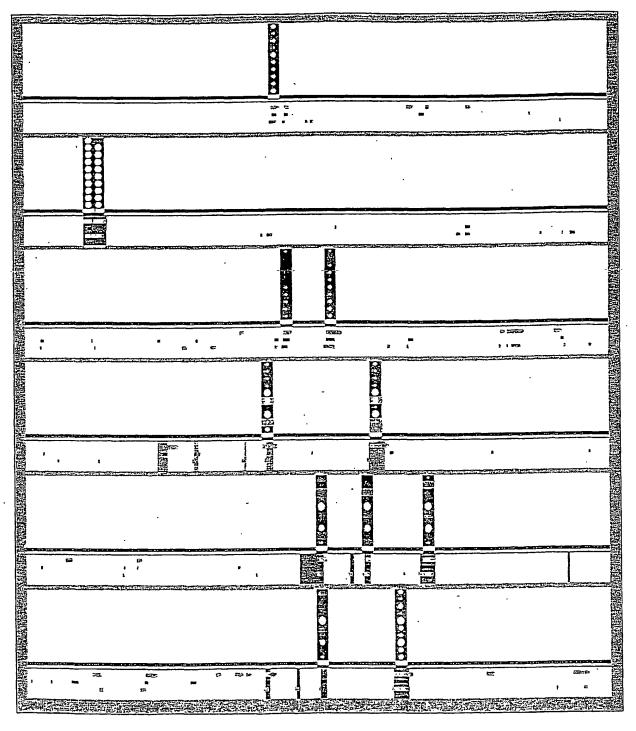
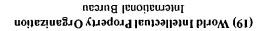


Fig. 10

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> (21) International Application Number: PCT/US01/00663

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English (26) Publication Language:

4 October 2000 (04.10.2000) 0.8324200 (0002.60.72) 0005 radmatqa2 72 625,352/03 SN (0002.90.12) 0005 redmetqs 12 788,452/08 SO (0002.80.E0) 0002 tenguA & 996,259/60  $S\Omega$ 0002.30.05) 0002 anut 05 804,803/90 26 May 2000 (26.05.2000)  $S\Omega$ 954,702/03 4 February 2000 (04.02.2000) 215,081/03 (30) Priority Data:

CA 94086 (US). ICA, INC. [--/US]; 928 East Arques Avenue, Sunnyvale, (71) Applicant (for all designated States except US): AEOM-

(72) Inventors; and

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PCT/US 01/00663

### INTERNATIONAL SEARCH REPORT

Fex (+31-70) 340-3016 Luzzatto, E European Patent Office, P.B. 5616 Patentiaan 2 NL – 2260 HV Rijswijk Tet (+31-70) 340-2046, Tx. 31 651 epo nl, A2I ent to esembs gnillem bas emsM racilto beshortuA 2002 Jaugua S 03 00 C 0 Date of mailing of the international search report Date of the actual completion of the international search P. document published prior to the international filing date but .g. qocament member of the same patent lamity O document referring to an oral disclosure, use, exhibition or council be considered to invalve an inventive step when the citation or other epecies reason (sa abecilied)

which is cited to establish the publication date of enother which may throw doubts on brooking distincts) or "X" document of particular relevance; the defined invention cannot be considered novel or cannot be considered to involve an inventive step when the document is latten alone eteb gate E' earlier document but published on or after the international Considered to be of particular relevance. The pier document published after the international filing date or phority date and not in conflict with the application but cited to understand the principle or theory understand the principle. Special categories of cited documents: X Patent family members are listed in annex. Further documents are listed in the continuation of box C. abstract; figures 1,2 155N: 0027-8424 4209-4213, XP002086258 vol. 91, 1 May 1994 (1994-05-01), pages SCIENCE: MYSHINGLON' NS' SCIENCES OF USA, NATIONAL ACADEMY OF PROCEEDINGS OF THE NATIONAL ACADEMY OF spliced form of HLA-6 mRNA" KIRSZENBAUM ET AL: "An alternatively X 1-57 Helevani to dam No. Custion of document, with indication, where appropriate, or the relevant passages C. DOCUMENTS CONSIDERED TO BE RELEVANT BIO212, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH Electronne data base consulted during the international search (name of data base and, where practical, search terms used) Documentation searched other than minimum documentation to the extent that such documents are included, in the fields searched B. FIELDS SEARCHED According to International Patent Classification (IPC) or to both national classification and IPC A CLASSIFICATION OF SUBJECT MATTER 19/00 COJKIT/47

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X No protest accompanied the payment of additional search fees.
Remark on Protest  The additional search fees were accompanied by the applicant's protest.
4. Ho required additional search fees were timely paid by the applicant. Consequently, this intermational Search Report is restricted to the invention first mentioned in the dalms; it is covered by claims Nos.:
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I-27 (partially)
3. X covers only those claims for which lees were paid, specifically claims Nos.:
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This international Searching Authority found multiple inventions in this international application, as follows:
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
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255 LOWING MINIORINA PROPERTY AND ACCOUNT WITH THE
an extent that no meaningful intermational Search can be carried out, specifically:
S. Claims Nos:  Decause they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful international Search can be carried out, specifically:  See FURTHER INFORMATION sheet PCT/ISA/210
an extent that no meaningful international Search can be carried out, specifically:  —— because they relate to parts of the international Search can be carried out, specifically:
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This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID I (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13233(see p. 91 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons gene expression (claim 22), a method for dentifying exons (claim 24) comprising using the said arrays, the peptide (claim 24) comprising using the said arrays, the peptide encoded by SEQ ID 1 or 13233 (claims 26-27) having the encoded by SEQ ID 26233 (claims 26-27) having the sequence SEQ ID 26233 (see ISA form 206), which is the encoded by SEQ ID 13233 (see p. 69 of the description).

2. Claims: 1-27(partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13234(see p. 91 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sor identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 13234 having the sequence SEQ ID 26234, which is the translation from SEQ ID 13234 (see p. 69 of the description).

...Inventions 3-13232: similar subject-matter as above related to SEQ IDs 3-13232.

Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCI are made for the subject-matter for which a search has ben performed and which has been identified as inventions 1-2 in PCI form 206.

1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description fragments).

2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID I or 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and concisesness (Art. 6 PCI) to such an extent as to render a meaningful and concisesness (Art. 6 PCI) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID I and 2 as such.

3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID I and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. 26233 and 26234 (Art. 6 PCI).

4) Claims 15-21 relate to nucleic probes, solely defined in that they code for polypeptides having the sequence SEQ ID 26233 or 26234. However, a peptide is potentially coded by an extremely large number of nucleic an extent as to render a meaningful search over their whole scope an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID i, 2, 13233 and 13234.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCI). The applicant is advised that the EPO policy when acting as an international preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is preliminary examination on matter which has not been searched. This is receipt of the search report or during any Chapter II procedure.

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## TROGER HORAL SEARCH REPORT

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